There are more than 10,000 predictions to display.

To enable speedy output, the format was set to 'text' only.
In order to see the results in an html table (which allows for sorting), limit the number of predictions generated on the previous page.

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Predictions
Allele  Position        PepLength       Sequence        Proteasome      TAP     MHC     Processing      Total
HLA B*1517      1:174-182       9       AAVIGTAQY       1.097758        1.393069        -0.565859       2.490827        1.924968        3.680098
HLA B*1503      1:553-561       9       LQVSKGNQF       1.316494        1.095188        -0.664439       2.411682        1.747243        4.617842
HLA A*2902      1:199-207       9       VYSLGCVLY       1.447668        1.349451        -1.157117       2.797119        1.640003        14.358751
HLA B*1517      1:444-452       9       LTAAGFGRF       1.264045        1.143271        -0.779573       2.407316        1.627743        6.019677
HLA B*3501      1:429-437       9       IPDVSTLTY       1.587135        0.998491        -1.002849       2.585626        1.582776        10.065827
HLA B*4001      1:92-100        9       MEYVDGVTL       1.960528        0.479465        -0.870766       2.439993        1.569227        7.426191
HLA A*2603      1:81-89 9       ETPAGPLPY       0.838347        1.232245        -0.596182       2.070592        1.474410        3.946225
HLA B*1801      1:11-19 9       YELGEILGF       1.340749        1.097482        -1.045286       2.438231        1.392945        11.099052
HLA B*1517      1:324-332       9       RSIGSVGRW       1.364284        0.476685        -0.511633       1.840969        1.329336        3.248129
HLA B*3501      1:3-11  9       TPSHLSDRY       1.408193        1.130572        -1.216310       2.538765        1.322456        16.455443
HLA B*1517      1:369-377       9       SSADAIATL       1.558793        0.442595        -0.731442       2.001388        1.269946        5.388175
HLA B*4001      1:58-66 9       REAQNAAAL       1.509434        0.528379        -0.797866       2.037813        1.239947        6.278651
HLA A*2602      1:208-216       9       EVLTGEPPF       1.005134        1.056495        -0.823170       2.061629        1.238459        6.655340
HLA B*1503      1:441-449       9       VKKLTAAGF       1.183095        1.214009        -1.188167       2.397104        1.208937        15.422950
HLA A*0250      1:338-346       9       VLAVLTVVV       1.399873        0.245231        -0.446769       1.645104        1.198335        2.797491
HLA A*3101      1:153-161       9       KVMDFGIAR       1.467969        0.798713        -1.076933       2.266682        1.189749        11.938051
HLA A*1101      1:153-161       9       KVMDFGIAR       1.467969        0.798713        -1.087412       2.266682        1.179270        12.229597
HLA A*3201      1:340-348       9       AVLTVVVTI       1.737080        0.382942        -0.974764       2.120022        1.145258        9.435474
HLA B*1517      1:374-382       9       IATLQNRGF       1.437491        1.183631        -1.497402       2.621122        1.123720        31.434168
HLA B*5301      1:429-437       9       IPDVSTLTY       1.587135        0.998491        -1.463945       2.585626        1.121681        29.103506
HLA A*0219      1:338-346       9       VLAVLTVVV       1.399873        0.245231        -0.553393       1.645104        1.091711        3.575963
HLA B*1503      1:509-517       9       QKNLNVYGF       1.205828        1.152866        -1.293561       2.358694        1.065134        19.658965
HLA B*4001      1:427-435       9       REIPDVSTL       1.524929        0.472437        -0.948619       1.997366        1.048748        8.884207
HLA A*2602      1:81-89 9       ETPAGPLPY       0.838347        1.232245        -1.059918       2.070592        1.010674        11.479381
HLA A*0250      1:118-126       9       VIADACQAL       1.609592        0.433733        -1.046357       2.043325        0.996968        11.126466
HLA A*0101      1:192-200       9       SVDARSDVY       1.553332        1.216038        -1.776699       2.769370        0.992670        59.799748
HLA A*2403      1:436-444       9       TYAEAVKKL       1.577697        0.550199        -1.140717       2.127896        0.987179        13.826659
HLA A*3002      1:507-515       9       VAQKNLNVY       1.447705        1.245143        -1.727750       2.692848        0.965098        53.425695
HLA A*6801      1:24-32 9       EVHLARDLR       0.880960        0.651501        -0.608808       1.532461        0.923653        4.062636
HLA A*0250      1:162-170       9       AIADSGNSV       1.093291        0.318474        -0.501098       1.411765        0.910667        3.170284
HLA B*1517      1:46-54 9       LARDPSFYL       1.468873        0.401975        -0.962476       1.870848        0.908372        9.172251
HLA B*5801      1:324-332       9       RSIGSVGRW       1.364284        0.476685        -0.942721       1.840969        0.898248        8.764385
HLA A*2602      1:45-53 9       DLARDPSFY       1.045970        1.215443        -1.387112       2.261413        0.874300        24.384421
HLA A*0250      1:175-183       9       AVIGTAQYL       1.498806        0.636372        -1.275756       2.135178        0.859421        18.869320
HLA A*0211      1:201-209       9       SLGCVLYEV       1.046700        0.073642        -0.265097       1.120342        0.855245        1.841184
HLA A*2602      1:334-342       9       AVVAVLAVL       1.513669        0.593252        -1.260381       2.106921        0.846540        18.212989
HLA A*0211      1:340-348       9       AVLTVVVTI       1.737080        0.382942        -1.295304       2.120022        0.824718        19.738038
HLA A*0216      1:338-346       9       VLAVLTVVV       1.399873        0.245231        -0.823339       1.645104        0.821764        6.657933
HLA A*0203      1:144-152       9       IMISATNAV       0.995514        0.289158        -0.464808       1.284672        0.819864        2.916138
HLA A*3002      1:597-605       9       GSQHNRVVY       1.563391        1.181955        -1.927480       2.745346        0.817866        84.621341
HLA A*0250      1:328-336       9       SVGRWVAVV       1.311571        0.134409        -0.632683       1.445980        0.813297        4.292234
HLA A*0211      1:338-346       9       VLAVLTVVV       1.399873        0.245231        -0.836154       1.645104        0.808950        6.857306
HLA A*0206      1:334-342       9       AVVAVLAVL       1.513669        0.593252        -1.305787       2.106921        0.801134        20.220290
HLA B*1517      1:597-605       9       GSQHNRVVY       1.563391        1.181955        -1.952666       2.745346        0.792680        89.673967
HLA A*0202      1:144-152       9       IMISATNAV       0.995514        0.289158        -0.494881       1.284672        0.789790        3.125226
HLA A*0250      1:296-304       9       LLSSAAGNL       1.424780        0.448594        -1.101246       1.873374        0.772128        12.625422
HLA A*3002      1:199-207       9       VYSLGCVLY       1.447668        1.349451        -2.034208       2.797119        0.762912        108.195104
HLA A*0250      1:144-152       9       IMISATNAV       0.995514        0.289158        -0.527831       1.284672        0.756841        3.371558
HLA A*0202      1:118-126       9       VIADACQAL       1.609592        0.433733        -1.296404       2.043325        0.746921        19.788074
HLA A*0212      1:144-152       9       IMISATNAV       0.995514        0.289158        -0.541058       1.284672        0.743613        3.475827
HLA B*1801      1:92-100        9       MEYVDGVTL       1.960528        0.479465        -1.712934       2.439993        0.727059        51.633829
HLA A*0202      1:296-304       9       LLSSAAGNL       1.424780        0.448594        -1.147103       1.873374        0.726271        14.031470
HLA A*0211      1:144-152       9       IMISATNAV       0.995514        0.289158        -0.560554       1.284672        0.724117        3.635417
HLA A*8001      1:192-200       9       SVDARSDVY       1.553332        1.216038        -2.054371       2.769370        0.714999        113.336785
HLA B*3901      1:34-42 9       HRDVAVKVL       1.797280        0.410892        -1.493704       2.208172        0.714468        31.167638
HLA B*4403      1:11-19 9       YELGEILGF       1.340749        1.097482        -1.730743       2.438231        0.707488        53.795188
HLA B*1501      1:553-561       9       LQVSKGNQF       1.316494        1.095188        -1.709373       2.411682        0.702310        51.212091
HLA A*0250      1:216-224       9       FTGDSPVSV       1.347532        -0.048789       -0.598997       1.298743        0.699746        3.971884
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HLA A*0250	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.428278	1.120342	0.692064	2.680885
HLA B*1503	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-1.809301	2.500470	0.691170	64.461560
HLA A*0212	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.429843	1.120342	0.690499	2.690562
HLA A*2403	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-1.691390	2.374610	0.683220	49.134841
HLA A*0206	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-0.806179	1.488986	0.682807	6.399983
HLA A*2602	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-1.468696	2.135178	0.666482	29.423611
HLA A*6802	1:476-484	9	QTSAITNVV	1.187107	0.191059	-0.712820	1.378166	0.665346	5.162020
HLA A*0211	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.454155	1.113773	0.659617	2.845479
HLA B*4001	1:11-19	9	YELGEILGF	1.340749	1.097482	-1.779115	2.438231	0.659117	60.133243
HLA B*1503	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-1.783753	2.439993	0.656241	60.778854
HLA A*0219	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.491785	1.113773	0.621988	3.103022
HLA A*0219	1:144-152	9	IMISATNAV	0.995514	0.289158	-0.671276	1.284672	0.613395	4.691115
HLA A*0211	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-0.687628	1.298743	0.611114	4.871116
HLA A*0212	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-1.036442	1.645104	0.608661	10.875329
HLA A*0211	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-0.884337	1.488986	0.604649	7.661905
HLA A*0202	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-1.047659	1.645104	0.597445	11.159863
HLA A*0211	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-0.856077	1.445980	0.589903	7.179218
HLA A*6802	1:392-400	9	STIPPDHVI	1.394582	0.214468	-1.019625	1.609050	0.589425	10.462243
HLA A*6802	1:369-377	9	SSADAIATL	1.558793	0.442595	-1.412675	2.001388	0.588713	25.862759
HLA A*0250	1:268-276	9	EMRADLVRV	1.216414	0.187070	-0.824420	1.403484	0.579064	6.674522
HLA B*1501	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-1.844412	2.407316	0.562905	69.889432
HLA B*1501	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-2.183437	2.745346	0.561908	152.558883
HLA A*0203	1:162-170	9	AIADSGNSV	1.093291	0.318474	-0.867590	1.411765	0.544175	7.372073
HLA A*0203	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-1.343623	1.873374	0.529751	22.060913
HLA A*0206	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-1.608175	2.135178	0.527002	40.567243
HLA B*1517	1:579-587	9	RALGWTGML	1.320466	0.574247	-1.367833	1.894713	0.526881	23.325587
HLA A*0206	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.599866	1.113773	0.513907	3.979842
HLA B*1517	1:345-353	9	VVTIAINTF	1.511825	1.191327	-2.194818	2.703152	0.508334	156.609609
HLA A*3101	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-1.927264	2.428102	0.500838	84.579235
HLA A*0250	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-0.992394	1.488986	0.496592	9.826396
HLA A*0250	1:585-593	9	GMLDKGADV	0.832496	0.121837	-0.460518	0.954333	0.493816	2.887472
HLA B*5301	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-1.337219	1.828833	0.491614	21.737960
HLA B*1503	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-2.266952	2.745346	0.478394	184.906549
HLA A*6801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-1.329348	1.793234	0.463886	21.347549
HLA A*0203	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.652668	1.113773	0.461105	4.494363
HLA A*0202	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.653124	1.113773	0.460649	4.499082
HLA A*0202	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.662146	1.120342	0.458196	4.593524
HLA B*3501	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-1.603495	2.061629	0.458134	40.132417
HLA B*5801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-1.963169	2.407316	0.444148	91.868914
HLA A*6801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-1.499822	1.942822	0.443000	31.609814
HLA A*3301	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-1.350489	1.793234	0.442746	22.412416
HLA A*3001	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-0.927116	1.364704	0.437588	8.455050
HLA A*0206	1:144-152	9	IMISATNAV	0.995514	0.289158	-0.849146	1.284672	0.435525	7.065553
HLA A*3101	1:27-35	9	LARDLRLHR	1.122977	0.679742	-1.376169	1.802719	0.426551	23.777629
HLA A*2902	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-2.065559	2.490827	0.425268	116.294490
HLA A*0219	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.699329	1.120342	0.421013	5.004134
HLA A*0216	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.709046	1.120342	0.411295	5.117365
HLA A*0211	1:585-593	9	GMLDKGADV	0.832496	0.121837	-0.543647	0.954333	0.410686	3.496611
HLA B*3501	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-2.082475	2.490827	0.408352	120.913677
HLA A*0202	1:162-170	9	AIADSGNSV	1.093291	0.318474	-1.008700	1.411765	0.403065	10.202338
HLA A*0202	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.519795	0.918162	0.398366	3.309751
HLA A*0206	1:118-126	9	VIADACQAL	1.609592	0.433733	-1.650570	2.043325	0.392755	44.726983
HLA B*1501	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.038164	2.429816	0.391652	109.185293
HLA A*6801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-1.247553	1.638299	0.390746	17.682882
HLA A*0212	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.530316	0.918162	0.387845	3.390911
HLA A*3101	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-1.538217	1.922093	0.383876	34.531642
HLA B*5701	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-1.470637	1.840969	0.370333	29.555386
HLA A*0250	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.743574	1.113773	0.370198	5.540825
HLA A*2602	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-2.046552	2.407316	0.360765	111.314516
HLA B*3901	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-1.496941	1.857104	0.360162	31.400855
HLA A*0212	1:585-593	9	GMLDKGADV	0.832496	0.121837	-0.604170	0.954333	0.350163	4.019482
HLA A*3002	1:255-263	9	LAKNPENRY	1.439797	1.360506	-2.457890	2.800303	0.342413	287.005514
HLA B*3901	1:58-66	9	REAQNAAAL	1.509434	0.528379	-1.699970	2.037813	0.337843	50.115247
HLA A*6802	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-1.092854	1.430389	0.337536	12.383789
HLA A*3001	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-0.975920	1.303070	0.327151	9.460622

HLA A*0250	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.592893	0.918162	0.325269	3.916450
HLA A*0206	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-0.709507	1.028753	0.319246	5.122794
HLA A*2902	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-2.221485	2.538391	0.316906	166.527154
HLA A*6901	1:433-441	9	STLTYAEAV	1.049463	0.176908	-0.913132	1.226371	0.313239	8.187137
HLA A*0212	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.815281	1.113773	0.298492	6.535528
HLA A*3002	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-2.201862	2.490827	0.288965	159.170346
HLA A*0203	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.633238	0.918162	0.284924	4.297718
HLA A*3101	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-1.168648	1.449604	0.280956	14.745107
HLA B*3901	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-2.169153	2.439993	0.270840	147.622525
HLA B*4002	1:11-19	9	YELGEILGF	1.340749	1.097482	-2.170619	2.438231	0.267612	148.121707
HLA A*0203	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-1.378222	1.645104	0.266882	23.890322
HLA A*6801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-2.004454	2.266682	0.262229	101.030786
HLA A*2602	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-0.773549	1.028753	0.255204	5.936755
HLA B*1517	1:255-263	9	LAKNPENRY	1.439797	1.360506	-2.555638	2.800303	0.244665	359.449773
HLA A*0216	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-1.255673	1.488986	0.233313	18.016601
HLA A*0216	1:585-593	9	GMLDKGADV	0.832496	0.121837	-0.737268	0.954333	0.217065	5.460952
HLA A*3001	1:46-54	9	LARDPSFYL	1.468873	0.401975	-1.657143	1.870848	0.213704	45.409159
HLA A*0216	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-1.909210	2.120022	0.210812	81.135386
HLA A*0211	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-1.926893	2.135178	0.208285	84.506970
HLA B*1501	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-2.492089	2.692848	0.200758	310.519833
HLA A*3101	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-1.343938	1.538857	0.194918	22.076911
HLA A*0203	1:118-126	9	VIADACQAL	1.609592	0.433733	-1.863583	2.043325	0.179742	73.043792
HLA A*2403	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-2.248561	2.428102	0.179541	177.239503
HLA A*0206	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-1.947545	2.120022	0.172478	88.622604
HLA A*6801	1:145-153	9	MISATNAVK	0.938735	0.280828	-1.047133	1.219563	0.172431	11.146347
HLA A*3301	1:27-35	9	LARDLRLHR	1.122977	0.679742	-1.631233	1.802719	0.171486	42.779267
HLA B*5301	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-2.372054	2.538765	0.166711	235.534297
HLA A*2902	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-1.903896	2.070592	0.166696	80.148569
HLA A*0211	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.752441	0.918162	0.165720	5.655114
HLA A*0201	1:144-152	9	IMISATNAV	0.995514	0.289158	-1.121311	1.284672	0.163361	13.222407
HLA A*2602	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-2.338363	2.490827	0.152465	217.952844
HLA A*1101	1:549-557	9	SVIELQVSK	0.982858	0.255246	-1.087262	1.238104	0.150842	12.225363
HLA B*3501	1:345-353	9	VVTIAINTF	1.511825	1.191327	-2.556940	2.703152	0.146212	360.528689
HLA B*1501	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-2.344622	2.490827	0.146206	221.116712
HLA A*0201	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-0.986967	1.120342	0.133375	9.704361
HLA A*6801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-1.100687	1.233662	0.132975	12.609177
HLA B*1517	1:392-400	9	STIPPDHVI	1.394582	0.214468	-1.481144	1.609050	0.127906	30.279140
HLA A*8001	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-2.412587	2.538391	0.125803	258.575558
HLA A*0206	1:369-377	9	SSADAIATL	1.558793	0.442595	-1.878690	2.001388	0.122698	75.629373
HLA A*0201	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-0.997455	1.113773	0.116318	9.941572
HLA A*2601	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-1.954743	2.070592	0.115849	90.103846
HLA A*3101	1:40-48	9	KVLRADLAR	0.915954	0.778633	-1.583849	1.694587	0.110738	38.357379
HLA A*8001	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-2.475587	2.585626	0.110039	298.941742
HLA A*0211	1:433-441	9	STLTYAEAV	1.049463	0.176908	-1.117067	1.226371	0.109304	13.093849
HLA A*0202	1:369-377	9	SSADAIATL	1.558793	0.442595	-1.898360	2.001388	0.103028	79.133502
HLA A*0203	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.009980	2.106921	0.096941	102.324521
HLA A*3101	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-1.725358	1.822112	0.096754	53.132275
HLA B*1503	1:144-152	9	IMISATNAV	0.995514	0.289158	-1.192960	1.284672	0.091711	15.594103
HLA A*0202	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-2.049897	2.135178	0.085280	112.175360
HLA A*0216	1:144-152	9	IMISATNAV	0.995514	0.289158	-1.206987	1.284672	0.077685	16.105968
HLA B*4403	1:23-31	9	SEVHLARDL	1.447686	0.429685	-1.801223	1.877371	0.076148	63.273707
HLA A*3001	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-2.191210	2.266682	0.075473	155.313639
HLA A*3002	1:45-53	9	DLARDPSFY	1.045970	1.215443	-2.185947	2.261413	0.075466	153.442883
HLA B*4002	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-2.367632	2.439993	0.072361	233.148392
HLA B*3501	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-1.799292	1.866969	0.067677	62.992958
HLA A*6901	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-1.048350	1.113773	0.065423	11.177627
HLA B*1517	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-1.389236	1.431809	0.042573	24.503966
HLA A*6802	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-1.071647	1.113773	0.042126	11.793619
HLA A*2403	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.387984	2.429816	0.041832	244.333864
HLA A*0203	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-0.987117	1.028753	0.041636	9.707722
HLA B*0702	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-1.080195	1.118640	0.038446	12.028031
HLA A*3001	1:27-35	9	LARDLRLHR	1.122977	0.679742	-1.767616	1.802719	0.035103	58.562047
HLA A*6901	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.264436	1.298743	0.034306	18.383849
HLA A*0216	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-1.415147	1.445980	0.030834	26.010369
HLA A*6801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-1.244015	1.266360	0.022345	17.539399

HLA A*0206	1:162-170	9	AIADSGNSV	1.093291	0.318474	-1.390505	1.411765	0.021260	24.575655
HLA A*0216	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.280070	1.298743	0.018673	19.057675
HLA A*8001	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-2.053046	2.070592	0.017546	112.991502
HLA A*2902	1:45-53	9	DLARDPSFY	1.045970	1.215443	-2.246925	2.261413	0.014487	176.573401
HLA A*0212	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.286982	1.298743	0.011760	19.363421
HLA A*0203	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.299956	1.298743	-0.001213	19.950600
HLA A*3001	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-1.240218	1.238694	-0.001524	17.386732
HLA A*0250	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-1.622052	1.618772	-0.003279	41.884328
HLA B*1517	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-2.082100	2.070592	-0.011508	120.809062
HLA B*1503	1:11-19	9	YELGEILGF	1.340749	1.097482	-2.452533	2.438231	-0.014302	283.487174
HLA A*3101	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-1.542606	1.525910	-0.016696	34.882377
HLA A*1101	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-1.288627	1.266360	-0.022267	19.436888
HLA A*0203	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-1.145604	1.120342	-0.025262	13.983123
HLA A*6802	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.335367	1.298743	-0.036625	21.645489
HLA A*0212	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-1.658121	1.618772	-0.039349	45.511468
HLA A*3001	1:145-153	9	MISATNAVK	0.938735	0.280828	-1.261485	1.219563	-0.041922	18.259357
HLA A*2501	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-2.115354	2.070592	-0.044762	130.422981
HLA A*2601	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.075176	1.028753	-0.046423	11.889840
HLA A*0216	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-0.967015	0.918162	-0.048854	9.268621
HLA A*0211	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-0.824246	0.773768	-0.050478	6.671851
HLA B*4002	1:427-435	9	REIPDVSTL	1.524929	0.472437	-2.051227	1.997366	-0.053861	112.519367
HLA A*0211	1:579-587	9	RALGWTGML	1.320466	0.574247	-1.948747	1.894713	-0.054034	88.868417
HLA A*0201	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-1.703804	1.645104	-0.058700	50.559670
HLA A*6802	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-0.953421	0.887960	-0.065461	8.982992
HLA A*3002	1:192-200	9	SVDARSDVY	1.553332	1.216038	-2.837060	2.769370	-0.067690	687.162621
HLA A*0101	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-2.140160	2.070592	-0.069568	138.089286
HLA B*3901	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-1.324602	1.254080	-0.070522	21.115533
HLA A*0202	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.177733	2.106921	-0.070812	150.568093
HLA A*0203	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-1.561078	1.488986	-0.072092	36.398017
HLA B*4801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-2.450452	2.374610	-0.075842	282.131625
HLA A*0211	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-1.341481	1.261014	-0.080466	21.952337
HLA A*6801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-2.004364	1.922093	-0.082271	101.010019
HLA A*0211	1:162-170	9	AIADSGNSV	1.093291	0.318474	-1.494066	1.411765	-0.082301	31.193615
HLA B*1517	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-2.217984	2.135178	-0.082807	165.190218
HLA A*0219	1:118-126	9	VIADACQAL	1.609592	0.433733	-2.128262	2.043325	-0.084937	134.357586
HLA A*0206	1:433-441	9	STLTYAEAV	1.049463	0.176908	-1.315148	1.226371	-0.088777	20.660828
HLA A*0203	1:517-525	9	FTKFSQASV	0.794238	0.070907	-0.956748	0.865145	-0.091602	9.052070
HLA A*6801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-1.546558	1.449604	-0.096954	35.201235
HLA A*2601	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-2.508916	2.407316	-0.101600	322.787238
HLA A*0202	1:476-484	9	QTSAITNVV	1.187107	0.191059	-1.481496	1.378166	-0.103330	30.303721
HLA A*0216	1:162-170	9	AIADSGNSV	1.093291	0.318474	-1.518458	1.411765	-0.106693	32.995754
HLA A*6802	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-1.123951	1.014988	-0.108963	13.303053
HLA A*3001	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-0.910346	0.796898	-0.113447	8.134775
HLA A*0301	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-2.382852	2.266682	-0.116170	241.463999
HLA B*3901	1:244-252	9	SADLDAVVL	1.902706	0.406606	-2.426421	2.309312	-0.117109	266.944660
HLA A*8001	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-2.915932	2.797119	-0.118812	824.008590
HLA B*1503	1:255-263	9	LAKNPENRY	1.439797	1.360506	-2.920842	2.800303	-0.120539	833.378252
HLA A*0206	1:475-483	9	NQTSAITNV	1.108161	0.235536	-1.466610	1.343697	-0.122913	29.282599
HLA B*4001	1:23-31	9	SEVHLARDL	1.447686	0.429685	-2.002118	1.877371	-0.124747	100.488958
HLA B*1502	1:192-200	9	SVDARSDVY	1.553332	1.216038	-2.901403	2.769370	-0.132033	796.897609
HLA A*0250	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-0.910350	0.773768	-0.136582	8.134863
HLA A*3001	1:40-48	9	KVLRADLAR	0.915954	0.778633	-1.839562	1.694587	-0.144975	69.113387
HLA A*0219	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-1.065167	0.918162	-0.147006	11.618959
HLA A*6802	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-1.746584	1.598716	-0.147867	55.793506
HLA A*3101	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-1.424117	1.270418	-0.153699	26.553198
HLA A*0219	1:585-593	9	GMLDKGADV	0.832496	0.121837	-1.109535	0.954333	-0.155202	12.868706
HLA A*6801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-1.543010	1.386802	-0.156208	34.914850
HLA A*6801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-1.666861	1.509182	-0.157678	46.436655
HLA B*1503	1:427-435	9	REIPDVSTL	1.524929	0.472437	-2.158571	1.997366	-0.161204	144.069003
HLA A*6802	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-1.226943	1.049687	-0.177256	16.863331
HLA A*1101	1:192-200	9	SVDARSDVY	1.553332	1.216038	-2.952701	2.769370	-0.183332	896.811522
HLA A*0201	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.308740	2.120022	-0.188718	203.582402
HLA B*4403	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-2.628735	2.439993	-0.188742	425.339182
HLA A*2402	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-2.565652	2.374610	-0.191042	367.833872
HLA A*1101	1:145-153	9	MISATNAVK	0.938735	0.280828	-1.414789	1.219563	-0.195226	25.988989

HLA B*1501	1:255-263	9	LAKNPENRY	1.439797	1.360506	-2.999808	2.800303	-0.199505	999.558816
HLA B*1517	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-2.892418	2.692848	-0.199570	780.581211
HLA A*1101	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-1.436118	1.233662	-0.202456	27.297194
HLA A*0212	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-1.649320	1.445980	-0.203340	44.598441
HLA A*2403	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-2.614399	2.407316	-0.207082	411.527474
HLA A*0211	1:268-276	9	EMRADLVRV	1.216414	0.187070	-1.613744	1.403484	-0.210260	41.090722
HLA B*4501	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-1.315721	1.103143	-0.212578	20.688119
HLA B*3501	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-2.912234	2.692848	-0.219386	817.021810
HLA A*0203	1:475-483	9	NQTSAITNV	1.108161	0.235536	-1.565293	1.343697	-0.221596	36.752991
HLA B*1503	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-2.914560	2.692848	-0.221712	821.409346
HLA A*0202	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.255504	1.028753	-0.226751	18.009585
HLA A*0201	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-1.715749	1.488986	-0.226763	51.969557
HLA B*3501	1:192-200	9	SVDARSDVY	1.553332	1.216038	-2.997106	2.769370	-0.227737	993.359492
HLA A*6802	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-1.295135	1.067242	-0.227893	19.730351
HLA A*3001	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-1.193299	0.965301	-0.227998	15.606256
HLA A*2902	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-2.645196	2.407316	-0.237879	441.769658
HLA A*0219	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-1.685351	1.445980	-0.239371	48.456426
HLA B*4601	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-2.934079	2.692848	-0.241231	859.170113
HLA A*6802	1:459-467	9	STPELVGKV	0.780846	0.079303	-1.103910	0.860149	-0.243762	12.703115
HLA A*3301	1:372-380	9	DAIATLQNR	1.011737	0.626562	-1.888977	1.638299	-0.250678	77.441997
HLA B*2705	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-1.508125	1.257069	-0.251056	32.219962
HLA B*1503	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-2.742530	2.489515	-0.253015	552.752033
HLA A*6901	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-1.700698	1.445980	-0.254718	50.199364
HLA A*6802	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.363878	2.106921	-0.256957	231.141511
HLA A*0206	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.556214	1.298743	-0.257472	35.992688
HLA A*0216	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-1.375529	1.113773	-0.261757	23.742666
HLA A*2301	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-2.642339	2.374610	-0.267729	438.873047
HLA A*6801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-1.510334	1.238104	-0.272230	32.384227
HLA B*4002	1:44-52	9	ADLARDPSF	1.368587	1.094178	-2.735129	2.462765	-0.272364	543.412308
HLA B*4501	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-2.719482	2.439993	-0.279489	524.181755
HLA B*1501	1:192-200	9	SVDARSDVY	1.553332	1.216038	-3.061280	2.769370	-0.291911	1151.543318
HLA A*0206	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-1.210192	0.918162	-0.292030	16.225255
HLA A*2602	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.008675	2.703152	-0.305523	1020.176488
HLA B*4002	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.343936	2.037813	-0.306122	220.767693
HLA B*0702	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-2.175773	1.866969	-0.308805	149.890283
HLA A*3001	1:38-46	9	AVKVLRADL	1.192397	0.558614	-2.067645	1.751011	-0.316635	116.854510
HLA B*4402	1:11-19	9	YELGEILGF	1.340749	1.097482	-2.761326	2.438231	-0.323095	577.199875
HLA B*4001	1:14-22	9	GEILGFGGM	0.948298	0.046073	-1.320777	0.994371	-0.326406	20.930379
HLA A*0203	1:585-593	9	GMLDKGADV	0.832496	0.121837	-1.287067	0.954333	-0.332733	19.367193
HLA A*2301	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.037377	2.703152	-0.334224	1089.874820
HLA A*8001	1:45-53	9	DLARDPSFY	1.045970	1.215443	-2.596566	2.261413	-0.335154	394.971940
HLA B*1503	1:120-128	9	ADACQALNF	1.485501	1.040074	-2.860832	2.525575	-0.335256	725.824489
HLA A*6802	1:517-525	9	FTKFSQASV	0.794238	0.070907	-1.207851	0.865145	-0.342706	16.138064
HLA A*3301	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-1.793061	1.449604	-0.343457	62.095649
HLA B*1503	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.046812	2.703152	-0.343660	1113.812662
HLA A*2403	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.143968	2.797119	-0.346849	1393.054330
HLA A*0201	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.648281	1.298743	-0.349539	44.491926
HLA A*0202	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.655668	1.298743	-0.356925	45.255147
HLA A*6802	1:433-441	9	STLTYAEAV	1.049463	0.176908	-1.585860	1.226371	-0.359489	38.535419
HLA A*2402	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-2.849272	2.489515	-0.359757	706.760307
HLA A*0212	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.480112	2.120022	-0.360089	302.072833
HLA A*3001	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-1.095612	0.732039	-0.363573	12.462692
HLA A*2402	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.166086	2.797119	-0.368967	1465.838440
HLA B*3501	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.170574	2.800303	-0.370271	1481.063308
HLA A*6802	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-1.689496	1.312789	-0.376706	48.921061
HLA A*0301	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-1.652374	1.266360	-0.386014	44.913201
HLA B*1502	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.821708	2.429816	-0.391892	663.296938
HLA A*0211	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.499763	2.106921	-0.392842	316.055070
HLA A*0211	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.829090	2.429816	-0.399274	674.667942
HLA A*0301	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-1.703189	1.303070	-0.400118	50.488058
HLA A*6901	1:476-484	9	QTSAITNVV	1.187107	0.191059	-1.779768	1.378166	-0.401602	60.223748
HLA A*0211	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-2.023095	1.618772	-0.404322	105.461646
HLA A*3301	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-2.425200	2.015621	-0.409578	266.194762
HLA A*0219	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-1.902801	1.488986	-0.413815	79.946768
HLA A*2403	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-2.735031	2.316186	-0.418845	543.288850

HLA B*1501	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-2.920837	2.500470	-0.420367	833.369235
HLA A*0250	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.532308	2.106921	-0.425387	340.649557
HLA A*0206	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-2.745134	2.316186	-0.428948	556.075265
HLA B*3501	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-2.992295	2.554318	-0.437977	982.414357
HLA B*1502	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-2.852472	2.411682	-0.440790	711.987140
HLA B*4403	1:267-275	9	AEMRADLVR	1.301765	0.742764	-2.487221	2.044529	-0.442693	307.058561
HLA A*2902	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.876794	2.429816	-0.446978	752.998339
HLA A*0206	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-2.094011	1.645104	-0.448908	124.168490
HLA A*0206	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-1.572200	1.120342	-0.451858	37.342224
HLA A*6802	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-1.477380	1.022974	-0.454406	30.017856
HLA A*1101	1:249-257	9	AVVLKALAK	1.021065	0.298784	-1.774411	1.319849	-0.454562	59.485478
HLA A*2902	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.012895	2.554318	-0.458577	1030.136998
HLA B*4801	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-2.900317	2.439993	-0.460324	794.908355
HLA A*6901	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.356195	1.894713	-0.461482	227.088495
HLA B*1503	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-2.893278	2.429816	-0.463462	782.128308
HLA A*3301	1:24-32	9	EVHLARDLR	0.880960	0.651501	-1.996823	1.532461	-0.464362	99.271047
HLA A*3201	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-2.065545	1.598716	-0.466829	116.290715
HLA A*6901	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.469266	2.001388	-0.467878	294.622864
HLA A*3301	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-2.031492	1.561867	-0.469625	107.520582
HLA A*2301	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-2.787612	2.316186	-0.471426	613.214289
HLA A*6801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-2.034349	1.561867	-0.472482	108.230229
HLA B*4501	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.511209	2.037813	-0.473396	324.496079
HLA A*6802	1:243-251	9	LSADLDAVV	0.948699	0.148803	-1.572905	1.097502	-0.475403	37.402878
HLA A*2602	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.480957	2.001388	-0.479569	302.661712
HLA A*2602	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.177975	2.692848	-0.485127	1506.518609
HLA A*3301	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-1.758167	1.270418	-0.487748	57.301583
HLA A*2403	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.201436	2.703152	-0.498284	1590.144011
HLA B*3501	1:374-382	9	IATLQNRGF	1.437491	1.183631	-3.119552	2.621122	-0.498430	1316.898207
HLA A*0206	1:11-19	9	YELGEILGF	1.340749	1.097482	-2.938177	2.438231	-0.499945	867.314612
HLA B*3901	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-2.895402	2.374610	-0.520792	785.962706
HLA B*5801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.020258	2.490827	-0.529431	1047.751452
HLA A*0211	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-1.840403	1.306673	-0.533730	69.247371
HLA B*2705	1:578-586	9	LRALGWTGM	0.993924	0.288236	-1.817200	1.282160	-0.535040	65.644716
HLA A*0206	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.407935	1.870848	-0.537088	255.820586
HLA A*2902	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.285078	2.745346	-0.539732	1927.871681
HLA A*0203	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-1.987688	1.445980	-0.541708	97.204821
HLA A*6802	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-0.951509	0.409720	-0.541789	8.943521
HLA A*0212	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-2.031501	1.488986	-0.542515	107.522908
HLA A*3002	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.319047	2.772331	-0.546716	2084.716376
HLA A*2403	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-3.038584	2.489515	-0.549069	1092.909634
HLA A*3101	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-2.565318	2.015621	-0.549697	367.551409
HLA B*5101	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-2.416878	1.866969	-0.549909	261.142544
HLA B*1517	1:192-200	9	SVDARSDVY	1.553332	1.216038	-3.323680	2.769370	-0.554311	2107.075816
HLA B*1503	1:374-382	9	IATLQNRGF	1.437491	1.183631	-3.176226	2.621122	-0.555104	1500.467122
HLA A*0219	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-1.865308	1.298743	-0.566565	73.334415
HLA A*3001	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-1.487600	0.920120	-0.567480	30.732644
HLA A*0206	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-1.301488	0.732039	-0.569449	20.021095
HLA B*1517	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-2.000234	1.430389	-0.569845	100.053908
HLA A*0250	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-1.371930	0.798791	-0.573139	23.546702
HLA B*5801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-2.182437	1.609050	-0.573387	152.207698
HLA A*2403	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.012552	2.438231	-0.574321	1029.323672
HLA B*2705	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-2.784191	2.208172	-0.576020	608.403097
HLA A*0250	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.448906	1.870848	-0.578058	281.129105
HLA B*1502	1:45-53	9	DLARDPSFY	1.045970	1.215443	-2.841975	2.261413	-0.580562	694.983750
HLA A*3301	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-2.091187	1.509182	-0.582005	123.363681
HLA A*6802	1:265-273	9	TAAEMRADL	1.001324	0.415888	-2.001075	1.417212	-0.583864	100.247874
HLA A*0206	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-1.774998	1.190001	-0.584997	59.565985
HLA A*0250	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-1.425310	0.839877	-0.585433	26.626273
HLA A*3101	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-2.650971	2.064862	-0.586109	447.683324
HLA B*4801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.626292	2.037813	-0.588479	422.952822
HLA A*2602	1:392-400	9	STIPPDHVI	1.394582	0.214468	-2.198808	1.609050	-0.589758	158.054851
HLA B*1501	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.150100	2.554318	-0.595783	1412.863516
HLA A*6801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-1.811495	1.208137	-0.603358	64.788098
HLA A*2402	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-2.733015	2.127896	-0.605119	540.772918
HLA A*0219	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-1.381431	0.773768	-0.607663	24.067523

HLA A*3201	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-2.875638	2.266682	-0.608956	750.996774
HLA A*6901	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-1.755770	1.144551	-0.611219	56.986258
HLA A*3101	1:521-529	9	SQASVDSPR	0.518283	0.661153	-1.792046	1.179436	-0.612610	61.950696
HLA A*0201	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.644503	1.028753	-0.615750	44.106564
HLA A*0211	1:64-72	9	AALNHPAIV	1.169288	0.295731	-2.082992	1.465019	-0.617974	121.057672
HLA A*0211	1:118-126	9	VIADACQAL	1.609592	0.433733	-2.662972	2.043325	-0.619647	460.226993
HLA A*0201	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-1.538969	0.918162	-0.620807	34.591474
HLA A*6901	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-2.703317	2.081726	-0.621591	505.030310
HLA A*0201	1:118-126	9	VIADACQAL	1.609592	0.433733	-2.670777	2.043325	-0.627452	468.572802
HLA A*3201	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.182963	1.554751	-0.628212	152.392258
HLA A*6801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-2.892301	2.261413	-0.630888	780.370097
HLA A*1101	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-1.428200	0.796898	-0.631302	26.804039
HLA A*0216	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-2.768605	2.135178	-0.633427	586.955171
HLA A*3002	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.172472	2.538391	-0.634081	1487.551488
HLA A*0211	1:459-467	9	STPELVGKV	0.780846	0.079303	-1.495753	0.860149	-0.635604	31.315016
HLA A*2301	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.136116	2.500470	-0.635646	1368.094433
HLA A*0216	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-1.900292	1.261014	-0.639277	79.486187
HLA A*2402	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.072755	2.429816	-0.642939	1182.374798
HLA A*2902	1:192-200	9	SVDARSDVY	1.553332	1.216038	-3.414074	2.769370	-0.644705	2594.622909
HLA B*3901	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.758855	2.106921	-0.651933	573.924243
HLA A*6901	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.683575	1.028753	-0.654822	48.258650
HLA A*0219	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.781997	2.120022	-0.661975	605.336689
HLA B*1503	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.126765	2.462765	-0.664000	1338.952361
HLA B*3901	1:239-247	9	RHEGLSADL	1.161744	0.529922	-2.355697	1.691666	-0.664031	226.828197
HLA B*1517	1:288-296	9	LTDAERTSL	1.232510	0.352954	-2.252686	1.585464	-0.667222	178.931260
HLA B*5401	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-1.615215	0.942253	-0.672962	41.230115
HLA B*5101	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-1.615304	0.942253	-0.673051	41.238592
HLA B*1503	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-2.497512	1.822112	-0.675399	314.421297
HLA A*0301	1:145-153	9	MISATNAVK	0.938735	0.280828	-1.896636	1.219563	-0.677073	78.819897
HLA B*1501	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.116282	2.438231	-0.678051	1307.018466
HLA A*0202	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-2.995368	2.316186	-0.679182	989.390708
HLA A*6802	1:456-464	9	NSPSTPELV	0.868149	0.229670	-1.777122	1.097819	-0.679303	59.858008
HLA B*1502	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.479827	2.800303	-0.679524	3018.748524
HLA A*2902	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.268571	2.585626	-0.682945	1855.968676
HLA A*3001	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.803279	2.120022	-0.683256	635.738675
HLA A*0250	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-1.759130	1.075727	-0.683403	57.428822
HLA A*0219	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.713686	1.028753	-0.684933	51.723293
HLA A*6901	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-2.290630	1.598716	-0.691914	195.267696
HLA A*0211	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.562818	1.870848	-0.691971	365.441816
HLA B*5801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-2.292482	1.598716	-0.693766	196.101898
HLA B*1517	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.282395	2.585626	-0.696769	1915.997826
HLA B*1503	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.734744	2.037813	-0.696931	542.930394
HLA A*3002	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.105178	2.407316	-0.697862	1274.025314
HLA A*0250	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.818043	2.120022	-0.698021	657.722647
HLA A*0250	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-1.895564	1.194908	-0.700657	78.625695
HLA A*0219	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-2.574608	1.873374	-0.701234	375.498284
HLA A*6802	1:146-154	9	ISATNAVKV	1.443784	0.185540	-2.331211	1.629324	-0.701886	214.393053
HLA B*0702	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.742582	2.037813	-0.704769	552.817824
HLA A*0203	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-2.840537	2.135178	-0.705359	692.686567
HLA A*0212	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-2.840941	2.135178	-0.705763	693.331412
HLA A*3201	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.409394	2.703152	-0.706242	2566.812079
HLA A*0101	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.293517	2.585626	-0.707892	1965.701070
HLA B*1501	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.816060	2.106921	-0.709139	654.726367
HLA B*1503	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.481636	2.772331	-0.709305	3031.349694
HLA A*6901	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-1.843481	1.132158	-0.711323	69.739867
HLA A*0250	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-1.973300	1.261014	-0.712285	94.037172
HLA B*5701	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.513598	2.800303	-0.713295	3262.859949
HLA B*3901	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-2.581849	1.866969	-0.714880	381.811556
HLA B*1503	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.205947	2.490827	-0.715120	1606.746894
HLA B*1502	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.409474	2.692848	-0.716626	2567.284252
HLA A*1101	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-2.242607	1.525910	-0.716697	174.826366
HLA A*0203	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-2.837121	2.120022	-0.717098	687.259282
HLA A*0211	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-2.591994	1.873374	-0.718620	390.835627
HLA B*4501	1:267-275	9	AEMRADLVR	1.301765	0.742764	-2.766692	2.044529	-0.722164	584.376108
HLA B*1517	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-2.056166	1.332686	-0.723480	113.806193

HLA A*0206	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-2.322400	1.598716	-0.723684	210.087464
HLA A*6802	1:477-485	9	TSAITNVVI	1.425064	0.225264	-2.374145	1.650328	-0.723817	236.671082
HLA A*6802	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-2.031125	1.306673	-0.724452	107.429879
HLA A*0216	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-2.605959	1.873374	-0.732585	403.607738
HLA A*6901	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.052172	1.312789	-0.739382	112.764337
HLA B*5401	1:140-148	9	KPANIMISA	1.205138	-0.289626	-1.666241	0.915512	-0.750729	46.370381
HLA B*1503	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-2.150361	1.394783	-0.755579	141.371364
HLA A*0216	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.311343	1.554751	-0.756592	204.806371
HLA B*3501	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-2.833357	2.070592	-0.762765	681.328788
HLA B*4403	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.809256	2.037813	-0.771443	644.548678
HLA A*3002	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-3.311867	2.538765	-0.773102	2050.533892
HLA B*5801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-2.209658	1.431809	-0.777848	162.053252
HLA A*0250	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.092475	1.312789	-0.779685	123.729950
HLA B*4402	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.243403	2.462765	-0.780638	1751.471032
HLA A*0201	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-2.888269	2.106921	-0.781348	773.159155
HLA B*5301	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-2.650135	1.866969	-0.783166	446.821951
HLA B*1501	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.489117	2.703152	-0.785965	3084.017256
HLA B*4002	1:23-31	9	SEVHLARDL	1.447686	0.429685	-2.664292	1.877371	-0.786922	461.628377
HLA B*1517	1:146-154	9	ISATNAVKV	1.443784	0.185540	-2.420313	1.629324	-0.790988	263.216177
HLA A*6802	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-1.923923	1.132158	-0.791765	83.931075
HLA A*0212	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.204733	1.411765	-0.792968	160.226089
HLA B*1501	1:144-152	9	IMISATNAV	0.995514	0.289158	-2.079398	1.284672	-0.794726	120.059797
HLA B*4402	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.320678	2.525575	-0.795102	2092.558079
HLA A*0250	1:517-525	9	FTKFSQASV	0.794238	0.070907	-1.661800	0.865145	-0.796655	45.898674
HLA A*2402	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.500766	2.703152	-0.797613	3167.856833
HLA A*0206	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-2.198587	1.398961	-0.799626	157.974496
HLA B*4403	1:427-435	9	REIPDVSTL	1.524929	0.472437	-2.797692	1.997366	-0.800325	627.612460
HLA B*4002	1:155-163	9	MDFGIARAI	1.445600	0.187062	-2.435814	1.632662	-0.803153	272.781227
HLA A*3201	1:155-163	9	MDFGIARAI	1.445600	0.187062	-2.437215	1.632662	-0.804553	273.662174
HLA B*3901	1:427-435	9	REIPDVSTL	1.524929	0.472437	-2.803025	1.997366	-0.805659	635.367342
HLA A*6802	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-1.926766	1.120342	-0.806424	84.482287
HLA B*5701	1:374-382	9	IATLQNRGF	1.437491	1.183631	-3.427687	2.621122	-0.806565	2677.239134
HLA A*0211	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-2.002631	1.194908	-0.807723	100.607540
HLA A*1101	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.558751	2.745346	-0.813405	3620.352314
HLA A*0211	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.368661	1.554751	-0.813910	233.701499
HLA B*0702	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.709285	1.894713	-0.814572	512.017890
HLA B*1501	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.817798	2.001388	-0.816410	657.352698
HLA A*0202	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-2.307232	1.488986	-0.818246	202.876556
HLA A*3301	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-3.085184	2.266682	-0.818502	1216.701210
HLA B*5801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.521963	2.703152	-0.818810	3326.309068
HLA A*3001	1:249-257	9	AVVLKALAK	1.021065	0.298784	-2.141015	1.319849	-0.821166	138.361480
HLA A*0206	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.196813	2.374610	-0.822203	1573.304089
HLA A*1101	1:40-48	9	KVLRADLAR	0.915954	0.778633	-2.517567	1.694587	-0.822980	329.281369
HLA B*1503	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.238478	2.407316	-0.831162	1731.723053
HLA A*6901	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-1.425602	0.593391	-0.832211	26.644140
HLA B*1502	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.421057	2.585626	-0.835431	2636.676921
HLA A*0203	1:268-276	9	EMRADLVRV	1.216414	0.187070	-2.239675	1.403484	-0.836191	173.649994
HLA B*1517	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-2.439799	1.598716	-0.841083	275.295559
HLA A*6801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-2.644679	1.802719	-0.841960	441.244187
HLA A*2301	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-2.971196	2.127896	-0.843300	935.828626
HLA A*0216	1:118-126	9	VIADACQAL	1.609592	0.433733	-2.892418	2.043325	-0.849093	780.581211
HLA B*1517	1:477-485	9	TSAITNVVI	1.425064	0.225264	-2.508578	1.650328	-0.858250	322.535877
HLA A*6901	1:117-125	9	EVIADACQA	1.033905	-0.225946	-1.669196	0.807959	-0.861238	46.687038
HLA A*0202	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.237886	2.374610	-0.863276	1729.363817
HLA A*0216	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-2.485201	1.618772	-0.866428	305.633288
HLA B*2705	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-2.122985	1.254080	-0.868905	132.734938
HLA A*6801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-2.052322	1.179436	-0.872886	112.803387
HLA B*3901	1:9-17	9	DRYELGEIL	1.564982	0.473277	-2.913141	2.038259	-0.874881	818.729711
HLA A*0219	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.288873	1.411765	-0.877108	194.479123
HLA A*0201	1:585-593	9	GMLDKGADV	0.832496	0.121837	-1.835042	0.954333	-0.880708	68.397742
HLA B*1503	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.466712	2.585626	-0.881086	2928.951028
HLA B*5801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-2.314370	1.430389	-0.883980	206.238433
HLA A*0216	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-1.659869	0.773768	-0.886101	45.695019
HLA B*1503	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.425977	2.538391	-0.887586	2666.715833
HLA B*1503	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.443264	2.554318	-0.888947	2775.008068

HLA A*6802	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.011659	2.120022	-0.891637	1027.209805
HLA A*6802	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-2.340322	1.445980	-0.894342	218.938436
HLA A*6901	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.017185	2.120022	-0.897163	1040.363591
HLA A*6802	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.033965	2.135178	-0.898788	1081.347217
HLA A*0101	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.644921	2.745346	-0.899575	4414.896715
HLA B*1502	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.338275	2.438231	-0.900044	2179.089978
HLA A*6901	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.771448	1.870848	-0.900600	590.809962
HLA A*6901	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-2.390408	1.488986	-0.901422	245.701797
HLA B*1503	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-2.763925	1.857104	-0.906821	580.663809
HLA A*0206	1:226-234	9	YQHVREDPI	0.574108	0.335010	-1.816655	0.909118	-0.907536	65.562378
HLA A*0203	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.914400	2.001388	-0.913012	821.107228
HLA B*4403	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.438960	2.525575	-0.913385	2747.641034
HLA A*2602	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-2.755485	1.840969	-0.914516	569.489090
HLA A*0250	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.943752	1.028753	-0.914999	87.852159
HLA A*0219	1:268-276	9	EMRADLVRV	1.216414	0.187070	-2.318787	1.403484	-0.915303	208.346702
HLA A*3002	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.619109	2.703152	-0.915957	4160.151107
HLA B*0702	1:140-148	9	KPANIMISA	1.205138	-0.289626	-1.834229	0.915512	-0.918717	68.269834
HLA B*0702	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-1.746264	0.826538	-0.919726	55.752472
HLA A*0206	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.360074	2.439993	-0.920081	2291.256369
HLA A*6802	1:117-125	9	EVIADACQA	1.033905	-0.225946	-1.728859	0.807959	-0.920901	53.562291
HLA B*1801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-2.959698	2.037813	-0.921885	911.376752
HLA A*0206	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.625321	2.703152	-0.922169	4220.084470
HLA B*0702	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.793946	1.870848	-0.923099	622.223598
HLA A*2301	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.721147	2.797119	-0.924028	5261.956327
HLA A*0301	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-2.450442	1.525910	-0.924532	282.125520
HLA A*0212	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-1.698504	0.773768	-0.924735	49.946354
HLA A*0206	1:348-356	9	IAINTFGGI	0.883060	0.298110	-2.107591	1.181170	-0.926421	128.112476
HLA B*1502	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.418238	2.490827	-0.927410	2619.615406
HLA A*3001	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-2.415209	1.487180	-0.928030	260.141413
HLA A*3201	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.379603	2.449598	-0.930005	2396.638902
HLA A*8001	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.623526	2.692848	-0.930678	4202.678201
HLA A*8001	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.380448	2.449598	-0.930850	2401.311048
HLA B*1502	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.338524	2.407316	-0.931208	2180.339932
HLA A*0206	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.826139	1.894713	-0.931426	670.099234
HLA A*0212	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.960913	1.028753	-0.932160	91.393030
HLA A*0203	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-1.775496	0.839877	-0.935619	59.634340
HLA A*0203	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-1.711929	0.773768	-0.938160	51.514413
HLA A*0206	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-2.387631	1.445980	-0.941651	244.135672
HLA B*1517	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-2.341807	1.398961	-0.942846	219.688278
HLA A*0201	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.946160	2.001388	-0.944772	883.405733
HLA B*1517	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-1.974728	1.028753	-0.945975	94.346990
HLA A*6802	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-2.386908	1.440103	-0.946804	243.729220
HLA B*4402	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.387285	2.439993	-0.947292	2439.413486
HLA A*2501	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.650827	2.703152	-0.947675	4475.351521
HLA A*2403	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.846796	1.894713	-0.952082	702.741811
HLA A*0206	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-1.845098	0.892112	-0.952985	69.999923
HLA A*0212	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-2.207111	1.249564	-0.957547	161.105701
HLA A*0206	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.271163	1.312789	-0.958373	186.707847
HLA A*0206	1:427-435	9	REIPDVSTL	1.524929	0.472437	-2.956343	1.997366	-0.958977	904.363199
HLA A*3301	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-2.485426	1.525910	-0.959516	305.792060
HLA B*4402	1:23-31	9	SEVHLARDL	1.447686	0.429685	-2.839874	1.877371	-0.962503	691.630618
HLA B*1517	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.072365	2.106921	-0.965444	1181.313453
HLA A*3001	1:549-557	9	SVIELQVSK	0.982858	0.255246	-2.205504	1.238104	-0.967400	160.510653
HLA A*0206	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.375374	2.407316	-0.968057	2373.414173
HLA B*1503	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-3.268909	2.297586	-0.971323	1857.415084
HLA A*0250	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.288621	2.316186	-0.972435	1943.663805
HLA A*0206	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-2.238646	1.262230	-0.976415	173.239012
HLA B*5301	1:575-583	9	EPRLRALGW	1.410483	0.250517	-2.640201	1.661000	-0.979201	436.717785
HLA A*0301	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-2.518084	1.538857	-0.979227	329.673505
HLA B*4002	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.433354	2.449598	-0.983756	2712.402415
HLA A*3002	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.417927	2.429816	-0.988111	2617.745392
HLA A*0216	1:412-420	9	AGDEITVNV	1.300588	0.029163	-2.318453	1.329751	-0.988702	208.186711
HLA A*6802	1:478-486	9	SAITNVVII	1.257201	0.311030	-2.558603	1.568231	-0.990373	361.912234
HLA A*3002	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.546256	2.554318	-0.991939	3517.679555
HLA B*3901	1:369-377	9	SSADAIATL	1.558793	0.442595	-2.997168	2.001388	-0.995779	993.499225

HLA A*0301	1:487-495	9	IVGSGPATK	0.962871	0.205808	-2.164590	1.168679	-0.995911	146.079721
HLA A*3101	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-2.361303	1.363134	-0.998169	229.775072
HLA A*6901	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-2.066038	1.067242	-0.998797	116.422905
HLA A*6802	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.411234	1.411765	-0.999469	257.771066
HLA B*1509	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.774673	2.772331	-1.002342	5952.140944
HLA B*1517	1:517-525	9	FTKFSQASV	0.794238	0.070907	-1.867935	0.865145	-1.002789	73.779304
HLA B*1501	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.046873	2.043325	-1.003548	1113.969339
HLA A*6801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-2.274175	1.270418	-1.003756	188.007256
HLA A*2902	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-3.543319	2.538765	-1.004554	3493.971984
HLA A*2603	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.267678	2.261413	-1.006265	1852.157173
HLA B*1503	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-2.265909	1.257069	-1.008840	184.462938
HLA A*0201	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.145147	2.135178	-1.009970	1396.842679
HLA A*3201	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.905364	1.894713	-1.010650	804.199420
HLA A*1101	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-2.110820	1.099547	-1.011272	129.068308
HLA A*3201	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.551106	2.538391	-1.012715	3557.178115
HLA B*1503	1:453-461	9	KQANSPSTP	0.696748	0.084681	-1.799748	0.781429	-1.018319	63.059105
HLA A*0250	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.020324	2.001388	-1.018936	1047.910174
HLA A*6901	1:392-400	9	STIPPDHVI	1.394582	0.214468	-2.631141	1.609050	-1.022092	427.701983
HLA A*2603	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.085198	2.061629	-1.023569	1216.740704
HLA B*1501	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.094944	2.070592	-1.024352	1244.353291
HLA A*2602	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-1.679163	0.654207	-1.024956	47.770835
HLA B*3501	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.798248	2.772331	-1.025917	6284.170202
HLA A*0216	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-1.824779	0.798791	-1.025988	66.800423
HLA A*0250	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-2.275739	1.249564	-1.026176	188.685865
HLA A*0201	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-2.473627	1.445980	-1.027647	297.596001
HLA A*8001	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-3.570047	2.538765	-1.031282	3715.755761
HLA A*3001	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.166829	2.135178	-1.031651	1468.346471
HLA B*1501	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.029449	1.997366	-1.032083	1070.161830
HLA B*0702	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.076246	2.043325	-1.032922	1191.918331
HLA B*3501	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.475166	2.439993	-1.035173	2986.520894
HLA A*2301	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-3.525496	2.489515	-1.035981	3353.483896
HLA B*5801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.732415	2.692848	-1.039568	5400.268698
HLA A*3001	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-1.956924	0.916314	-1.040609	90.557339
HLA A*0203	1:476-484	9	QTSAITNVV	1.187107	0.191059	-2.418879	1.378166	-1.040713	262.348987
HLA A*2902	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.737302	2.692848	-1.044455	5461.378774
HLA A*6901	1:459-467	9	STPELVGKV	0.780846	0.079303	-1.905456	0.860149	-1.045307	80.436994
HLA B*1502	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.748669	2.703152	-1.045517	5606.206706
HLA B*1801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.818181	2.772331	-1.045850	6579.319394
HLA A*0202	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.165955	2.120022	-1.045932	1465.394426
HLA A*0212	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.272723	1.226371	-1.046352	187.379738
HLA A*6802	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.075465	1.028753	-1.046711	118.977425
HLA A*2902	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.820159	2.772331	-1.047828	6609.357389
HLA B*5101	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.635255	2.585626	-1.049629	4317.722895
HLA A*6802	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-2.006319	0.956046	-1.050273	101.465692
HLA B*0702	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-2.036111	0.985326	-1.050784	108.670257
HLA A*1101	1:487-495	9	IVGSGPATK	0.962871	0.205808	-2.219897	1.168679	-1.051218	165.919262
HLA B*1503	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.427448	2.374610	-1.052838	2675.762217
HLA A*8001	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.827029	2.772331	-1.054698	6714.738906
HLA B*4402	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.611116	2.554318	-1.056799	4084.286112
HLA A*0203	1:64-72	9	AALNHPAIV	1.169288	0.295731	-2.522492	1.465019	-1.057473	333.036382
HLA A*3002	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.645823	2.585626	-1.060197	4424.077743
HLA A*6901	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-2.183696	1.120342	-1.063354	152.649696
HLA A*3201	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.200703	2.135178	-1.065526	1587.462294
HLA B*1517	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-3.466628	2.397104	-1.069523	2928.380653
HLA B*1503	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-2.325173	1.254080	-1.071092	211.432883
HLA B*1801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.657185	2.585626	-1.071559	4541.348802
HLA A*6802	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-2.562090	1.488986	-1.073104	364.829460
HLA A*2301	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.485470	2.411682	-1.073788	3058.231792
HLA A*6901	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-2.097916	1.022974	-1.074943	125.289953
HLA B*1502	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-3.849312	2.772331	-1.076980	7068.245837
HLA A*2501	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.078568	2.001388	-1.077180	1198.306155
HLA A*8001	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.569258	2.490827	-1.078431	3709.007682
HLA A*6801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-2.607205	1.525910	-1.081295	404.766639
HLA B*1503	1:478-486	9	SAITNVVII	1.257201	0.311030	-2.649730	1.568231	-1.081500	446.406377
HLA A*0216	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.310065	1.226371	-1.083694	204.204516

HLA A*0206	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.514421	2.429816	-1.084605	3269.043901
HLA A*0206	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.496926	2.411682	-1.085244	3139.977149
HLA A*3201	1:476-484	9	QTSAITNVV	1.187107	0.191059	-2.465709	1.378166	-1.087543	292.219589
HLA B*0801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-2.033320	0.944464	-1.088856	107.974078
HLA A*0202	1:46-54	9	LARDPSFYL	1.468873	0.401975	-2.959891	1.870848	-1.089043	911.781138
HLA A*0216	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-1.930624	0.839877	-1.090746	85.236089
HLA B*1502	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.162332	2.070592	-1.091740	1453.220881
HLA B*1501	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.532766	2.439993	-1.092773	3410.087571
HLA A*0211	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.095240	2.001388	-1.093852	1245.201788
HLA A*0203	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.649444	1.554751	-1.094692	446.111843
HLA B*3501	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-2.924451	1.828833	-1.095618	840.332135
HLA B*1503	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.158713	2.061629	-1.097084	1441.164058
HLA B*0702	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-1.650236	0.552387	-1.097849	44.692636
HLA A*0250	1:64-72	9	AALNHPAIV	1.169288	0.295731	-2.564674	1.465019	-1.099656	367.006988
HLA B*5301	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.590694	2.490827	-1.099867	3896.677232
HLA A*6901	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.235316	2.135178	-1.100139	1719.158946
HLA A*0203	1:459-467	9	STPELVGKV	0.780846	0.079303	-1.960298	0.860149	-1.100149	91.263582
HLA A*6901	1:79-87	9	EAETPAGPL	0.986891	0.274759	-2.363521	1.261650	-1.101871	230.951520
HLA B*1503	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-2.340712	1.236758	-1.103954	219.135140
HLA B*4801	1:579-587	9	RALGWTGML	1.320466	0.574247	-2.998864	1.894713	-1.104150	997.387362
HLA A*2601	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.367023	2.261413	-1.105611	2328.217031
HLA B*2705	1:9-17	9	DRYELGEIL	1.564982	0.473277	-3.145415	2.038259	-1.107156	1397.704416
HLA A*2603	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.515624	2.407316	-1.108307	3278.111257
HLA B*3501	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.907593	2.797119	-1.110473	8083.379545
HLA A*0216	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-2.417667	1.306673	-1.110994	261.617660
HLA B*1509	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.554855	2.439993	-1.114862	3588.024416
HLA B*4002	1:267-275	9	AEMRADLVR	1.301765	0.742764	-3.162242	2.044529	-1.117714	1452.922164
HLA A*2601	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.610275	2.490827	-1.119448	4076.383565
HLA B*1503	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.919505	2.797119	-1.122385	8308.160160
HLA A*2402	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-3.551895	2.428102	-1.123793	3563.649958
HLA A*0203	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-2.320037	1.194908	-1.125129	208.947201
HLA B*1517	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.186827	2.061629	-1.125198	1537.543317
HLA A*3201	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.232534	2.106921	-1.125613	1708.182394
HLA B*3501	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.154029	2.028058	-1.125971	1425.701312
HLA A*0101	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.534039	2.407316	-1.126723	3420.101166
HLA B*1503	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.389964	2.261413	-1.128551	2454.504504
HLA A*1101	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.055679	1.922093	-1.133586	1136.787023
HLA B*1502	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.880945	2.745346	-1.135599	7602.301900
HLA A*6901	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-1.545707	0.409720	-1.135988	35.132365
HLA A*0212	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.010090	1.873374	-1.136716	1023.504368
HLA B*1517	1:244-252	9	SADLDAVVL	1.902706	0.406606	-3.446892	2.309312	-1.137580	2798.284423
HLA B*4002	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-3.627370	2.489515	-1.137855	4240.039426
HLA A*2902	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.939302	2.800303	-1.138999	8695.641382
HLA B*5701	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.549268	2.407316	-1.141952	3542.161141
HLA A*0201	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.371312	1.226371	-1.144941	235.131989
HLA B*1503	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.272363	2.120022	-1.152341	1872.245136
HLA A*0201	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.564590	1.411765	-1.152825	366.935518
HLA B*3501	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.560316	2.407316	-1.152999	3633.419920
HLA A*6801	1:350-358	9	INTFGGITR	1.090401	0.639154	-2.884388	1.729555	-1.154833	766.280111
HLA A*0202	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-2.231795	1.075727	-1.156067	170.527568
HLA B*1501	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.195069	2.037813	-1.157256	1567.001288
HLA B*1503	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.008685	1.851066	-1.157619	1020.198565
HLA B*3501	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.598373	2.438231	-1.160141	3966.181194
HLA A*0212	1:268-276	9	EMRADLVRV	1.216414	0.187070	-2.563641	1.403484	-1.160157	366.134421
HLA A*6801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-3.590093	2.428102	-1.161991	3891.284336
HLA A*3001	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.964653	2.800303	-1.164349	9218.336639
HLA A*2602	1:255-263	9	LAKNPENRY	1.439797	1.360506	-3.969281	2.800303	-1.168978	9317.106275
HLA B*4403	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.632431	2.462765	-1.169665	4289.737185
HLA A*2902	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.611614	2.438231	-1.173383	4088.973052
HLA A*6801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.244362	2.070592	-1.173770	1755.341210
HLA A*0206	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.226325	1.049687	-1.176638	168.393374
HLA A*0301	1:249-257	9	AVVLKALAK	1.021065	0.298784	-2.501849	1.319849	-1.182000	317.577046
HLA B*1509	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-3.390697	2.208172	-1.182525	2458.650924
HLA B*1502	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-3.980972	2.797119	-1.183853	9571.325517
HLA A*6802	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-2.829405	1.645104	-1.184301	675.157203

HLA A*6801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-2.985077	1.799748	-1.185329	966.222359
HLA A*0202	1:475-483	9	NQTSAITNV	1.108161	0.235536	-2.529756	1.343697	-1.186060	338.654061
HLA B*1503	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.057587	1.870848	-1.186739	1141.791719
HLA B*1517	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.599449	2.411682	-1.187766	3976.020502
HLA A*2301	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.617746	2.429816	-1.187930	4147.118110
HLA A*0216	1:268-276	9	EMRADLVRV	1.216414	0.187070	-2.592154	1.403484	-1.188670	390.979431
HLA A*0101	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.881904	2.692848	-1.189056	7619.100497
HLA B*0702	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.019464	1.828833	-1.190631	1045.837344
HLA A*3101	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-2.429400	1.238694	-1.190706	268.782126
HLA A*0201	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-2.809693	1.618772	-1.190921	645.197575
HLA A*6801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-3.260380	2.064862	-1.195518	1821.295177
HLA B*0702	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-3.782713	2.585626	-1.197087	6063.357066
HLA A*2902	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.697619	2.500470	-1.197149	4984.475853
HLA A*6802	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.241002	2.043325	-1.197677	1741.814033
HLA B*1503	1:9-17	9	DRYELGEIL	1.564982	0.473277	-3.240306	2.038259	-1.202047	1739.027051
HLA B*3501	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.949823	2.745346	-1.204477	8908.869853
HLA B*0702	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.315424	2.106921	-1.208503	2067.397906
HLA A*3201	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.638323	2.429816	-1.208507	4348.336990
HLA A*0216	1:459-467	9	STPELVGKV	0.780846	0.079303	-2.069173	0.860149	-1.209024	117.266144
HLA A*3001	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.954681	2.745346	-1.209335	9009.098795
HLA A*6802	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.292568	2.081726	-1.210842	1961.409534
HLA A*2403	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-3.228470	2.015621	-1.212849	1692.269909
HLA B*3501	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.713483	2.500470	-1.213013	5169.912814
HLA A*0201	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-1.987927	0.773768	-1.214159	97.258475
HLA B*1503	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-3.481124	2.266682	-1.214442	3027.776762
HLA B*5701	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-3.907696	2.692848	-1.214849	8085.303903
HLA A*0202	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.534709	1.312789	-1.221920	342.538193
HLA A*0206	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-2.239012	1.014988	-1.224024	173.385277
HLA A*6901	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.286967	2.061629	-1.225338	1936.275319
HLA A*0206	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-2.192859	0.965301	-1.227558	155.904602
HLA A*2602	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.001276	2.772331	-1.228945	10029.431950
HLA B*1503	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-3.437992	2.208172	-1.229820	2741.523707
HLA A*0219	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.365017	2.135178	-1.229839	2317.485372
HLA B*1503	1:614-622	9	VNRDGIITL	1.888708	0.385349	-3.504788	2.274057	-1.230731	3197.332958
HLA A*2602	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.001281	2.769370	-1.231911	10029.540467
HLA A*6801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.002507	2.769370	-1.233138	10057.903539
HLA A*0203	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.663716	2.429816	-1.233900	4610.164560
HLA A*0250	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.283652	1.049687	-1.233965	192.155329
HLA A*3201	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.979826	2.745346	-1.234480	9546.090295
HLA A*0211	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-2.033301	0.798791	-1.234510	107.969405
HLA A*2403	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-2.206072	0.968816	-1.237257	160.720930
HLA A*2602	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.776182	2.538391	-1.237791	5972.849556
HLA A*0301	1:549-557	9	SVIELQVSK	0.982858	0.255246	-2.476804	1.238104	-1.238700	299.780648
HLA B*4601	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.729723	2.490827	-1.238896	5366.892044
HLA A*1101	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-1.992937	0.750403	-1.242534	98.386737
HLA B*5801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-3.988472	2.745346	-1.243126	9738.041988
HLA A*2301	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.653886	2.407316	-1.246570	4506.985726
HLA B*3501	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.275457	1.028753	-1.246704	188.563412
HLA B*4002	1:14-22	9	GEILGFGGM	0.948298	0.046073	-2.244515	0.994371	-1.250144	175.596037
HLA A*6801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-2.001752	0.750403	-1.251349	100.404187
HLA B*5801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.626125	2.374610	-1.251515	4227.899622
HLA B*2705	1:615-623	9	NRDGIITLR	0.950398	0.693822	-2.899701	1.644220	-1.255481	793.782458
HLA B*1801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.255089	1.997366	-1.257723	1799.240827
HLA A*0202	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.688372	2.429816	-1.258556	4879.461812
HLA B*5801	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.154649	1.894713	-1.259935	1427.738969
HLA A*0301	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.030687	2.769370	-1.261318	10732.161250
HLA B*4402	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.299753	2.037813	-1.261940	1994.127888
HLA A*0203	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-2.883593	1.618772	-1.264821	764.880216
HLA A*0203	1:143-151	9	NIMISATNA	0.971550	-0.064300	-2.172592	0.907250	-1.265342	148.796349
HLA A*6801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.758321	2.490827	-1.267494	5732.192822
HLA A*0202	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.133295	0.865145	-1.268149	135.923575
HLA A*6802	1:144-152	9	IMISATNAV	0.995514	0.289158	-2.552899	1.284672	-1.268227	357.189525
HLA A*3001	1:614-622	9	VNRDGIITL	1.888708	0.385349	-3.543343	2.274057	-1.269286	3494.161010
HLA A*0250	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-2.668587	1.398961	-1.269627	466.216196
HLA B*2705	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-2.665354	1.394783	-1.270572	462.758564

HLA A*0202	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.497582	1.226371	-1.271211	314.472331
HLA A*3201	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.042406	2.769370	-1.273037	11025.706321
HLA A*3101	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-3.070016	1.793234	-1.276781	1174.939933
HLA A*6802	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-2.811046	1.534036	-1.277010	647.211208
HLA A*6802	1:191-199	9	DSVDARSDV	0.837527	0.035965	-2.151268	0.873492	-1.277776	141.666887
HLA A*3201	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.118861	1.840969	-1.277892	1314.805336
HLA A*0206	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-2.354024	1.075727	-1.278297	225.956171
HLA A*2402	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.688691	2.407316	-1.281375	4883.053172
HLA B*1517	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.732580	2.449598	-1.282982	5402.314125
HLA A*3101	1:254-262	9	ALAKNPENR	1.033268	0.766480	-3.083051	1.799748	-1.283302	1210.739210
HLA A*6802	1:155-163	9	MDFGIARAI	1.445600	0.187062	-2.916218	1.632662	-1.283557	824.552621
HLA A*2601	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.345911	2.061629	-1.284282	2217.741838
HLA B*5801	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.286088	2.001388	-1.284700	1932.361617
HLA A*2301	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.723252	2.438231	-1.285021	5287.524318
HLA A*2902	1:345-353	9	VVTIAINTF	1.511825	1.191327	-3.989148	2.703152	-1.285996	9753.226151
HLA A*0202	1:243-251	9	LSADLDAVV	0.948699	0.148803	-2.386259	1.097502	-1.288757	243.365573
HLA A*3301	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.086502	2.797119	-1.289382	12203.981904
HLA B*3901	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.062217	2.772331	-1.289886	11540.304762
HLA A*6802	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.161824	1.870848	-1.290976	1451.523731
HLA A*1101	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-2.595133	1.303070	-1.292063	393.670668
HLA A*0301	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-2.090403	0.796898	-1.293504	123.140976
HLA A*6801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.094391	2.800303	-1.294088	12427.710434
HLA B*3901	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.430920	2.135178	-1.295743	2697.242883
HLA B*1502	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.797679	2.500470	-1.297209	6275.948392
HLA A*3301	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-3.244493	1.942822	-1.301671	1755.873078
HLA A*0206	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-3.568445	2.266682	-1.301762	3702.071575
HLA A*2501	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.072235	2.769370	-1.302866	11809.607997
HLA B*1501	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.843574	2.538391	-1.305184	6975.481700
HLA A*6801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-2.404876	1.099547	-1.305329	254.025000
HLA A*2501	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.000266	2.692848	-1.307418	10006.128077
HLA A*3101	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-2.407780	1.099547	-1.308233	255.729261
HLA B*0702	1:575-583	9	EPRLRALGW	1.410483	0.250517	-2.969622	1.661000	-1.308622	932.442737
HLA B*4501	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-1.888892	0.579907	-1.308985	77.426916
HLA A*6901	1:138-146	9	DVKPANIMI	1.366995	0.210559	-2.887691	1.577554	-1.310137	772.130894
HLA A*0301	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.118882	2.797119	-1.321763	13148.680038
HLA A*3101	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.067565	2.745346	-1.322219	11683.277870
HLA A*6901	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-2.264805	0.942253	-1.322552	183.994510
HLA B*1501	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.095815	2.772331	-1.323484	12468.520210
HLA A*6802	1:138-146	9	DVKPANIMI	1.366995	0.210559	-2.904396	1.577554	-1.326841	802.408957
HLA B*3801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.100434	2.772331	-1.328103	12601.841155
HLA B*1503	1:475-483	9	NQTSAITNV	1.108161	0.235536	-2.672187	1.343697	-1.328490	470.096229
HLA B*3501	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.759806	2.429816	-1.329990	5751.825018
HLA A*2403	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.743923	2.411682	-1.332241	5545.275745
HLA A*1101	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.130160	2.797119	-1.333040	13494.589726
HLA B*5701	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.036443	2.703152	-1.333291	10875.354629
HLA B*0702	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-2.307932	0.974301	-1.333631	203.203887
HLA B*3501	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.377479	2.043325	-1.334154	2384.946658
HLA B*1517	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.797975	2.462765	-1.335210	6280.227826
HLA B*1801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.132551	2.797119	-1.335432	13569.113059
HLA B*1503	1:226-234	9	YQHVREDPI	0.574108	0.335010	-2.247278	0.909118	-1.338159	176.716746
HLA B*7301	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-2.596796	1.257069	-1.339728	395.181397
HLA B*4601	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.769688	2.429816	-1.339872	5884.202353
HLA A*6901	1:144-152	9	IMISATNAV	0.995514	0.289158	-2.627852	1.284672	-1.343180	424.474871
HLA A*0212	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.450989	2.106921	-1.344068	2824.810747
HLA B*5701	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.089523	2.745346	-1.344177	12289.182471
HLA B*3501	1:244-252	9	SADLDAVVL	1.902706	0.406606	-3.654347	2.309312	-1.345035	4511.767190
HLA A*0206	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.899842	1.554751	-1.345091	794.040156
HLA A*0202	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.048628	2.703152	-1.345476	11184.790576
HLA B*1801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.048849	2.703152	-1.345697	11190.479819
HLA A*2603	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.146531	2.800303	-1.346228	14012.992734
HLA B*1517	1:614-622	9	VNRDGIITL	1.888708	0.385349	-3.621402	2.274057	-1.347345	4182.175013
HLA B*5301	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.149825	2.800303	-1.349522	14119.680668
HLA B*1517	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.788389	2.438231	-1.350158	6143.127087
HLA A*0250	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.781698	2.429816	-1.351882	6049.203109
HLA B*4601	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.152428	2.800303	-1.352125	14204.570420

HLA B*1801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.907475	2.554318	-1.353158	8081.193332
HLA A*2403	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.473535	2.120022	-1.353513	2975.329134
HLA A*0250	1:479-487	9	AITNVVIII	1.197409	0.357342	-2.909410	1.554751	-1.354658	811.726209
HLA A*6802	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.763067	2.407316	-1.355750	5795.177609
HLA B*4501	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-2.460282	1.104337	-1.355945	288.590490
HLA A*0211	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-2.605706	1.249564	-1.356142	403.371992
HLA A*0211	1:412-420	9	AGDEITVNV	1.300588	0.029163	-2.686425	1.329751	-1.356674	485.763240
HLA A*6802	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-2.226809	0.869990	-1.356819	168.581142
HLA B*2705	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.733834	2.374610	-1.359224	5417.943331
HLA B*1502	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-2.608953	1.249564	-1.359389	406.399091
HLA A*3201	1:392-400	9	STIPPDHVI	1.394582	0.214468	-2.968494	1.609050	-1.359445	930.024561
HLA B*5301	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.052932	2.692848	-1.360084	11296.193245
HLA B*1501	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.157559	2.797119	-1.360440	14373.395618
HLA A*0206	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-2.093758	0.732827	-1.360931	124.095964
HLA A*2602	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.180944	1.819741	-1.361203	1516.855636
HLA B*1503	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.406843	2.043325	-1.363518	2551.775912
HLA A*3201	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.738529	2.374610	-1.363919	5476.823298
HLA B*1502	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-3.904971	2.538765	-1.366206	8034.723683
HLA A*3001	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-3.795414	2.428102	-1.367313	6243.303683
HLA A*6802	1:79-87	9	EAETPAGPL	0.986891	0.274759	-2.629135	1.261650	-1.367485	425.730538
HLA A*2402	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.817664	2.449598	-1.368066	6571.493507
HLA A*2602	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.450238	2.081726	-1.368511	2819.924765
HLA A*0301	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-2.468670	1.099547	-1.369122	294.218297
HLA B*1517	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.895230	2.525575	-1.369654	7856.515669
HLA A*0202	1:585-593	9	GMLDKGADV	0.832496	0.121837	-2.326930	0.954333	-1.372597	212.290200
HLA B*4002	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-2.478932	1.104337	-1.374595	301.253588
HLA B*1517	1:63-71	9	AAALNHPAI	1.199473	0.385466	-2.959787	1.584939	-1.374849	911.564128
HLA A*0203	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-2.636136	1.261014	-1.375122	432.649563
HLA B*2705	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-2.992957	1.616917	-1.376040	983.914262
HLA A*6802	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-1.969437	0.593391	-1.376046	93.204527
HLA B*1503	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.146315	2.769370	-1.376945	14006.020065
HLA A*3002	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.751634	2.374610	-1.377024	5644.612805
HLA B*0801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.197264	1.819741	-1.377523	1574.939127
HLA A*0206	1:585-593	9	GMLDKGADV	0.832496	0.121837	-2.332193	0.954333	-1.377859	214.878415
HLA A*3101	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.752851	2.374610	-1.378241	5660.453015
HLA A*3001	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.176647	2.797119	-1.379527	15019.192912
HLA B*5301	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.000806	2.621122	-1.379684	10018.586196
HLA A*6901	1:268-276	9	EMRADLVRV	1.216414	0.187070	-2.783388	1.403484	-1.379904	607.278481
HLA A*6801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.179034	2.797119	-1.381914	15101.972403
HLA A*2603	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.154529	2.772331	-1.382197	14273.436384
HLA A*8001	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.183070	2.800303	-1.382767	15242.987292
HLA A*3201	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.822932	2.439993	-1.382939	6651.684297
HLA B*1503	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.384396	2.001388	-1.383007	2423.235116
HLA A*0211	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-2.325769	0.942253	-1.383516	211.723615
HLA A*3101	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.182262	2.797119	-1.385142	15214.646444
HLA A*3201	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.387365	2.001388	-1.385977	2439.862224
HLA B*1517	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.886988	2.500470	-1.386518	7708.821465
HLA B*4601	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.132420	2.745346	-1.387074	13565.002867
HLA A*0211	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.439649	1.049687	-1.389962	275.200259
HLA A*3201	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-3.751225	2.358694	-1.392531	5639.301914
HLA A*0206	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-2.410261	1.017549	-1.392713	257.194383
HLA B*1502	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.947215	2.554318	-1.392897	8855.532599
HLA B*5101	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.423204	2.028058	-1.395147	2649.746622
HLA A*6901	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.504257	2.106921	-1.397336	3193.426175
HLA B*1502	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.018987	2.621122	-1.397865	10446.883556
HLA A*6801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-2.195025	0.796898	-1.398127	156.684184
HLA B*1502	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.838734	2.439993	-1.398741	6898.175902
HLA A*0301	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.144684	2.745346	-1.399338	13953.533571
HLA A*3001	1:63-71	9	AAALNHPAI	1.199473	0.385466	-2.984438	1.584939	-1.399499	964.801618
HLA A*3201	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-3.889384	2.489515	-1.399869	7751.476992
HLA B*1502	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.461896	2.061629	-1.400267	2896.647620
HLA A*3201	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.627800	1.226371	-1.401429	424.424354
HLA A*2902	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.930176	2.525575	-1.404601	8514.834691
HLA B*1501	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.780829	2.374610	-1.406219	6037.106778
HLA A*0212	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.450482	2.043325	-1.407157	2821.511781

HLA A*0206	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.016419	1.609050	-1.407370	1038.530398
HLA B*5801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.029724	2.621122	-1.408602	10708.383111
HLA A*2501	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.947445	2.538391	-1.409054	8860.228774
HLA B*1503	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.859856	2.449598	-1.410258	7241.960218
HLA B*1501	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.873126	2.462765	-1.410361	7466.653986
HLA A*2403	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.910863	2.500470	-1.410393	8144.481744
HLA A*0206	1:244-252	9	SADLDAVVL	1.902706	0.406606	-3.721974	2.309312	-1.412662	5271.986117
HLA B*4002	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.938507	2.525575	-1.412932	8679.755560
HLA B*1501	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.442229	1.028753	-1.413475	276.839830
HLA B*0702	1:63-71	9	AAALNHPAI	1.199473	0.385466	-2.998652	1.584939	-1.413714	996.901862
HLA A*3001	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-2.684132	1.266360	-1.417771	483.205144
HLA B*1501	1:120-128	9	ADACQALNF	1.485501	1.040074	-3.944889	2.525575	-1.419313	8808.231006
HLA A*0101	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.216437	2.797119	-1.419318	16460.289664
HLA A*3201	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.105394	1.685171	-1.420223	1274.659567
HLA B*3901	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.450186	2.028058	-1.422128	2819.589164
HLA A*6802	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-2.105646	0.682948	-1.422698	127.539894
HLA A*6801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.196448	2.772331	-1.424117	15719.837603
HLA A*0202	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.864588	2.439993	-1.424595	7321.296537
HLA A*6901	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.832160	2.407316	-1.424844	6794.545411
HLA A*0211	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.865161	2.439993	-1.425168	7330.967124
HLA A*3001	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.800151	2.374610	-1.425541	6311.767922
HLA A*2402	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.837794	2.411682	-1.426112	6883.264695
HLA A*2601	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.198675	2.772331	-1.426344	15800.665055
HLA A*3101	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-2.729956	1.303070	-1.426885	536.977272
HLA B*1517	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-3.858291	2.429816	-1.428475	7215.914485
HLA A*0250	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-2.452684	1.022974	-1.429710	283.585343
HLA A*2601	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.230215	2.800303	-1.429912	16990.840133
HLA B*1503	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.060054	1.629324	-1.430730	1148.295990
HLA B*1501	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.051983	2.621122	-1.430861	11271.531300
HLA B*1509	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-3.288123	1.857104	-1.431019	1941.435901
HLA B*5801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.232778	2.800303	-1.432475	17091.419811
HLA B*4403	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-3.987339	2.554318	-1.433022	9712.682473
HLA A*2403	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.206570	2.772331	-1.434238	16090.503589
HLA A*3301	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.358185	1.922093	-1.436092	2281.312075
HLA A*2602	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-3.976376	2.538765	-1.437611	9470.578189
HLA A*0211	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-2.221786	0.783751	-1.438035	166.642508
HLA A*3002	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.509355	2.070592	-1.438763	3231.136187
HLA A*0211	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.467805	1.028753	-1.439052	293.633138
HLA B*5801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.208684	2.769370	-1.439315	16169.037678
HLA B*1801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-3.939964	2.500470	-1.439494	8708.917479
HLA A*0101	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.240069	2.800303	-1.439766	17380.753237
HLA B*0801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-3.249690	1.809179	-1.440511	1777.011264
HLA B*4402	1:267-275	9	AEMRADLVR	1.301765	0.742764	-3.485221	2.044529	-1.440693	3056.478557
HLA B*1502	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-3.980385	2.538391	-1.441994	9558.389314
HLA B*1501	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.313056	1.870848	-1.442208	2056.154721
HLA A*0211	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.758462	2.316186	-1.442276	5734.053755
HLA A*0216	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.443739	2.001388	-1.442351	2778.042247
HLA A*0216	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.552684	2.106921	-1.445763	3570.133577
HLA A*2601	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.215512	2.769370	-1.446142	16425.241983
HLA B*1501	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.287113	1.840969	-1.446144	1936.924881
HLA A*0203	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-2.756364	1.306673	-1.449691	570.642503
HLA B*1517	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-2.750138	1.298743	-1.451395	562.520016
HLA B*3501	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.714348	2.261413	-1.452935	5180.215531
HLA A*1101	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.945396	2.490827	-1.454569	8818.529757
HLA B*1501	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.590394	2.135178	-1.455216	3893.979850
HLA A*1101	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.148321	2.692848	-1.455473	14070.878221
HLA A*0206	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-2.762924	1.306673	-1.456250	579.327145
HLA A*0301	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.257605	2.800303	-1.457302	18096.940136
HLA B*4403	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.906959	2.449598	-1.457361	8071.581014
HLA A*2301	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.908476	2.449598	-1.458878	8099.838830
HLA A*3001	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.229705	2.769370	-1.460335	16970.905508
HLA A*8001	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.206480	2.745346	-1.461134	16087.196111
HLA A*0211	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-2.537077	1.075727	-1.461350	344.411213
HLA B*1801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.157113	2.692848	-1.464265	14358.629098
HLA A*3001	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.167864	2.703152	-1.464712	14718.522654

HLA A*0219	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.083967	1.618772	-1.465195	1213.296393
HLA B*5801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.115995	1.650328	-1.465667	1306.156110
HLA A*2501	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.238067	2.772331	-1.465736	17300.825768
HLA B*1503	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.000405	1.534036	-1.466369	1000.933266
HLA B*3501	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.929772	2.462765	-1.467007	8506.915315
HLA A*6802	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-2.542749	1.075727	-1.467022	348.938540
HLA B*0801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-2.429447	0.961636	-1.467812	268.811209
HLA A*2501	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.875743	2.407316	-1.468427	7511.788514
HLA A*3001	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.162211	2.692848	-1.469364	14528.184941
HLA B*1517	1:147-155	9	SATNAVKVM	1.243941	0.165923	-2.880384	1.409864	-1.470520	759.248655
HLA B*3901	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.909454	2.438231	-1.471223	8118.088157
HLA A*8001	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.879249	2.407316	-1.471932	7572.665682
HLA B*1801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-3.830713	2.358694	-1.472019	6771.940331
HLA A*3101	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-2.859840	1.386802	-1.473038	724.169341
HLA A*6901	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.885684	1.411765	-1.473920	768.571842
HLA B*5301	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.177436	2.703152	-1.474284	15046.518468
HLA A*2603	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.178493	2.703152	-1.475341	15083.193090
HLA B*1503	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-2.670843	1.195398	-1.475445	468.643785
HLA A*0211	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-2.876761	1.398961	-1.477801	752.941310
HLA A*0206	1:64-72	9	AALNHPAIV	1.169288	0.295731	-2.943252	1.465019	-1.478233	877.508942
HLA A*3101	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.278722	2.800303	-1.478419	18998.631578
HLA A*0206	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.345040	0.865145	-1.479894	221.329741
HLA B*1517	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.019602	2.538765	-1.480837	10461.701374
HLA A*3001	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.971781	2.490827	-1.480954	9370.891324
HLA B*0801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-3.944513	2.462765	-1.481747	8800.610056
HLA A*2603	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.251215	2.769370	-1.481845	17832.595174
HLA A*6901	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-2.369864	0.887960	-1.481904	234.349718
HLA A*0211	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.080931	1.598716	-1.482215	1204.845533
HLA B*4402	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.255037	2.772331	-1.482706	17990.248514
HLA A*6802	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.167961	1.685171	-1.482790	1472.180278
HLA B*5701	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.377606	1.894713	-1.482892	2385.643484
HLA A*1101	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.284117	2.800303	-1.483814	19236.087262
HLA B*5101	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.024062	2.538765	-1.485296	10569.675192
HLA B*1503	1:64-72	9	AALNHPAIV	1.169288	0.295731	-2.951931	1.465019	-1.486912	895.221592
HLA A*0216	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.381764	1.894713	-1.487051	2408.596942
HLA A*3301	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-3.915431	2.428102	-1.487329	8230.587817
HLA B*1517	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.485470	1.997366	-1.488104	3058.231792
HLA B*0702	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.624099	2.135178	-1.488922	4208.229454
HLA A*0301	1:40-48	9	KVLRADLAR	0.915954	0.778633	-3.186090	1.694587	-1.491503	1534.933702
HLA B*4801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.490719	1.997366	-1.493353	3095.416891
HLA A*2601	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.186463	2.692848	-1.493615	15362.529997
HLA A*6801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.239089	2.745346	-1.493743	17341.587776
HLA A*0250	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.722339	1.226371	-1.495968	527.641412
HLA B*1501	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-3.894126	2.397104	-1.497021	7836.564690
HLA B*0801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.250024	1.751011	-1.499013	1778.376896
HLA A*0301	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-2.732799	1.233662	-1.499137	540.503837
HLA B*4601	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.204737	2.703152	-1.501585	16022.749326
HLA A*2602	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.940528	2.438231	-1.502297	8720.232249
HLA A*0101	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.763884	2.261413	-1.502472	5806.098127
HLA B*1517	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.622958	2.120022	-1.502935	4197.179684
HLA A*3201	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.574328	2.070592	-1.503736	3752.562389
HLA B*3501	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.505352	2.001388	-1.503964	3201.486986
HLA B*1517	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.301393	2.797119	-1.504273	20016.700992
HLA A*0202	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.123246	1.618772	-1.504473	1328.145322
HLA B*0803	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.275344	2.769370	-1.505974	18851.406637
HLA A*2603	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-3.998452	2.490827	-1.507625	9964.425284
HLA A*0201	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.381214	1.873374	-1.507840	2405.549795
HLA A*6901	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.196418	1.685171	-1.511247	1571.874823
HLA A*2902	1:616-624	9	RDGIITLRF	1.386647	1.062951	-3.960889	2.449598	-1.511291	9138.789812
HLA A*0203	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-2.748944	1.236758	-1.512186	560.976208
HLA B*1503	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.594477	2.081726	-1.512751	3930.765221
HLA A*3001	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.285082	2.772331	-1.512751	19278.905603
HLA B*1503	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.164512	1.650328	-1.514184	1460.534942
HLA B*0803	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.314597	2.800303	-1.514294	20634.626272
HLA A*2601	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.217810	2.703152	-1.514657	16512.376133

HLA A*3101	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.219529	2.703152	-1.516377	16577.895428
HLA B*5801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.313969	2.797119	-1.516850	20604.842299
HLA B*2705	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.262631	2.745346	-1.517285	18307.569782
HLA A*6802	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-2.513902	0.995952	-1.517950	326.514117
HLA A*0203	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-2.917421	1.398961	-1.518461	826.839685
HLA B*1503	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.653943	2.135178	-1.518765	4507.570939
HLA B*1517	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-2.674151	1.154939	-1.519211	472.227133
HLA B*5101	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.319533	2.800303	-1.519230	20870.501046
HLA B*2705	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-2.668606	1.149326	-1.519280	466.236374
HLA A*2601	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.058153	2.538391	-1.519762	11432.801652
HLA A*0202	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-3.648379	2.127896	-1.520483	4450.194470
HLA A*0211	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-1.617465	0.096922	-1.520543	41.444352
HLA A*3001	1:228-236	9	HVREDPIPP	0.388485	0.064198	-1.973502	0.452683	-1.520819	94.080933
HLA A*0211	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.129932	1.609050	-1.520883	1348.752402
HLA B*3801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.291353	2.769370	-1.521984	19559.292992
HLA B*3501	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.047777	2.525575	-1.522202	11162.907941
HLA A*0203	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-2.411009	0.887960	-1.523049	257.637227
HLA B*3501	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-3.936322	2.411682	-1.524640	8636.195672
HLA A*6801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-3.933583	2.407316	-1.526267	8581.890604
HLA A*2602	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.272468	2.745346	-1.527122	18726.990574
HLA B*1503	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.400720	1.873374	-1.527346	2516.052945
HLA B*5801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.634625	2.106921	-1.527704	4311.467379
HLA A*6801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-3.394282	1.865170	-1.529112	2479.032308
HLA B*5101	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-2.504814	0.974301	-1.530513	319.752652
HLA A*2501	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.023253	2.490827	-1.532426	10550.023299
HLA A*3201	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.178341	1.645104	-1.533237	1507.790561
HLA A*3201	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.572279	2.037813	-1.534466	3734.901653
HLA B*0803	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-3.933325	2.397104	-1.536220	8576.785145
HLA A*2501	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.282639	2.745346	-1.537293	19170.741558
HLA A*2601	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.335206	2.797119	-1.538087	21637.460592
HLA A*0216	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.852007	1.312789	-1.539218	711.224897
HLA B*1509	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.310316	2.769370	-1.540946	20432.233628
HLA A*2403	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.234477	2.692848	-1.541629	17158.401242
HLA A*0101	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.080200	2.538391	-1.541810	12028.188796
HLA B*4501	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.980521	2.438231	-1.542290	9561.388954
HLA A*3201	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.604721	2.061629	-1.543092	4024.582732
HLA B*2705	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-3.903331	2.358694	-1.544637	8004.440953
HLA A*2402	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.664844	2.120022	-1.544822	4622.151547
HLA B*1501	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.130672	2.585626	-1.545046	13510.514038
HLA B*5701	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.037712	2.490827	-1.546885	10907.171690
HLA A*0211	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.628850	2.081726	-1.547124	4254.515110
HLA A*0211	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.921948	2.374610	-1.547338	8355.035979
HLA A*0250	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.030197	1.482642	-1.547555	1072.004462
HLA A*0216	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.864494	2.316186	-1.548308	7319.712412
HLA A*0203	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-2.861706	1.312789	-1.548916	727.286666
HLA B*0801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.319906	2.769370	-1.550537	20888.460997
HLA B*4402	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.350852	2.800303	-1.550548	22431.148501
HLA A*0250	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.445459	1.894713	-1.550745	2789.065214
HLA A*2402	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.323323	2.772331	-1.550991	21053.417109
HLA A*2601	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.296611	2.745346	-1.551265	19797.543221
HLA A*6802	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-1.769134	0.216497	-1.552637	58.767067
HLA B*4601	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.325992	2.772331	-1.553660	21183.202104
HLA B*1501	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.427795	1.873374	-1.554421	2677.905461
HLA A*2501	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.351554	2.797119	-1.554435	22467.461520
HLA B*5301	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-3.994867	2.439993	-1.554874	9882.502684
HLA A*6901	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.604851	1.049687	-1.555163	402.578453
HLA B*4402	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.352405	2.797119	-1.555285	22511.504457
HLA B*5701	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-2.987215	1.431809	-1.555406	970.990798
HLA A*6901	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.355743	2.800303	-1.555440	22685.227466
HLA A*2603	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.248289	2.692848	-1.555442	17712.890658
HLA B*3901	1:25-33	9	VHLARDLRL	1.381366	0.381622	-3.318643	1.762988	-1.555655	2082.777448
HLA A*0216	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.325517	2.769370	-1.556147	21160.065795
HLA B*5301	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.328529	2.772331	-1.556198	21307.331050
HLA A*0203	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-2.429654	0.873256	-1.556398	268.939213
HLA A*3001	1:138-146	9	DVKPANIMI	1.366995	0.210559	-3.134518	1.577554	-1.556964	1363.070836

HLA B*4601	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.354136	2.797119	-1.557017	22601.438982
HLA B*1503	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.664990	2.106921	-1.558069	4623.702137
HLA B*1503	1:162-170	9	AIADSGNSV	1.093291	0.318474	-2.970040	1.411765	-1.558275	933.341075
HLA A*2403	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.303829	2.745346	-1.558483	20129.311366
HLA A*3201	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.209072	1.650328	-1.558745	1618.349374
HLA A*0212	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.023844	1.465019	-1.558825	1056.436957
HLA B*5101	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-2.704112	1.144551	-1.559561	505.954624
HLA B*0801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.359916	2.800303	-1.559613	22904.236726
HLA A*6802	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.263343	2.703152	-1.560190	18337.604094
HLA A*3201	1:11-19	9	YELGEILGF	1.340749	1.097482	-3.998457	2.438231	-1.560226	9964.533098
HLA A*6901	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.330848	2.769370	-1.561478	21421.407122
HLA A*0216	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-2.178508	0.616515	-1.561993	150.837137
HLA B*3501	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.644582	2.081726	-1.562856	4411.458743
HLA B*4601	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.332326	2.769370	-1.562956	21494.424483
HLA B*0801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-3.287080	1.723131	-1.563949	1936.778186
HLA A*0301	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.336592	2.772331	-1.564261	21706.634124
HLA B*4001	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.364760	2.800303	-1.564457	23161.168267
HLA A*2402	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.066193	2.500470	-1.565722	11646.424259
HLA B*4801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.366039	2.800303	-1.565736	23229.431514
HLA B*2705	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-3.994336	2.428102	-1.566234	9870.427374
HLA B*2705	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.363482	2.797119	-1.566363	23093.105621
HLA B*0702	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.215378	1.648439	-1.566940	1642.019468
HLA A*0203	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.272012	2.703152	-1.568860	18707.346561
HLA B*1509	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.366640	2.797119	-1.569521	23261.624976
HLA A*0101	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.344365	2.772331	-1.572033	22098.590917
HLA A*6901	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.438385	0.865145	-1.573239	274.400448
HLA A*2301	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.001535	2.428102	-1.573433	10035.402119
HLA B*0702	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.342934	2.769370	-1.573564	22025.904206
HLA A*0301	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.266785	2.692848	-1.573937	18483.515995
HLA B*4001	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.343380	2.769370	-1.574011	22048.555808
HLA B*4402	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.319979	2.745346	-1.574633	20891.964423
HLA B*0702	1:235-243	9	PPSARHEGL	1.512930	0.077910	-3.165527	1.590840	-1.574687	1463.952309
HLA A*6801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.278220	2.703152	-1.575067	18976.649280
HLA B*0802	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.321976	2.745346	-1.576630	20988.255376
HLA B*1501	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.115522	2.538765	-1.576757	13047.352436
HLA B*5801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.350774	2.772331	-1.578443	22427.144307
HLA B*0802	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.378796	2.800303	-1.578493	23921.933852
HLA B*3501	1:147-155	9	SATNAVKVM	1.243941	0.165923	-2.988456	1.409864	-1.578592	973.768322
HLA A*0250	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.263956	1.685171	-1.578785	1836.353359
HLA B*1503	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.118351	2.538765	-1.579586	13132.613825
HLA A*6801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-3.224100	1.644220	-1.579879	1675.327009
HLA A*2403	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.380819	2.800303	-1.580516	24033.620086
HLA A*0201	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.136525	1.554751	-1.581773	1369.382855
HLA A*1101	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-2.790009	1.208137	-1.581871	616.607412
HLA A*2403	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.351841	2.769370	-1.582471	22482.295085
HLA A*0250	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-2.889740	1.306673	-1.583066	775.781967
HLA B*4801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.380288	2.797119	-1.583169	24004.253698
HLA A*3101	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.356634	2.772331	-1.584302	22731.787792
HLA B*4402	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.353770	2.769370	-1.584400	22582.372709
HLA A*0201	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.381759	2.797119	-1.584640	24085.684086
HLA B*1501	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.646575	2.061629	-1.584946	4431.743182
HLA B*4001	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-3.959634	2.374610	-1.585024	9112.427035
HLA B*1501	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.034695	2.449598	-1.585097	10831.669762
HLA B*0702	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.331226	2.745346	-1.585880	21440.073128
HLA B*4402	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.583383	1.997366	-1.586017	3831.623574
HLA B*0803	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.383173	2.797119	-1.586054	24164.253087
HLA A*0202	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.141261	1.554751	-1.586510	1384.399545
HLA B*3901	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.356784	2.769370	-1.587414	22739.659648
HLA B*0803	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.291269	2.703152	-1.588116	19555.484073
HLA A*3101	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.281664	2.692848	-1.588816	19127.749528
HLA B*1503	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.659586	2.070592	-1.588994	4566.527036
HLA B*3801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.174964	2.585626	-1.589339	14961.128887
HLA B*0802	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.386618	2.797119	-1.589498	24356.659269
HLA B*0802	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.359101	2.769370	-1.589731	22861.280503
HLA A*0206	1:412-420	9	AGDEITVNV	1.300588	0.029163	-2.920034	1.329751	-1.590283	831.828776

HLA A*3201	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.159385	1.568231	-1.591155	1443.395594
HLA A*0206	1:476-484	9	QTSAITNVV	1.187107	0.191059	-2.969796	1.378166	-1.591630	932.816098
HLA A*2402	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.907922	2.316186	-1.591736	8089.504091
HLA A*0206	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.361955	2.769370	-1.592586	23012.042989
HLA B*1503	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-2.914546	1.321448	-1.593097	821.382684
HLA A*6801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.132244	1.538857	-1.593387	1355.951402
HLA B*1801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.362982	2.769370	-1.593612	23066.510614
HLA A*6801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-3.345380	1.751118	-1.594262	2215.032006
HLA A*2603	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.033403	2.438231	-1.595172	10799.488690
HLA A*0203	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.368247	2.772331	-1.595916	23347.860913
HLA B*0801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.299365	2.703152	-1.596213	19923.466146
HLA A*3001	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.703714	2.106921	-1.596793	5054.917367
HLA B*3901	1:144-152	9	IMISATNAV	0.995514	0.289158	-2.881953	1.284672	-1.597282	761.997396
HLA A*1101	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.136234	1.538857	-1.597377	1368.464545
HLA B*3501	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-2.168777	0.571232	-1.597545	147.494801
HLA A*0211	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.036204	2.438231	-1.597973	10869.355169
HLA A*0250	1:614-622	9	VNRDGIITL	1.888708	0.385349	-3.872412	2.274057	-1.598355	7454.384372
HLA A*8001	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.123999	2.525575	-1.598424	13304.523827
HLA B*1509	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.344200	2.745346	-1.598854	22090.223937
HLA B*4801	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.368393	2.769370	-1.599023	23355.693406
HLA A*2501	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.400170	2.800303	-1.599866	25128.672730
HLA A*6901	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.397237	2.797119	-1.600118	24959.586886
HLA A*2403	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.221292	2.621122	-1.600170	16645.295503
HLA A*0212	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.303547	2.703152	-1.600395	20116.247925
HLA B*5301	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-2.543139	0.942253	-1.600886	349.252042
HLA B*0801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-3.348820	1.746933	-1.601887	2232.644887
HLA A*0201	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.402446	2.800303	-1.602143	25260.747698
HLA B*2705	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.403738	2.800303	-1.603435	25336.021443
HLA A*6801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-3.619917	2.015621	-1.604296	4167.900365
HLA B*1801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.350013	2.745346	-1.604667	22387.868349
HLA A*0212	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.374447	2.769370	-1.605078	23683.582052
HLA B*5101	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.475927	1.870848	-1.605079	2991.760270
HLA B*0702	1:162-170	9	AIADSGNSV	1.093291	0.318474	-3.017415	1.411765	-1.605650	1040.915306
HLA B*1509	1:9-17	9	DRYELGEIL	1.564982	0.473277	-3.645268	2.038259	-1.607009	4418.432977
HLA B*0801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-3.904792	2.297586	-1.607206	8031.420872
HLA A*3001	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.229216	2.621122	-1.608094	16951.819619
HLA A*3101	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.377922	2.769370	-1.608553	23873.839878
HLA A*0201	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.378423	2.769370	-1.609053	23901.365713
HLA B*4001	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.406518	2.797119	-1.609398	25498.689392
HLA A*6901	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.382417	2.772331	-1.610086	24122.195979
HLA B*5101	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.303406	2.692848	-1.610558	20109.719385
HLA A*0201	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.926784	2.316186	-1.610598	8448.576961
HLA B*4801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.383782	2.772331	-1.611451	24198.134834
HLA A*2601	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.719507	2.106921	-1.612586	5242.124108
HLA A*8001	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.316314	2.703152	-1.613162	20716.390129
HLA B*5701	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.382807	2.769370	-1.613437	24143.868445
HLA A*6801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.153048	2.538765	-1.614283	14224.872034
HLA A*0203	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.415063	2.800303	-1.614760	26005.363917
HLA A*0301	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.105598	2.490827	-1.614771	12752.583302
HLA A*0202	1:412-420	9	AGDEITVNV	1.300588	0.029163	-2.944685	1.329751	-1.614934	880.409534
HLA B*4601	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.170073	2.554318	-1.615755	14793.561330
HLA A*3001	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.510474	1.894713	-1.615760	3239.467431
HLA B*4001	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.361236	2.745346	-1.615890	22973.979767
HLA B*3801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.413639	2.797119	-1.616520	25920.247718
HLA B*0801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.309491	2.692848	-1.616643	20393.472263
HLA B*0802	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.389160	2.772331	-1.616829	24499.649063
HLA A*0206	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.414250	2.797119	-1.617131	25956.732044
HLA A*0201	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.389613	2.772331	-1.617282	24525.242716
HLA A*0211	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.321133	2.703152	-1.617981	20947.532589
HLA B*5801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.203849	2.585626	-1.618223	15990.017274
HLA A*0206	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-2.855014	1.236758	-1.618256	716.166978
HLA B*2705	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.323135	2.703152	-1.619982	21044.307348
HLA B*5701	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.392477	2.772331	-1.620146	24687.512696
HLA B*5701	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.417337	2.797119	-1.620218	26141.905303
HLA B*5101	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.417579	2.797119	-1.620460	26156.476118

HLA B*0702	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.420861	2.800303	-1.620558	26354.905580
HLA B*0801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.366248	2.745346	-1.620902	23240.618717
HLA B*1517	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-2.811981	1.190001	-1.621980	648.606243
HLA B*0801	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.419233	2.797119	-1.622114	26256.284620
HLA B*3901	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.419520	2.797119	-1.622400	26273.619658
HLA B*5301	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.122872	2.500470	-1.622401	13270.020166
HLA B*3901	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.938780	2.316186	-1.622594	8685.204225
HLA B*2705	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.392233	2.769370	-1.622863	24673.626705
HLA B*3801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.369375	2.745346	-1.624029	23408.568183
HLA A*0219	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.519218	1.894713	-1.624505	3305.357215
HLA A*2602	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.744915	2.120022	-1.624892	5557.949923
HLA B*1503	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-3.492448	1.866969	-1.625479	3107.766415
HLA B*2705	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.397837	2.772331	-1.625505	24994.042940
HLA B*4801	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.371205	2.745346	-1.625859	23507.427162
HLA B*0801	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.398269	2.772331	-1.625938	25018.934887
HLA A*3201	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.423115	2.797119	-1.625995	26491.992337
HLA A*6802	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.426533	2.800303	-1.626230	26701.343969
HLA B*1509	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.426728	2.800303	-1.626425	26713.336120
HLA A*6802	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.424896	2.797119	-1.627776	26600.850988
HLA A*0202	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.213400	1.585464	-1.627936	1634.556870
HLA A*0301	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.331177	2.703152	-1.628025	21437.637509
HLA B*1501	1:614-622	9	VNRDGIITL	1.888708	0.385349	-3.902250	2.274057	-1.628193	7984.546274
HLA A*6901	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.374137	2.745346	-1.628791	23666.675516
HLA A*3201	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.247834	1.618772	-1.629062	1769.432857
HLA B*5301	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-2.773727	1.144551	-1.629176	593.918441
HLA B*3801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.332410	2.703152	-1.629258	21498.611059
HLA A*6901	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.332514	2.703152	-1.629362	21503.729092
HLA A*2403	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.078983	2.449598	-1.629385	11994.529116
HLA B*0802	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.332610	2.703152	-1.629458	21508.499266
HLA A*0212	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.375049	2.745346	-1.629703	23716.404917
HLA A*0212	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.430156	2.800303	-1.629853	26925.019549
HLA A*6801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.323027	2.692848	-1.630179	21039.071021
HLA B*0702	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.427767	2.797119	-1.630647	26777.288705
HLA B*1801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.042472	2.411682	-1.630790	11027.376587
HLA A*0212	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.428575	2.797119	-1.631455	26827.167687
HLA B*7301	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-2.885924	1.254080	-1.631844	768.996064
HLA B*4001	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.335094	2.703152	-1.631941	21631.842621
HLA A*6802	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.404298	2.772331	-1.631966	25368.663939
HLA A*0203	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.430436	2.797119	-1.633316	26942.358833
HLA A*0301	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.172098	2.538391	-1.633707	14862.709611
HLA A*0203	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.008870	2.374610	-1.634260	10206.336236
HLA A*0216	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.431434	2.797119	-1.634315	27004.376050
HLA A*0219	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.431664	2.797119	-1.634545	27018.696733
HLA A*6901	1:244-252	9	SADLDAVVL	1.902706	0.406606	-3.943907	2.309312	-1.634595	8788.335161
HLA A*3201	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.632045	1.997366	-1.634679	4285.932925
HLA A*0219	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.435196	2.800303	-1.634893	27239.283054
HLA A*2402	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-3.932939	2.297586	-1.635353	8569.179009
HLA A*0219	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.407859	2.772331	-1.635528	25577.577817
HLA A*0216	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.076704	2.439993	-1.636711	11931.751575
HLA A*0301	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.898637	2.261413	-1.637224	7918.387196
HLA A*6802	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.406793	2.769370	-1.637423	25514.834076
HLA B*1801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-2.222298	0.584529	-1.637769	166.839155
HLA B*5301	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.407392	2.769370	-1.638022	25550.056633
HLA A*0203	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.078104	2.439993	-1.638111	11970.285137
HLA A*6901	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-3.667194	2.028437	-1.638757	4647.224635
HLA B*5301	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.437399	2.797119	-1.640280	27377.859446
HLA B*4001	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.413757	2.772331	-1.641425	25927.259949
HLA A*2902	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.131480	2.489515	-1.641965	13535.680540
HLA B*1501	1:45-53	9	DLARDPSFY	1.045970	1.215443	-3.903909	2.261413	-1.642496	8015.100616
HLA B*5801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.762564	2.120022	-1.642542	5788.472320
HLA A*0202	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.050334	2.407316	-1.643017	11228.806111
HLA A*2301	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.389397	2.745346	-1.644051	24513.039299
HLA A*2602	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.441325	2.797119	-1.644206	27626.475277
HLA B*4402	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.347630	2.703152	-1.644478	22265.393075
HLA B*0702	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.347818	2.703152	-1.644666	22275.031425

HLA A*0101	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.348119	2.703152	-1.644967	22290.461464
HLA A*2403	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.780434	2.135178	-1.645257	6031.622377
HLA A*0212	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.417871	2.772331	-1.645539	26174.028455
HLA B*0803	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.418042	2.772331	-1.645711	26184.367194
HLA A*0250	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-1.746828	0.100651	-1.646177	55.824906
HLA B*5101	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.349435	2.703152	-1.646283	22358.093658
HLA A*0216	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.349489	2.703152	-1.646337	22360.875792
HLA B*1517	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.419165	2.772331	-1.646834	26252.165679
HLA B*1509	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.350346	2.703152	-1.647194	22405.073412
HLA B*5401	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.447951	2.800303	-1.647648	28051.173006
HLA A*0201	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.393236	2.745346	-1.647890	24730.689225
HLA B*1517	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.102979	1.454961	-1.648018	1267.590394
HLA B*1517	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.333590	1.685171	-1.648419	2155.709771
HLA A*6901	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.691920	2.043325	-1.648595	4919.485058
HLA B*0801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-2.464427	0.815296	-1.649130	291.357705
HLA B*1517	1:243-251	9	LSADLDAVV	0.948699	0.148803	-2.747507	1.097502	-1.650004	559.121970
HLA B*1509	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.343148	2.692848	-1.650300	22036.750226
HLA A*8001	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.205160	2.554318	-1.650842	16038.359559
HLA A*0211	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-2.267775	0.616515	-1.651259	185.256994
HLA B*3901	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.397143	2.745346	-1.651798	24954.186327
HLA A*0211	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.421209	2.769370	-1.651840	26376.015443
HLA A*0216	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.733811	2.081726	-1.652085	5417.650234
HLA A*2603	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.734041	2.081726	-1.652315	5420.523267
HLA A*3101	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-3.288325	1.635751	-1.652574	1942.339365
HLA A*0201	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.357014	2.703152	-1.653862	22751.718710
HLA A*0250	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.192496	2.538391	-1.654106	15577.444815
HLA B*4501	1:23-31	9	SEVHLARDL	1.447686	0.429685	-3.531793	1.877371	-1.654422	3402.458564
HLA A*3101	1:145-153	9	MISATNAVK	0.938735	0.280828	-2.873993	1.219563	-1.654430	748.158186
HLA A*0203	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.423909	2.769370	-1.654539	26540.478387
HLA A*0219	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.424513	2.769370	-1.655143	26577.404380
HLA B*1503	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.300387	1.645104	-1.655284	1997.042779
HLA A*0212	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.095411	2.439993	-1.655418	12456.923636
HLA A*0202	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.428563	2.772331	-1.656232	26826.442037
HLA A*1101	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.428676	2.772331	-1.656345	26833.409089
HLA A*6802	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.727406	2.070592	-1.656814	5338.340450
HLA B*3801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.457293	2.800303	-1.656990	28661.081829
HLA B*1801	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.457333	2.800303	-1.657029	28663.717856
HLA B*1502	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.055470	2.397104	-1.658365	11362.386475
HLA A*0203	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.403896	2.745346	-1.658550	25345.206467
HLA A*0211	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.142347	1.482642	-1.659705	1387.863998
HLA B*5401	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.488755	1.828833	-1.659922	3081.448960
HLA A*2603	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.071991	2.411682	-1.660309	11802.965444
HLA A*3101	1:372-380	9	DAIATLQNR	1.011737	0.626562	-3.299043	1.638299	-1.660744	1990.872569
HLA A*3101	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-3.603805	1.942822	-1.660982	4016.100390
HLA B*1503	1:521-529	9	SQASVDSPR	0.518283	0.661153	-2.840457	1.179436	-1.661021	692.559168
HLA A*3001	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.663543	2.001388	-1.662154	4608.319334
HLA B*4402	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.113135	2.449598	-1.663537	12975.835076
HLA A*0216	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.463850	2.800303	-1.663547	29097.119101
HLA B*0702	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.070863	2.407316	-1.663547	11772.355891
HLA B*0702	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.357395	2.692848	-1.664547	22771.667103
HLA B*0801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-3.059537	1.394783	-1.664754	1146.930129
HLA A*2402	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.103305	2.438231	-1.665074	12685.426453
HLA A*2602	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.077940	2.411682	-1.666258	11965.752941
HLA B*0802	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.359150	2.692848	-1.666302	22863.877867
HLA A*3001	1:487-495	9	IVGSGPATK	0.962871	0.205808	-2.836026	1.168679	-1.667347	685.528878
HLA A*0216	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.097257	2.429816	-1.667441	12510.005405
HLA A*0206	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.288731	2.621122	-1.667609	19441.560765
HLA B*2705	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.105861	2.438231	-1.667630	12760.312530
HLA B*5801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.168109	2.500470	-1.667638	14726.806043
HLA B*3901	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.787765	2.120022	-1.667742	6134.293298
HLA B*2705	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-3.659210	1.991397	-1.667813	4562.576041
HLA B*1501	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.100775	1.431809	-1.668966	1261.174329
HLA A*0219	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.415037	2.745346	-1.669691	26003.816416
HLA A*6901	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.134753	1.465019	-1.669735	1363.808442
HLA B*1517	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.110039	2.439993	-1.670046	12883.643402

HLA B*4002	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-2.739293	1.069099	-1.670193	548.646683
HLA B*5101	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.442754	2.772331	-1.670423	27717.494236
HLA A*1101	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-3.120337	1.449604	-1.670733	1319.279866
HLA A*2402	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.364916	2.692848	-1.672068	23169.439501
HLA B*2705	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.365017	2.692848	-1.672169	23174.829924
HLA B*1501	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-3.969972	2.297586	-1.672385	9331.936993
HLA B*1502	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.135183	2.462765	-1.672417	13651.578925
HLA B*1501	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.162080	2.489515	-1.672565	14523.784239
HLA B*0801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.173132	2.500470	-1.672661	14898.130220
HLA B*4402	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.365740	2.692848	-1.672892	23213.477077
HLA B*4402	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.295138	2.621122	-1.674016	19730.503708
HLA A*3001	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-2.208013	0.532852	-1.675161	161.440730
HLA B*3901	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.477378	2.800303	-1.677075	30017.763136
HLA A*0201	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.021175	1.343697	-1.677478	1049.964391
HLA A*0202	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.216207	2.538391	-1.677817	16451.565240
HLA A*3001	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.543524	0.865145	-1.678379	349.562044
HLA B*5301	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.424073	2.745346	-1.678727	26550.530964
HLA A*0203	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.676554	1.997366	-1.679188	4748.473448
HLA A*3201	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.168295	1.488986	-1.679308	1473.311648
HLA B*0702	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.451807	2.772331	-1.679475	28301.309554
HLA A*0202	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.278523	1.598716	-1.679807	1898.991674
HLA B*4402	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.170994	2.490827	-1.680167	14824.966977
HLA B*7301	1:9-17	9	DRYELGEIL	1.564982	0.473277	-3.718887	2.038259	-1.680628	5234.642594
HLA A*6802	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-2.623280	0.942253	-1.681027	420.029591
HLA A*0202	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-2.696960	1.014988	-1.681972	497.690943
HLA B*4801	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.385135	2.703152	-1.681983	24273.656154
HLA A*2902	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-3.998269	2.316186	-1.682083	9960.221469
HLA A*0216	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.165414	1.482642	-1.682772	1463.572207
HLA A*6802	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.428932	2.745346	-1.683586	26849.236824
HLA B*5701	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.554541	1.870848	-1.683693	3585.424310
HLA B*1517	1:433-441	9	STLTYAEAV	1.049463	0.176908	-2.910608	1.226371	-1.684237	813.968890
HLA A*6901	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.377643	2.692848	-1.684795	23858.475400
HLA A*2301	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.125301	2.439993	-1.685308	13344.458344
HLA A*2902	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.306644	2.621122	-1.685522	20260.194053
HLA B*3501	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-2.703313	1.017549	-1.685764	505.024846
HLA B*0803	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.431272	2.745346	-1.685926	26994.297674
HLA A*3101	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.177145	2.490827	-1.686317	15036.428253
HLA A*6801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.224783	2.538391	-1.686392	16779.647932
HLA B*5101	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.455775	2.769370	-1.686405	28561.092237
HLA A*0206	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.173736	1.487180	-1.686556	1491.887343
HLA A*0202	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.090917	1.403484	-1.687433	1232.868292
HLA A*0212	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.380627	2.692848	-1.687779	24022.960875
HLA A*2301	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-3.986991	2.297586	-1.689405	9704.908994
HLA A*6802	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.033289	1.343697	-1.689592	1079.663738
HLA B*4002	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-3.549165	1.859413	-1.689752	3541.318083
HLA A*0202	1:244-252	9	SADLDAVVL	1.902706	0.406606	-3.999171	2.309312	-1.689859	9980.934315
HLA B*0802	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.311141	2.621122	-1.690019	20471.068665
HLA B*1503	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-3.681535	1.991397	-1.690138	4803.247021
HLA A*0203	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.229616	2.538391	-1.691225	16967.417059
HLA B*3901	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.586061	1.894713	-1.691348	3855.327264
HLA A*6801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-3.443692	1.752221	-1.691471	2777.741686
HLA A*0203	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-2.883020	1.190001	-1.693019	763.871230
HLA B*0802	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.278821	2.585626	-1.693195	19002.948849
HLA B*3501	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.231695	2.538391	-1.693304	17048.847622
HLA A*2301	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.386451	2.692848	-1.693603	24347.305621
HLA B*3501	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.010721	2.316186	-1.694535	10249.938645
HLA A*0202	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.492215	2.797119	-1.695096	31060.992171
HLA A*6801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-3.389691	1.694587	-1.695104	2452.964670
HLA B*3801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.388500	2.692848	-1.695652	24462.433509
HLA A*0219	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.008469	1.312789	-1.695679	1019.690928
HLA A*0203	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.107440	2.411682	-1.695758	12806.786377
HLA B*4801	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.389792	2.692848	-1.696944	24535.328381
HLA A*0216	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.469590	2.772331	-1.697259	29484.229538
HLA A*0201	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-2.429311	0.732039	-1.697272	268.726877
HLA A*2501	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.758908	2.061629	-1.697279	5739.950699

HLA B*1517	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.779711	2.081726	-1.697984	6021.580580
HLA A*3201	1:144-152	9	IMISATNAV	0.995514	0.289158	-2.983484	1.284672	-1.698813	962.684838
HLA B*4601	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.320358	2.621122	-1.699236	20910.169087
HLA A*6801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-2.868247	1.168679	-1.699568	738.323330
HLA B*0702	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.320806	2.621122	-1.699684	20931.786498
HLA B*1517	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.189324	2.489515	-1.699809	15464.091711
HLA A*0250	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.403452	2.703152	-1.700300	25319.305022
HLA A*3001	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.286506	2.585626	-1.700880	19342.213146
HLA A*0206	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.738782	2.037813	-1.700969	5480.024166
HLA A*0216	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-2.896003	1.194908	-1.701096	787.051965
HLA A*0201	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.394284	2.692848	-1.701436	24790.431738
HLA B*4402	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.060361	2.358694	-1.701667	11491.088908
HLA A*3201	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.109400	2.407316	-1.702083	12864.699193
HLA A*0216	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.011468	2.309312	-1.702156	10267.587249
HLA B*1801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.241069	2.538765	-1.702304	17420.855335
HLA B*0803	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.395938	2.692848	-1.703090	24885.027656
HLA A*0101	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.258479	2.554318	-1.704162	18133.396515
HLA A*8001	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.142744	2.438231	-1.704512	13891.320357
HLA A*2601	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-2.359724	0.654207	-1.705517	228.941254
HLA A*2402	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.326696	2.621122	-1.705574	21217.609650
HLA B*0801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.326844	2.621122	-1.705722	21224.842332
HLA A*0206	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.392229	1.685171	-1.707057	2467.338508
HLA B*1501	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.352198	1.645104	-1.707094	2250.081305
HLA B*0702	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.016900	2.309312	-1.707588	10396.817276
HLA A*2403	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.246180	2.538391	-1.707789	17627.048693
HLA A*3301	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.508253	2.800303	-1.707950	32229.451075
HLA B*4402	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.197505	2.489515	-1.707990	15758.153384
HLA B*3901	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.411175	2.703152	-1.708022	25773.567590
HLA A*3001	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-2.458858	0.750403	-1.708455	287.645926
HLA A*2601	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.330315	2.621122	-1.709193	21395.116820
HLA B*1501	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.791293	2.081726	-1.709567	6184.341501
HLA B*4001	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.403297	2.692848	-1.710449	25310.266310
HLA B*5301	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.582171	1.870848	-1.711323	3820.942502
HLA B*1503	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.310189	1.598716	-1.711473	2042.628652
HLA A*1101	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.415890	2.703152	-1.712738	26054.932619
HLA B*3901	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.299353	2.585626	-1.713727	19922.927235
HLA A*3101	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.584600	1.870848	-1.713752	3842.376079
HLA A*0301	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.299475	2.585626	-1.713850	19928.532626
HLA A*3001	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-2.740543	1.026649	-1.713894	550.227996
HLA B*4403	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.486363	2.772331	-1.714031	30645.220955
HLA B*4601	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.300556	2.585626	-1.714930	19978.187515
HLA A*3001	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.269484	2.554318	-1.715167	18598.766666
HLA A*0219	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.408287	2.692848	-1.715439	25602.773897
HLA A*2301	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.487963	2.772331	-1.715631	30758.330298
HLA B*5401	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-2.860836	1.144551	-1.716286	725.832342
HLA B*1503	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.301393	1.584939	-1.716454	2001.672155
HLA A*0219	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.419889	2.703152	-1.716737	26295.944705
HLA A*0202	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.486788	2.769370	-1.717418	30675.243143
HLA A*0203	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.613296	1.894713	-1.718583	4104.842325
HLA A*0216	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.464524	2.745346	-1.719178	29142.331489
HLA B*2705	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.131687	2.411682	-1.720004	13542.126009
HLA A*2501	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.305748	2.585626	-1.720123	20218.477401
HLA A*0211	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.520987	2.800303	-1.720684	33188.461268
HLA A*2501	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-3.848908	2.127896	-1.721012	7061.671887
HLA A*6901	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.307207	2.585626	-1.721582	20286.516434
HLA A*3201	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.493928	2.772331	-1.721597	31183.732671
HLA A*1101	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.149872	2.428102	-1.721770	14121.208469
HLA A*0211	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-2.912248	1.190001	-1.722246	817.048330
HLA B*2705	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.343533	2.621122	-1.722411	22056.310388
HLA B*0801	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.163198	2.439993	-1.723205	14561.232737
HLA B*3901	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.805456	2.081726	-1.723730	6389.342353
HLA A*3201	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.345476	2.621122	-1.724354	22155.210917
HLA A*6802	1:348-356	9	IAINTFGGI	0.883060	0.298110	-2.905993	1.181170	-1.724823	805.366235
HLA A*2603	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.470461	2.745346	-1.725116	29543.465843
HLA A*0211	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.259271	1.534036	-1.725235	1816.650491

HLA B*2705	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-3.534556	1.809179	-1.725377	3424.174110
HLA A*0203	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-2.098884	0.373369	-1.725515	125.569520
HLA A*3001	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.264188	2.538391	-1.725798	18373.352480
HLA A*2602	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.226592	2.500470	-1.726122	16849.691265
HLA B*4403	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.216339	2.489515	-1.726824	16456.550059
HLA A*0212	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.165125	2.438231	-1.726894	14625.971442
HLA A*1101	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.312682	2.585626	-1.727056	20543.847246
HLA B*0702	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.755501	2.028058	-1.727444	5695.100717
HLA A*0250	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.497159	2.769370	-1.727789	31416.560793
HLA A*0203	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.420854	2.692848	-1.728007	26354.477852
HLA A*0101	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.219013	2.490827	-1.728185	16558.176558
HLA A*0206	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.601742	1.873374	-1.728368	3997.069617
HLA B*4501	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.726340	1.997366	-1.728973	5325.245096
HLA B*3901	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.422567	2.692848	-1.729719	26458.620107
HLA A*2301	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.530820	2.800303	-1.730517	33948.431390
HLA A*2902	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.142283	2.411682	-1.730601	13876.598665
HLA A*1101	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-2.955845	1.224706	-1.731139	903.326582
HLA A*0206	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.533132	2.800303	-1.732829	34129.631992
HLA A*1101	1:521-529	9	SQASVDSPR	0.518283	0.661153	-2.912506	1.179436	-1.733070	817.534690
HLA A*0101	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.355283	2.621122	-1.734161	22661.186199
HLA A*0101	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.273053	2.538765	-1.734288	18752.233997
HLA B*4402	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.146277	2.411682	-1.734595	14004.807781
HLA B*1517	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.778014	2.043325	-1.734689	5998.106522
HLA B*5101	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.174903	2.439993	-1.734910	14959.024645
HLA B*4002	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.289556	2.554318	-1.735238	19478.512855
HLA A*0211	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.532836	2.797119	-1.735716	34106.375591
HLA B*5101	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.481546	2.745346	-1.736200	30307.234740
HLA B*1801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.358154	2.621122	-1.737032	22811.492967
HLA A*6802	1:143-151	9	NIMISATNA	0.971550	-0.064300	-2.644552	0.907250	-1.737302	441.115303
HLA A*0301	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.359178	2.621122	-1.738056	22865.362208
HLA B*5301	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.293038	2.554318	-1.738720	19635.308681
HLA A*2603	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.535873	2.797119	-1.738754	34345.785592
HLA A*0301	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.293183	2.554318	-1.738866	19641.895726
HLA A*0203	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.146230	2.407316	-1.738914	14003.292574
HLA A*6802	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-2.865361	1.126330	-1.739032	733.434651
HLA B*1503	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.558831	1.819741	-1.739090	3621.018289
HLA A*0216	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.277938	2.538391	-1.739547	18964.333889
HLA A*2601	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.169443	2.429816	-1.739627	14772.128422
HLA A*3301	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.821743	2.081726	-1.740017	6633.500849
HLA A*2402	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.540387	2.800303	-1.740084	34704.581780
HLA B*2705	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.240698	2.500470	-1.740228	17405.971003
HLA A*2603	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.876096	2.135178	-1.740918	7517.886680
HLA B*5801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.876406	2.135178	-1.741228	7523.257160
HLA A*0250	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.542017	2.800303	-1.741714	34835.123754
HLA B*1503	1:147-155	9	SATNAVKVM	1.243941	0.165923	-3.151604	1.409864	-1.741740	1417.763792
HLA A*6802	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.434641	2.692848	-1.741793	27204.527931
HLA A*2403	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-3.599181	1.857104	-1.742077	3973.569137
HLA A*1101	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.296529	2.554318	-1.742212	19793.794988
HLA A*2602	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-3.870382	2.127896	-1.742486	7419.622808
HLA A*0206	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.514820	2.772331	-1.742488	32720.484018
HLA A*6901	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.363713	2.621122	-1.742591	23105.352119
HLA A*0211	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.514961	2.772331	-1.742629	32731.106593
HLA A*0211	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.281046	2.538391	-1.742655	19100.553901
HLA B*1801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.205583	2.462765	-1.742817	16053.985000
HLA A*3001	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.268885	2.525575	-1.743310	18573.126952
HLA B*3501	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.102163	2.358694	-1.743469	12652.117660
HLA B*5401	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.540676	2.797119	-1.743556	34727.682461
HLA A*3002	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.365158	2.621122	-1.744036	23182.353540
HLA A*8001	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.366694	2.621122	-1.745572	23264.519541
HLA A*3201	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.271272	2.525575	-1.745697	18675.494238
HLA A*0250	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.827588	2.081726	-1.745862	6723.390060
HLA B*5801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.301585	2.554318	-1.747268	20025.582588
HLA A*0301	1:254-262	9	ALAKNPENR	1.033268	0.766480	-3.548277	1.799748	-1.748529	3534.083706
HLA A*3201	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.211532	2.462765	-1.748766	16275.402918
HLA A*3001	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-2.766476	1.017549	-1.748928	584.085331

HLA A*3001	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.347833	1.598716	-1.749117	2227.577734
HLA A*8001	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.238833	2.489515	-1.749318	17331.364839
HLA B*0801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-3.410625	1.661000	-1.749626	2574.098754
HLA B*5301	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.187887	2.438231	-1.749655	15412.977053
HLA A*3201	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.831507	2.081726	-1.749781	6784.334440
HLA B*0801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.336590	2.585626	-1.750964	21706.516693
HLA A*2601	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.752381	2.001388	-1.750993	5654.331842
HLA A*0250	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.191021	2.439993	-1.751028	15524.611641
HLA B*5301	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-2.736445	0.985326	-1.751119	545.061092
HLA B*5401	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.523656	2.772331	-1.751325	33393.053437
HLA B*0801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.163273	2.411682	-1.751591	14563.753745
HLA A*3001	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.290902	2.538765	-1.752137	19538.987327
HLA A*3001	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.242597	2.489515	-1.753081	17482.222350
HLA A*0211	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-2.593775	0.839877	-1.753898	392.441615
HLA A*2402	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.499297	2.745346	-1.753951	31571.605824
HLA A*0206	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.254887	2.500470	-1.754416	17984.020777
HLA A*0211	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.029273	2.274057	-1.755216	10697.266102
HLA A*0201	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.185156	2.429816	-1.755340	15316.390494
HLA B*1517	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.309728	2.554318	-1.755411	20404.618277
HLA B*4402	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.341994	2.585626	-1.756368	21978.292659
HLA A*2601	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.257361	2.500470	-1.756890	18086.761146
HLA A*0250	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-2.900218	1.143250	-1.756968	794.727761
HLA B*1509	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.295876	2.538765	-1.757111	19764.048501
HLA A*2402	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.526649	2.769370	-1.757280	33623.999949
HLA A*0216	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.195536	2.438231	-1.757305	15686.875689
HLA A*0203	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.356033	1.598716	-1.757316	2270.035092
HLA A*3101	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.378463	2.621122	-1.757341	23903.563977
HLA A*2501	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.379308	2.621122	-1.758186	23950.162967
HLA A*3201	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.559260	2.800303	-1.758957	36246.011856
HLA A*0206	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.222574	2.462765	-1.759809	16694.535054
HLA A*0211	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.070643	2.309312	-1.761331	11766.370822
HLA A*0201	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.656231	1.894713	-1.761518	4531.385062
HLA A*0216	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.160513	1.398961	-1.761553	1447.148597
HLA B*5101	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.383126	2.621122	-1.762004	24161.638710
HLA B*1509	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.843908	2.081726	-1.762182	6980.842354
HLA A*0219	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.192153	2.429816	-1.762337	15565.145924
HLA A*2501	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.262842	2.500470	-1.762372	18316.485725
HLA B*5701	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.348711	2.585626	-1.763085	22320.870597
HLA B*7301	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.535664	2.772331	-1.763333	34329.252759
HLA B*0803	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.288999	2.525575	-1.763423	19453.554606
HLA A*0250	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.561241	2.797119	-1.764121	36411.690622
HLA A*0201	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.386068	2.621122	-1.764946	24325.845340
HLA A*2601	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.319401	2.554318	-1.765084	20864.179206
HLA B*1801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.256085	2.490827	-1.765258	18033.707985
HLA A*3201	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.266054	2.500470	-1.765584	18452.444078
HLA B*4403	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.177699	2.411682	-1.766017	15055.638030
HLA B*4001	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.388079	2.621122	-1.766957	24438.756284
HLA B*4601	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.267818	2.500470	-1.767348	18527.565661
HLA A*0206	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.513513	2.745346	-1.768168	32622.211998
HLA A*8001	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.197985	2.429816	-1.768169	15775.553956
HLA B*4403	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.513542	2.745346	-1.768196	32624.329857
HLA B*5401	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-2.743277	0.974301	-1.768976	553.703775
HLA B*5401	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.461914	2.692848	-1.769066	28967.700130
HLA A*6802	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.390847	2.621122	-1.769725	24594.998122
HLA A*0216	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.462713	2.692848	-1.769865	29021.031259
HLA A*3002	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.771403	2.001388	-1.770015	5907.486304
HLA A*6802	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.145215	2.374610	-1.770605	13970.604082
HLA B*4403	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.568226	2.797119	-1.771106	37002.056584
HLA A*2403	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.297452	2.525575	-1.771877	19835.923075
HLA B*1503	1:578-586	9	LRALGWTGM	0.993924	0.288236	-3.054175	1.282160	-1.772016	1132.857898
HLA B*1801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-3.810818	2.038259	-1.772559	6468.710032
HLA B*2705	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.262079	2.489515	-1.772563	18284.309719
HLA A*2301	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.542292	2.769370	-1.772923	34857.179870
HLA A*3101	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-2.570083	0.796898	-1.773185	371.606112
HLA A*3001	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.236617	2.462765	-1.773852	17243.173586

HLA A*0203	1:348-356	9	IAINTFGGI	0.883060	0.298110	-2.955535	1.181170	-1.774365	902.681742
HLA A*3001	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.239409	1.465019	-1.774390	1735.436928
HLA B*4001	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.186124	2.411682	-1.774442	15350.566877
HLA B*2705	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.171713	2.397104	-1.774608	14849.528939
HLA B*4001	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.360694	2.585626	-1.775068	22945.287475
HLA B*1503	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.697342	1.922093	-1.775249	4981.294944
HLA A*0206	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.343608	1.568231	-1.775378	2206.015168
HLA A*1101	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-3.718417	1.942822	-1.775595	5228.981889
HLA A*1101	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.846220	2.070592	-1.775628	7018.102775
HLA B*1801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.050164	2.274057	-1.776107	11224.433207
HLA B*1509	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.397611	2.621122	-1.776489	24981.065670
HLA B*5801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.226235	2.449598	-1.776637	16835.841406
HLA A*6901	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.315520	2.538765	-1.776755	20678.543940
HLA A*0211	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-2.773454	0.995952	-1.777502	593.545846
HLA A*0250	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.087000	2.309312	-1.777688	12217.986638
HLA A*3001	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.278497	2.500470	-1.778026	18988.767212
HLA A*0211	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.523546	2.745346	-1.778200	33384.563838
HLA A*0202	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.578714	2.800303	-1.778411	37906.524193
HLA A*0202	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.190499	2.411682	-1.778817	15505.977846
HLA A*0206	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.471695	2.692848	-1.778847	29627.494225
HLA A*0202	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.225274	1.445980	-1.779294	1679.864810
HLA B*5101	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-3.526680	1.746933	-1.779748	3362.639929
HLA A*0206	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.364759	1.584939	-1.779820	2316.106675
HLA A*0201	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.244958	1.465019	-1.779940	1757.754903
HLA A*3201	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.472928	2.692848	-1.780081	29711.761602
HLA A*1101	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.318530	2.538391	-1.780139	20822.345357
HLA B*5401	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.365853	2.585626	-1.780227	23219.505812
HLA B*4801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.401462	2.621122	-1.780340	25203.552909
HLA A*0203	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.402030	2.621122	-1.780908	25236.570837
HLA B*4001	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.335274	2.554318	-1.780957	21640.855490
HLA B*3901	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.320092	2.538765	-1.781327	20897.390242
HLA A*0203	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.466543	1.685171	-1.781372	2927.810389
HLA B*4402	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.320557	2.538765	-1.781792	20919.786642
HLA A*0212	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.403548	2.621122	-1.782426	25324.921605
HLA A*0202	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.043603	1.261014	-1.782588	1105.612027
HLA A*3101	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.191007	2.407316	-1.783690	15524.107731
HLA B*1801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-3.661094	1.877371	-1.783724	4582.414838
HLA B*4601	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.191895	2.407316	-1.784578	15555.886051
HLA A*6802	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.323106	2.538391	-1.784716	21042.941224
HLA A*3001	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.192492	2.407316	-1.785175	15577.276271
HLA B*3801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.339635	2.554318	-1.785318	21859.240542
HLA B*4601	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.324039	2.538391	-1.785649	21088.184263
HLA B*1509	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.371482	2.585626	-1.785857	23522.438316
HLA A*0212	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-2.980839	1.194908	-1.785931	956.838435
HLA B*7301	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.583514	2.797119	-1.786394	38327.806195
HLA B*1509	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.341195	2.554318	-1.786878	21937.903772
HLA B*4001	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.287596	2.500470	-1.787126	19390.826737
HLA B*4801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.198957	2.411682	-1.787275	15810.925967
HLA B*0802	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.227489	2.439993	-1.787496	16884.548465
HLA B*5801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.326309	2.538765	-1.787543	21198.678589
HLA A*0211	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-3.313512	1.525910	-1.787602	2058.313826
HLA A*2602	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-3.174789	1.386802	-1.787986	1495.507512
HLA A*2501	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.049887	2.261413	-1.788475	11217.270187
HLA A*6901	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-3.859194	2.070592	-1.788602	7230.920388
HLA B*5401	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.558165	2.769370	-1.788796	36154.750441
HLA B*3801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.410770	2.621122	-1.789648	25749.596415
HLA B*0802	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.329037	2.538765	-1.790271	21332.243988
HLA B*4601	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.228758	2.438231	-1.790527	16933.946093
HLA A*2602	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.411762	2.621122	-1.790640	25808.449209
HLA A*2601	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.329673	2.538765	-1.790908	21363.541700
HLA A*0301	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.330174	2.538765	-1.791408	21388.173234
HLA B*1501	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.150647	2.358694	-1.791953	14146.441062
HLA B*0702	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.331311	2.538765	-1.792545	21444.249117
HLA B*0803	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.222852	2.429816	-1.793036	16705.195696
HLA B*3801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.283922	2.490827	-1.793095	19227.451798

HLA A*0202	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-3.753838	1.960098	-1.793740	5673.329055
HLA A*0202	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-2.635281	0.839877	-1.795404	431.798428
HLA A*3101	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.381275	2.585626	-1.795649	24058.857056
HLA B*4801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.381806	2.585626	-1.796180	24088.290245
HLA B*3501	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.667664	1.870848	-1.796816	4652.255550
HLA A*0202	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-3.657669	1.859413	-1.798255	4546.412671
HLA A*2501	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.237240	2.438231	-1.799009	17267.911484
HLA A*2601	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.384870	2.585626	-1.799244	24258.821778
HLA A*0211	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.492246	2.692848	-1.799398	31063.176723
HLA A*6802	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.239505	2.439993	-1.799512	17358.201173
HLA A*0219	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.906554	2.106921	-1.799633	8064.073893
HLA A*3301	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.502931	2.703152	-1.799779	31836.940460
HLA A*0216	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.143747	1.343697	-1.800051	1392.346101
HLA B*0801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.207448	2.407316	-1.800132	16123.092439
HLA A*3001	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.233023	1.431809	-1.801213	1710.105620
HLA B*5101	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.630307	1.828833	-1.801474	4268.809271
HLA B*2705	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.231390	2.429816	-1.801574	17036.861628
HLA B*5401	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.505314	2.703152	-1.802161	32012.065957
HLA B*4001	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.327881	2.525575	-1.802305	21275.540188
HLA A*1101	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.341653	2.538765	-1.802888	21961.058901
HLA A*6901	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.831122	2.028058	-1.803064	6778.317900
HLA B*1517	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.243290	1.440103	-1.803187	1751.016279
HLA A*0206	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.207099	1.403484	-1.803615	1611.011782
HLA A*3001	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.253237	2.449598	-1.803640	17915.851629
HLA A*0250	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-2.994043	1.190001	-1.804041	986.376502
HLA B*2705	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.699208	1.894713	-1.804494	5002.737878
HLA A*2301	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.330075	2.525575	-1.804500	21383.314065
HLA A*0212	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.391234	2.585626	-1.805609	24616.962198
HLA A*0301	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-2.556320	0.750403	-1.805917	360.014145
HLA A*6901	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.296849	2.490827	-1.806021	19808.363531
HLA A*0201	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.180721	2.374610	-1.806111	15160.747076
HLA A*2902	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.867769	2.061629	-1.806140	7375.121854
HLA A*2402	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.344792	2.538391	-1.806402	22120.359901
HLA A*0212	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.236486	2.429816	-1.806670	17237.950493
HLA B*1502	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.332434	2.525575	-1.806858	21499.774141
HLA A*3002	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.729352	1.922093	-1.807259	5362.306586
HLA A*0201	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.392891	2.585626	-1.807265	24711.029871
HLA B*4801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.308070	2.500470	-1.807599	20326.833889
HLA A*6802	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.117219	2.309312	-1.807907	13098.414269
HLA A*0206	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.426888	1.618772	-1.808116	2672.319247
HLA A*3101	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.346561	2.538391	-1.808171	22210.654217
HLA A*0219	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.246424	2.438231	-1.808193	17636.968963
HLA B*0702	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.083142	2.274057	-1.809085	12109.934425
HLA B*1503	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-2.999550	1.190001	-1.809548	998.964167
HLA B*1509	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.083927	2.274057	-1.809869	12131.835682
HLA B*1503	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.238015	2.428102	-1.809914	17298.766789
HLA B*5801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.335542	2.525575	-1.809967	21654.206114
HLA B*4402	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.207152	2.397104	-1.810048	16112.105942
HLA A*0250	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.582600	2.772331	-1.810269	38247.232175
HLA A*0219	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.431406	2.621122	-1.810284	27002.623019
HLA A*0206	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-2.597342	0.786863	-1.810478	395.677699
HLA A*2501	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.349642	2.538765	-1.810876	22368.740215
HLA B*5801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.349853	2.538391	-1.811462	22379.633983
HLA A*6901	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.251598	2.439993	-1.811604	17848.327104
HLA B*1517	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-2.728231	0.916314	-1.811917	534.849239
HLA B*5401	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.557625	2.745346	-1.812279	36109.791983
HLA B*7301	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.252385	2.439993	-1.812392	17880.703186
HLA A*2402	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.338059	2.525575	-1.812483	21780.034568
HLA B*3901	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.224322	2.411682	-1.812640	16761.865259
HLA B*1801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-2.988254	1.175404	-1.812850	973.315381
HLA A*3301	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.585532	2.772331	-1.813201	38506.333639
HLA A*3001	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.253367	2.439993	-1.813374	17921.183174
HLA A*2403	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.253430	2.439993	-1.813437	17923.801059
HLA B*4801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.367859	2.554318	-1.813542	23327.029171
HLA B*3801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.352867	2.538765	-1.814102	22535.508840

HLA A*3301	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.559554	2.745346	-1.814208	36270.531008
HLA A*3301	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.583798	2.769370	-1.814429	38352.903660
HLA B*7301	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.559824	2.745346	-1.814478	36293.103278
HLA A*3002	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.709386	1.894713	-1.814672	5121.364861
HLA B*3901	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.369170	2.554318	-1.814853	23397.553290
HLA B*3901	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.465415	1.650328	-1.815087	2920.217469
HLA B*5701	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.369659	2.554318	-1.815342	23423.896368
HLA B*0802	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.369828	2.554318	-1.815511	23433.022034
HLA B*0801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.341153	2.525575	-1.815577	21935.767607
HLA A*0203	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.341263	2.525575	-1.815688	21941.345809
HLA A*0203	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.384677	1.568231	-1.816447	2424.808759
HLA A*0203	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.042964	1.226371	-1.816593	1103.986326
HLA B*1509	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.317228	2.500470	-1.816758	20760.032576
HLA B*7301	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.617156	2.800303	-1.816853	41414.863814
HLA A*6901	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.342527	2.525575	-1.816952	22005.299567
HLA A*0202	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.317693	2.500470	-1.817223	20782.281767
HLA B*5301	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-3.564404	1.746933	-1.817471	3667.783537
HLA A*3002	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.246081	2.428102	-1.817979	17623.044012
HLA B*1503	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-3.833659	2.015621	-1.818038	6818.037366
HLA A*0202	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.900380	2.081726	-1.818654	7950.236574
HLA B*5801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.308178	2.489515	-1.818663	20331.892951
HLA B*4601	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.357801	2.538765	-1.819036	22792.989329
HLA B*1801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.216315	2.397104	-1.819211	16455.659802
HLA B*4501	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.616663	2.797119	-1.819543	41367.840068
HLA A*0250	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.149320	1.329751	-1.819569	1410.328173
HLA B*1501	1:162-170	9	AIADSGNSV	1.093291	0.318474	-3.231369	1.411765	-1.819604	1703.604963
HLA B*3801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-3.511841	1.691666	-1.820175	3249.683148
HLA A*0216	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-2.816516	0.995952	-1.820564	655.413875
HLA A*3101	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.375009	2.554318	-1.820691	23714.223864
HLA B*4801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.137062	2.316186	-1.820876	13710.789785
HLA A*0206	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.311704	2.490827	-1.820877	20497.665018
HLA B*4403	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.621315	2.800303	-1.821012	41813.336744
HLA B*5301	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.228354	2.407316	-1.821038	16918.196369
HLA A*2902	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.284370	2.462765	-1.821605	19247.329577
HLA B*0702	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-2.966201	1.144551	-1.821651	925.126924
HLA B*2705	1:136-144	9	HRDVKPANI	1.262411	0.208757	-3.292954	1.471168	-1.821785	1963.150512
HLA A*2902	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.180707	2.358694	-1.822012	15160.254977
HLA A*3101	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.928959	2.106921	-1.822038	8491.006780
HLA A*0201	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.360614	2.538391	-1.822223	22941.067393
HLA B*4601	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.347889	2.525575	-1.822313	22278.646882
HLA B*1503	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.139210	2.316186	-1.823024	13778.752574
HLA A*2602	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.269064	1.445980	-1.823084	1858.078397
HLA A*6901	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.377840	2.554318	-1.823523	23869.319887
HLA A*2403	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.409866	2.585626	-1.824240	25696.020781
HLA B*5801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.653388	1.828833	-1.824555	4501.819642
HLA B*3501	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.645456	1.819741	-1.825715	4420.345650
HLA B*5301	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.135277	2.309312	-1.825965	13654.533386
HLA B*1801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.364373	2.538391	-1.825982	23140.503098
HLA A*6901	1:143-151	9	NIMISATNA	0.971550	-0.064300	-2.733344	0.907250	-1.826094	541.182646
HLA B*0803	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.447432	2.621122	-1.826310	28017.655470
HLA B*4402	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.327065	2.500470	-1.826595	21235.638537
HLA A*3001	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.223716	2.397104	-1.826612	16738.486181
HLA B*0802	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.318212	2.490827	-1.827385	20807.143621
HLA A*6901	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.365865	2.538391	-1.827474	23220.133895
HLA A*2403	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.290277	2.462765	-1.827512	19510.890350
HLA A*6901	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.328043	2.500470	-1.827572	21283.483454
HLA A*3201	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.382250	2.554318	-1.827933	24112.932372
HLA B*4601	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.268230	2.439993	-1.828236	18545.114580
HLA A*1101	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.450202	2.621122	-1.829080	28196.930465
HLA A*2601	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.267351	2.438231	-1.829120	18507.630211
HLA B*3901	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.680191	1.851066	-1.829125	4788.406555
HLA A*0202	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.096083	2.266682	-1.829400	12476.212259
HLA B*1801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.319176	2.489515	-1.829661	20853.346221
HLA A*2601	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.965278	2.135178	-1.830100	9231.611656
HLA B*3901	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-3.958314	2.127896	-1.830418	9084.764071

HLA B*0802	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.269736	2.438231	-1.831504	18609.535830
HLA B*0801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.321405	2.489515	-1.831890	20960.682279
HLA B*4402	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.370437	2.538391	-1.832046	23465.878491
HLA B*4002	1:199-207	9	VYSLGCVLY	1.447668	1.349451	-4.629475	2.797119	-1.832355	42606.375193
HLA B*4501	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.577748	2.745346	-1.832402	37822.334016
HLA B*5701	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.371297	2.538765	-1.832531	23512.387415
HLA A*2603	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.453738	2.621122	-1.832616	28427.443711
HLA A*0206	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.418359	2.585626	-1.832733	26203.497539
HLA A*0301	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.358873	2.525575	-1.833297	22849.286981
HLA B*0801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.371802	2.538391	-1.833411	23539.751199
HLA A*6801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.915501	2.081726	-1.833775	8231.923722
HLA A*0216	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.454983	2.621122	-1.833861	28509.069014
HLA A*3101	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.334469	2.500470	-1.833998	21600.736126
HLA B*0803	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.419706	2.585626	-1.834080	26284.850910
HLA B*2705	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.419734	2.585626	-1.834108	26286.557343
HLA B*5701	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.324013	2.489515	-1.834498	21086.929369
HLA B*0702	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-3.581452	1.746933	-1.834519	3814.622446
HLA A*2403	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.388887	2.554318	-1.834570	24484.279201
HLA A*0202	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.464128	1.629324	-1.834803	2911.572957
HLA B*4801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.373700	2.538765	-1.834935	23642.873153
HLA B*5801	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.273189	2.438231	-1.834958	18758.118876
HLA A*0250	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.580361	2.745346	-1.835015	38050.551255
HLA A*0202	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.580420	2.745346	-1.835074	38055.697835
HLA B*1501	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-3.795189	1.960098	-1.835091	6240.062069
HLA B*3501	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.324916	2.489515	-1.835400	21130.780834
HLA B*4801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.325193	2.489515	-1.835678	21144.274332
HLA A*0203	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-2.568659	0.732827	-1.835832	370.389836
HLA A*6802	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.336468	2.500470	-1.835998	21700.411200
HLA B*5301	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-3.864372	2.028058	-1.836314	7317.653562
HLA A*0203	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.886460	1.049687	-1.836772	769.945171
HLA A*0101	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.362679	2.525575	-1.837103	23050.418673
HLA B*4002	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.637449	2.800303	-1.837146	43395.903977
HLA B*1502	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.866170	1.028753	-1.837417	734.800845
HLA A*2602	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.268538	1.430389	-1.838148	1855.828113
HLA A*6901	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.105044	2.266682	-1.838361	12736.312037
HLA A*2501	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.392877	2.554318	-1.838559	24710.227780
HLA A*0212	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.393001	2.554318	-1.838684	24717.313814
HLA A*0216	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.304029	1.465019	-1.839011	2013.859045
HLA B*0702	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.393488	2.554318	-1.839170	24745.008930
HLA A*0219	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.424893	2.585626	-1.839267	26600.707081
HLA A*2601	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.364878	2.525575	-1.839302	23167.434082
HLA A*3001	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.277679	2.438231	-1.839448	18953.051803
HLA B*4001	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.378077	2.538391	-1.839687	23882.365619
HLA A*0201	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.394098	2.554318	-1.839781	24779.839036
HLA B*4002	1:597-605	9	GSQHNRVVY	1.563391	1.181955	-4.585229	2.745346	-1.839883	38479.470379
HLA A*6802	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.378749	2.538765	-1.839984	23919.345692
HLA A*2301	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-3.697314	1.857104	-1.840210	4980.971575
HLA B*3901	1:289-297	9	TDAERTSLL	1.288079	0.301720	-3.431409	1.589799	-1.841610	2700.279683
HLA A*0250	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-2.786315	0.944464	-1.841851	611.385804
HLA B*4501	1:255-263	9	LAKNPENRY	1.439797	1.360506	-4.642484	2.800303	-1.842181	43901.937376
HLA B*5801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.254330	2.411682	-1.842648	17960.977453
HLA B*4001	1:267-275	9	AEMRADLVR	1.301765	0.742764	-3.887392	2.044529	-1.842864	7715.997869
HLA A*2501	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.273145	2.429816	-1.843329	18756.190867
HLA A*2902	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-3.978905	2.135178	-1.843727	9525.867575
HLA A*2603	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.382433	2.538391	-1.844043	24123.109485
HLA B*3801	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.284103	2.439993	-1.844110	19235.462882
HLA A*0212	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.153575	2.309312	-1.844263	14242.120399
HLA B*1517	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.382654	2.538391	-1.844264	24135.379920
HLA A*3002	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.256019	2.411682	-1.844337	18030.976501
HLA B*3501	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.294480	2.449598	-1.844882	19700.639178
HLA B*4403	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.614269	2.769370	-1.844899	41140.419948
HLA A*0250	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.538394	2.692848	-1.845547	34545.736164
HLA A*0206	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-3.907504	2.061629	-1.845875	8081.717969
HLA B*4001	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.385340	2.538765	-1.846574	24285.083490
HLA A*0301	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.274785	2.428102	-1.846683	18827.150059

HLA A*2902	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.144275	2.297586	-1.846689	13940.405001
HLA B*5301	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.372509	2.525575	-1.846934	23578.114006
HLA A*0301	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.255070	2.407316	-1.847754	17991.611120
HLA B*3501	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-2.833136	0.985326	-1.847810	680.982400
HLA A*0219	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.386230	2.538391	-1.847839	24334.927443
HLA B*4601	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.122383	2.274057	-1.848326	13255.096381
HLA A*0202	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.541301	2.692848	-1.848453	34777.692630
HLA B*5101	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.348934	2.500470	-1.848464	22332.345122
HLA B*0801	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.387259	2.538765	-1.848494	24392.658190
HLA B*0702	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.339527	2.490827	-1.848700	21853.801440
HLA B*4002	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.621381	2.772331	-1.849049	41819.670978
HLA B*1517	1:575-583	9	EPRLRALGW	1.410483	0.250517	-3.510286	1.661000	-1.849286	3238.065722
HLA B*4801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.387708	2.538391	-1.849317	24417.875877
HLA A*1101	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.339005	2.489515	-1.849490	21827.570879
HLA B*1801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.931534	2.081726	-1.849808	8541.501534
HLA A*2301	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.470962	2.621122	-1.849840	29577.528589
HLA B*4801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.279914	2.429816	-1.850097	19050.812815
HLA A*3001	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-3.083788	1.233662	-1.850127	1212.797647
HLA A*3001	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.280080	2.429816	-1.850264	19058.131679
HLA A*6802	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.435957	2.585626	-1.850331	27287.070049
HLA A*2603	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.375916	2.525575	-1.850340	23763.796055
HLA A*2603	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.435997	2.585626	-1.850371	27289.579704
HLA B*4403	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.553816	2.703152	-1.850664	35794.514104
HLA B*1502	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-3.932967	2.081726	-1.851241	8569.735326
HLA A*2403	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.390936	2.538765	-1.852171	24600.054777
HLA A*6801	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.853639	2.001388	-1.852251	7139.033131
HLA A*0203	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.406772	2.554318	-1.852454	25513.591814
HLA A*2603	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.353704	2.500470	-1.853233	22578.952260
HLA B*3901	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.897161	2.043325	-1.853836	7891.530832
HLA A*3002	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.354387	2.500470	-1.853917	22614.525796
HLA A*0201	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.392752	2.538765	-1.853987	24703.143777
HLA B*0803	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.605087	1.751011	-1.854077	4027.980683
HLA B*1509	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.266470	2.411682	-1.854787	18470.121685
HLA A*0202	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.161787	1.306673	-1.855113	1451.398096
HLA B*1801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.380690	2.525575	-1.855114	24026.470093
HLA A*0101	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.345838	2.489515	-1.856323	22173.676622
HLA B*4001	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.319225	2.462765	-1.856460	20855.715456
HLA B*7301	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.051868	1.195398	-1.856470	1126.855536
HLA B*4601	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.268262	2.411682	-1.856580	18546.519212
HLA A*6901	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.295002	2.438231	-1.856771	19724.313769
HLA B*4403	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.489615	1.632662	-1.856953	3087.556334
HLA A*0201	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.382776	2.525575	-1.857201	24142.170501
HLA B*0802	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.395788	2.538391	-1.857397	24876.413132
HLA B*3901	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.131518	2.274057	-1.857461	13536.852215
HLA A*0301	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-3.065735	1.208137	-1.857598	1163.415654
HLA B*4501	1:67-75	9	NHPAIVAVY	1.468693	1.303638	-4.630161	2.772331	-1.857829	42673.733145
HLA B*2705	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.348713	2.490827	-1.857886	22320.991351
HLA B*4801	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.296123	2.438231	-1.857891	19775.278428
HLA B*3901	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.479117	2.621122	-1.857995	30138.174649
HLA B*0801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.307675	2.449598	-1.858077	20308.368008
HLA B*5401	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.397195	2.538765	-1.858430	24957.156490
HLA B*7301	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.627987	2.769370	-1.858618	42460.720909
HLA B*1503	1:267-275	9	AEMRADLVR	1.301765	0.742764	-3.903214	2.044529	-1.858685	8002.276089
HLA A*2603	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.678631	1.819741	-1.858890	4771.236659
HLA A*3101	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.348725	2.489515	-1.859210	22321.595129
HLA A*3001	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.271159	2.411682	-1.859477	18670.645314
HLA A*3101	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.385105	2.525575	-1.859529	24271.949082
HLA B*2705	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.385274	2.525575	-1.859698	24281.405140
HLA A*0212	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.398238	2.538391	-1.859848	25017.175403
HLA B*2705	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.414170	2.554318	-1.859853	25951.958099
HLA A*3101	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.398922	2.538765	-1.860157	25056.590403
HLA B*4501	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.629759	2.769370	-1.860389	42634.274311
HLA B*5401	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-2.625192	0.764421	-1.860772	421.883333
HLA A*0211	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.546491	1.685171	-1.861320	3519.583096
HLA A*0212	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.470608	1.609050	-1.861558	2955.340712

HLA A*3201	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.352618	2.490827	-1.861791	22522.589597
HLA B*3901	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.220591	2.358694	-1.861897	16618.482460
HLA A*0301	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.362881	2.500470	-1.862410	23061.145386
HLA A*0202	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.300667	2.438231	-1.862435	19983.267910
HLA A*0101	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.363121	2.500470	-1.862650	23073.874238
HLA A*0250	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.124206	2.261413	-1.862793	13310.859223
HLA B*3501	1:79-87	9	EAETPAGPL	0.986891	0.274759	-3.124702	1.261650	-1.863052	1332.607575
HLA B*5301	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.983115	2.120022	-1.863093	9618.665390
HLA B*1501	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-3.984022	2.120022	-1.864000	9638.772239
HLA B*2705	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.130747	2.266682	-1.864065	13512.853132
HLA A*0203	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.449908	2.585626	-1.864282	28177.869128
HLA B*0702	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.304597	2.439993	-1.864604	20164.952313
HLA A*0212	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.390701	2.525575	-1.865126	24586.750020
HLA B*5801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.295171	2.429816	-1.865355	19731.998123
HLA B*5701	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.403835	2.538391	-1.865444	25341.641734
HLA A*0203	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.366024	2.500470	-1.865554	23228.677514
HLA A*2603	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.706642	1.840969	-1.865672	5089.106258
HLA B*5801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.329001	2.462765	-1.866236	21330.512982
HLA B*2705	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.316140	2.449598	-1.866542	20708.098359
HLA A*2501	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.973491	2.106921	-1.866570	9407.870407
HLA A*2602	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.225770	2.358694	-1.867075	16817.817214
HLA A*3301	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-3.254079	1.386802	-1.867277	1795.060204
HLA B*3801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.368014	2.500470	-1.867544	23335.359637
HLA B*5701	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.368059	2.500470	-1.867589	23337.758353
HLA B*0802	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.393250	2.525575	-1.867675	24731.491980
HLA A*0101	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.297824	2.429816	-1.868008	19852.885326
HLA A*0216	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.453735	2.585626	-1.868110	28427.289922
HLA A*0301	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.357940	2.489515	-1.868425	22800.265635
HLA A*3002	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.478008	1.609050	-1.868959	3006.134683
HLA B*4002	1:192-200	9	SVDARSDVY	1.553332	1.216038	-4.638750	2.769370	-1.869381	43526.160008
HLA A*6802	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.423765	2.554318	-1.869448	26531.721388
HLA B*1517	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.050731	1.181170	-1.869561	1123.908852
HLA B*0802	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.371649	2.500470	-1.871179	23531.475070
HLA B*4002	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.574682	2.703152	-1.871530	37556.252280
HLA B*2705	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.410486	2.538391	-1.872096	25732.746333
HLA B*4001	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.362319	2.489515	-1.872804	23031.347434
HLA A*6901	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-3.740643	1.866969	-1.873674	5503.554427
HLA A*0203	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.364631	2.490827	-1.873804	23154.277827
HLA B*0801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.428206	2.554318	-1.873888	26804.391636
HLA B*1503	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-3.834026	1.960098	-1.873928	6823.793827
HLA B*3901	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.399646	2.525575	-1.874070	25098.375645
HLA B*4001	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.323687	2.449598	-1.874089	21071.078494
HLA B*0702	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.374581	2.500470	-1.874111	23690.886335
HLA B*4801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.365078	2.490827	-1.874250	23178.089858
HLA B*0702	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.412913	2.538391	-1.874523	25876.954183
HLA B*3901	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.560236	1.685171	-1.875064	3632.751664
HLA A*0219	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.429428	2.554318	-1.875110	26879.902367
HLA A*2603	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.149176	2.274057	-1.875119	14098.613889
HLA B*1501	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.141846	2.266682	-1.875164	13862.642507
HLA A*2403	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.366349	2.490827	-1.875522	23246.025700
HLA A*6901	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.192116	2.316186	-1.875930	15563.798691
HLA A*6901	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.365968	2.489515	-1.876453	23225.661760
HLA A*0201	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.377175	2.500470	-1.876705	23832.803951
HLA A*6901	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.521864	1.645104	-1.876760	3325.553365
HLA A*2602	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-3.021621	1.144551	-1.877070	1051.044182
HLA A*8001	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.378481	2.500470	-1.878011	23904.598525
HLA B*0702	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.340927	2.462765	-1.878162	21924.378238
HLA A*0202	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.729366	1.851066	-1.878300	5362.480646
HLA B*3501	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.253000	2.374610	-1.878390	17906.065103
HLA B*4801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.404276	2.525575	-1.878701	25367.428795
HLA B*4403	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.238034	2.358694	-1.879339	17299.515480
HLA B*4601	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.342241	2.462765	-1.879475	21990.780719
HLA A*3301	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.572382	2.692848	-1.879534	37357.869606
HLA B*5701	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.330082	2.449598	-1.880484	21383.661112
HLA A*3201	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.466211	2.585626	-1.880585	29255.749191

HLA B*5701	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.406325	2.525575	-1.880750	25487.380404
HLA B*5701	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.292948	2.411682	-1.881266	19631.272552
HLA B*3801	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.419987	2.538391	-1.881597	26301.920226
HLA B*0702	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.632746	1.751011	-1.881735	4292.848051
HLA B*4801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-3.988843	2.106921	-1.881922	9746.369259
HLA A*0203	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.131685	1.249564	-1.882121	1354.206665
HLA B*1502	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.166951	1.284672	-1.882279	1468.759596
HLA A*0212	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.421334	2.538765	-1.882568	26383.579167
HLA B*1801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.290019	2.407316	-1.882702	19499.283111
HLA B*2705	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.322918	2.439993	-1.882925	21033.835996
HLA B*0801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-3.473831	1.590840	-1.882991	2977.357947
HLA A*0206	1:243-251	9	LSADLDAVV	0.948699	0.148803	-2.981327	1.097502	-1.883825	957.915730
HLA A*3201	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.295538	2.411682	-1.883855	19748.657827
HLA B*1509	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.193967	2.309312	-1.884655	15630.288673
HLA B*2705	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.423422	2.538765	-1.884657	26510.773746
HLA A*6801	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.470393	2.585626	-1.884767	29538.831227
HLA A*0202	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.517480	1.632662	-1.884818	3292.151271
HLA B*5801	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.324878	2.439993	-1.884885	21128.951870
HLA B*4403	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.385657	2.500470	-1.885186	24302.826216
HLA A*1101	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.410961	2.525575	-1.885385	25760.882387
HLA A*6801	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.506566	2.621122	-1.885444	32104.505027
HLA A*3001	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.419713	1.534036	-1.885677	2628.530450
HLA A*0212	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.757160	1.870848	-1.886312	5716.894073
HLA A*2601	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.376280	2.489515	-1.886765	23783.731135
HLA B*4801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.160858	2.274057	-1.886801	14482.984182
HLA A*0201	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.326875	2.439993	-1.886882	21226.335097
HLA A*6901	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.076928	1.190001	-1.886926	1193.789761
HLA B*0801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.284227	2.397104	-1.887123	19240.978944
HLA A*2403	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.185067	2.297586	-1.887481	15313.242139
HLA B*5401	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.083347	1.195398	-1.887949	1211.564787
HLA B*1517	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.371295	1.482642	-1.888653	2351.228436
HLA A*0212	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.263284	2.374610	-1.888674	18335.124152
HLA B*1517	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.708601	1.819741	-1.888860	5112.119406
HLA B*4601	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.378594	2.489515	-1.889079	23910.806750
HLA A*0206	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.414680	2.525575	-1.889104	25982.442185
HLA A*0203	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.427985	2.538765	-1.889220	26790.764276
HLA B*5101	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.443971	2.554318	-1.889653	27795.276530
HLA B*0803	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.444098	2.554318	-1.889780	27803.397662
HLA B*0702	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.415483	2.525575	-1.889908	26030.558933
HLA A*6801	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.444417	2.554318	-1.890100	27823.861398
HLA B*5301	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.538550	1.648439	-1.890111	3455.810850
HLA A*0216	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.444514	2.554318	-1.890196	27830.033566
HLA A*0201	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.197001	1.306673	-1.890327	1573.985148
HLA A*6802	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.415930	2.525575	-1.890354	26057.328952
HLA B*4801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.353246	2.462765	-1.890480	22555.145642
HLA B*1517	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.719498	1.828833	-1.890665	5242.010672
HLA A*0206	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.287803	2.397104	-1.890699	19400.060330
HLA A*0212	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.303284	2.411682	-1.891601	20104.063030
HLA B*0801	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.329946	2.438231	-1.891715	21376.952537
HLA A*1101	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.299583	2.407316	-1.892267	19933.492556
HLA B*4001	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.202185	2.309312	-1.892874	15928.889427
HLA A*0101	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.343209	2.449598	-1.893611	22039.850070
HLA B*5101	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.419313	2.525575	-1.893738	26261.114547
HLA B*0802	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.343453	2.449598	-1.893855	22052.253806
HLA A*0202	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.227004	1.332686	-1.894318	1686.566825
HLA B*1502	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.192684	2.297586	-1.895098	15584.188054
HLA A*0211	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.516765	2.621122	-1.895643	32867.380526
HLA A*0250	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.429830	1.534036	-1.895794	2690.480786
HLA A*0206	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.450275	2.554318	-1.895957	28201.659672
HLA B*4001	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.386824	2.490827	-1.895997	24368.257510
HLA A*6802	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.386928	2.490827	-1.896101	24374.058702
HLA B*1801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.345882	2.449598	-1.896284	22175.955924
HLA A*2403	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.255152	2.358694	-1.896458	17995.018084
HLA A*0211	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.163283	2.266682	-1.896600	14564.068901
HLA A*0201	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.387461	2.490827	-1.896634	24404.009526

HLA B*4403	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.589679	2.692848	-1.896831	38875.770576
HLA A*3002	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.181720	1.284672	-1.897048	1519.566042
HLA A*3101	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.346702	2.449598	-1.897104	22217.864818
HLA A*0301	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.326978	2.429816	-1.897162	21231.388312
HLA A*0212	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.397914	2.500470	-1.897444	24998.505433
HLA A*0219	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.423136	2.525575	-1.897560	26493.282237
HLA A*6901	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.327613	2.429816	-1.897797	21262.423025
HLA B*0801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.272813	2.374610	-1.898203	18741.889206
HLA B*4403	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.389580	2.490827	-1.898753	24523.385282
HLA A*0201	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.769782	1.870848	-1.898934	5885.475806
HLA A*0201	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.388450	2.489515	-1.898935	24459.654546
HLA A*3201	1:40-48	9	KVLRADLAR	0.915954	0.778633	-3.593960	1.694587	-1.899373	3926.089703
HLA B*1501	1:243-251	9	LSADLDAVV	0.948699	0.148803	-2.996961	1.097502	-1.899458	993.026362
HLA B*5801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.258183	2.358694	-1.899489	18121.040169
HLA B*0803	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.327688	2.428102	-1.899586	21266.104219
HLA B*0803	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.438661	2.538765	-1.899896	27457.510794
HLA A*8001	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.363085	2.462765	-1.900320	23072.001907
HLA B*2705	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.308004	2.407316	-1.900688	20323.755077
HLA B*2705	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.363464	2.462765	-1.900698	23092.106194
HLA B*0803	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.363511	2.462765	-1.900745	23094.604844
HLA B*0802	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.308119	2.407316	-1.900803	20329.143305
HLA A*3002	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.007850	2.106921	-1.900929	10182.400972
HLA B*4601	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.350595	2.449598	-1.900997	22417.925247
HLA A*0202	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.522392	2.621122	-1.901270	33296.003576
HLA B*5101	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.392557	2.490827	-1.901730	24692.054042
HLA A*0301	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.365139	2.462765	-1.902373	23181.350250
HLA A*0212	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.903848	2.001388	-1.902460	8013.973315
HLA A*0219	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.393492	2.490827	-1.902665	24745.276667
HLA A*3101	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.314425	2.411682	-1.902743	20626.478814
HLA B*1509	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.941332	2.037813	-1.903519	8736.381201
HLA A*0212	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.366309	2.462765	-1.903543	23243.887905
HLA A*3301	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.165393	2.261413	-1.903980	14634.994461
HLA B*1502	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.263129	2.358694	-1.904434	18328.578715
HLA A*1101	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.405578	2.500470	-1.905108	25443.571017
HLA A*0301	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.355278	2.449598	-1.905680	22660.941011
HLA B*1509	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.033929	2.127896	-1.906034	10812.583606
HLA B*0802	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.303234	2.397104	-1.906130	20101.779184
HLA B*1517	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.281135	2.374610	-1.906525	19104.480916
HLA B*1509	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.444953	2.538391	-1.906562	27858.202045
HLA A*0219	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.445458	2.538765	-1.906693	27890.623501
HLA B*5701	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.347158	2.439993	-1.907165	22241.195118
HLA A*0206	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.445585	2.538391	-1.907194	27898.772491
HLA B*0803	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.346000	2.438231	-1.907769	22181.955209
HLA A*3101	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.348016	2.439993	-1.908023	22285.156183
HLA B*0801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.217438	2.309312	-1.908126	16498.268004
HLA A*0202	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.266886	2.358694	-1.908191	18487.816228
HLA B*0801	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.399230	2.490827	-1.908403	25074.354189
HLA A*3101	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.338244	2.429816	-1.908428	21789.344935
HLA A*0203	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.398765	2.489515	-1.909249	25047.509972
HLA A*0206	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.399239	2.489515	-1.909724	25074.896793
HLA B*5401	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.530963	2.621122	-1.909841	33959.636331
HLA B*0803	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.399357	2.489515	-1.909841	25081.680331
HLA A*3001	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.269143	2.358694	-1.910449	18584.182883
HLA A*0212	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.465364	1.554751	-1.910612	2919.869933
HLA A*0219	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.350647	2.439993	-1.910654	22420.593533
HLA A*6901	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.309997	1.398961	-1.911036	2041.722721
HLA B*1517	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.269815	2.358694	-1.911121	18612.959113
HLA A*2301	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.496980	2.585626	-1.911354	31403.646480
HLA B*1509	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.349846	2.438231	-1.911615	22379.270772
HLA A*0203	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.350041	2.438231	-1.911810	22389.321787
HLA B*0802	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.374675	2.462765	-1.911910	23696.013492
HLA A*0203	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.782835	1.870848	-1.911988	6065.063015
HLA A*6901	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.361941	2.449598	-1.912343	23011.296045
HLA A*6802	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.732218	1.819741	-1.912477	5397.815208
HLA A*0201	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.350783	2.438231	-1.912552	22427.629626

HLA B*0803	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.352783	2.439993	-1.912790	22531.120342
HLA A*0250	1:459-467	9	STPELVGKV	0.780846	0.079303	-2.773144	0.860149	-1.912995	593.122143
HLA A*0202	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.808182	1.894713	-1.913468	6429.564562
HLA A*0206	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.447738	1.534036	-1.913702	2803.739560
HLA A*0203	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.188154	2.274057	-1.914097	15422.485589
HLA A*0216	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.440104	2.525575	-1.914528	27548.867281
HLA B*0702	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.500023	1.585464	-1.914559	3162.445929
HLA A*0301	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.354770	2.439993	-1.914777	22634.476350
HLA A*3101	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.377969	2.462765	-1.915204	23876.423115
HLA A*6801	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.415686	2.500470	-1.915215	26042.672480
HLA A*2402	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.501256	2.585626	-1.915630	31714.373928
HLA A*3201	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.225013	2.309312	-1.915701	16788.546342
HLA B*7301	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.618857	2.703152	-1.915705	41577.393973
HLA A*0216	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.416729	2.500470	-1.916258	26105.301927
HLA B*4001	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.323583	2.407316	-1.916267	21066.063434
HLA A*6901	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.379064	2.462765	-1.916299	23936.691713
HLA A*0216	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.407890	2.490827	-1.917063	25579.376714
HLA A*0212	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.233286	2.316186	-1.917100	17111.403425
HLA B*5801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.788037	1.870848	-1.917189	6138.144064
HLA B*3901	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.379959	2.462765	-1.917194	23986.080132
HLA B*1509	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.408940	2.490827	-1.918113	25641.308138
HLA A*2601	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.380904	2.462765	-1.918138	24038.301234
HLA B*0802	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.407836	2.489515	-1.918321	25576.194135
HLA B*1509	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.444234	2.525575	-1.918659	27812.123002
HLA A*0101	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.381768	2.462765	-1.919003	24086.205295
HLA A*0219	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.382591	2.462765	-1.919825	24131.854795
HLA A*0101	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.358057	2.438231	-1.919826	22806.433815
HLA B*7301	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.613122	2.692848	-1.920274	41031.951417
HLA A*6901	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.226985	1.306673	-1.920311	1686.493834
HLA B*0803	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.459026	2.538391	-1.920636	28775.739880
HLA B*1801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.295448	2.374610	-1.920838	19744.598399
HLA B*4402	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.218552	2.297586	-1.920966	16540.628595
HLA B*3801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.280146	2.358694	-1.921452	19061.018764
HLA B*1517	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.843654	1.922093	-1.921561	6976.764862
HLA A*2603	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.028648	2.106921	-1.921727	10681.883480
HLA A*6901	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.507335	1.584939	-1.922396	3216.138227
HLA A*3101	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.160692	1.238104	-1.922588	1447.743717
HLA B*3501	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.029578	2.106921	-1.922657	10704.791981
HLA A*2902	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.350814	2.428102	-1.922712	22429.206984
HLA B*0801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.353027	2.429816	-1.923211	22543.800559
HLA A*0301	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.361647	2.438231	-1.923416	22995.740235
HLA B*3801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.413035	2.489515	-1.923520	25884.234762
HLA B*3901	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.413087	2.489515	-1.923572	25887.315624
HLA B*4501	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.477945	2.554318	-1.923627	30056.925318
HLA B*1801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.185297	2.261413	-1.923885	15321.362900
HLA B*4501	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.616794	2.692848	-1.923947	41380.374510
HLA B*5801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.352318	2.428102	-1.924216	22506.998872
HLA B*3801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.199000	2.274057	-1.924943	15812.465679
HLA A*0201	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.388608	2.462765	-1.925842	24468.521863
HLA B*1503	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.224678	1.298743	-1.925935	1677.558073
HLA A*0216	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-2.975825	1.049687	-1.926138	945.855538
HLA A*0206	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.408825	1.482642	-1.926184	2563.453825
HLA B*0803	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.333825	2.407316	-1.926508	21568.740866
HLA A*6901	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.108176	1.181170	-1.927006	1282.850359
HLA B*5101	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.465727	2.538391	-1.927337	29223.163657
HLA B*5701	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.390250	2.462765	-1.927485	24561.225053
HLA B*4002	1:507-515	9	VAQKNLNVY	1.447705	1.245143	-4.620514	2.692848	-1.927666	41736.271768
HLA B*3801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.377429	2.449598	-1.927831	23846.732765
HLA B*3801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.136151	2.208172	-1.927979	13682.040513
HLA A*2601	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.339755	2.411682	-1.928072	21865.272434
HLA A*3002	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.325698	2.397104	-1.928594	21168.882099
HLA A*0201	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.237914	2.309312	-1.928602	17294.743127
HLA A*3101	1:24-32	9	EVHLARDLR	0.880960	0.651501	-3.461064	1.532461	-1.928603	2891.105557
HLA A*2301	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.467210	2.538391	-1.928819	29323.091481
HLA A*0216	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.467623	2.538765	-1.928858	29351.024479

HLA B*0803	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.429418	2.500470	-1.928948	26879.320704
HLA B*1517	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.780401	1.851066	-1.929335	6031.165569
HLA A*8001	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.369419	2.439993	-1.929426	23410.974424
HLA A*0101	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.369502	2.439993	-1.929509	23415.407621
HLA A*0206	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.203614	2.274057	-1.929557	15981.369192
HLA B*4801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.379243	2.449598	-1.929645	23946.535345
HLA A*3001	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-2.061800	0.132130	-1.929670	115.292209
HLA A*3201	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.357876	2.428102	-1.929775	22796.935512
HLA B*0802	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.341463	2.411682	-1.929781	21951.437651
HLA A*2301	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.392757	2.462765	-1.929991	24703.411061
HLA A*0212	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.420991	2.490827	-1.930163	26362.748488
HLA B*4601	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.305441	2.374610	-1.930831	20204.153734
HLA B*1503	1:23-31	9	SEVHLARDL	1.447686	0.429685	-3.808294	1.877371	-1.930923	6431.234374
HLA A*3301	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-3.456685	1.525646	-1.931038	2862.098054
HLA A*2501	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.456661	2.525575	-1.931085	28619.402833
HLA B*1517	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.193364	1.262230	-1.931133	1560.858836
HLA A*2902	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.371212	2.439993	-1.931219	23507.808682
HLA B*5301	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.469707	2.538391	-1.931317	29492.205938
HLA B*5701	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.361405	2.429816	-1.931589	22982.930151
HLA A*2501	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.394467	2.462765	-1.931702	24800.894797
HLA B*5701	1:369-377	9	SSADAIATL	1.558793	0.442595	-3.933174	2.001388	-1.931786	8573.816094
HLA A*0211	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.517458	2.585626	-1.931832	32919.876025
HLA B*1503	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-3.458122	1.525910	-1.932212	2871.589742
HLA A*0219	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.432722	2.500470	-1.932251	27084.552531
HLA B*3901	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.423223	2.490827	-1.932395	26498.585819
HLA A*0219	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.291405	2.358694	-1.932710	19561.621030
HLA B*5101	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.581170	1.648439	-1.932731	3812.146848
HLA B*4501	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.458387	2.525575	-1.932812	28733.427810
HLA A*3201	1:118-126	9	VIADACQAL	1.609592	0.433733	-3.976320	2.043325	-1.932995	9469.348635
HLA A*0101	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.344924	2.411682	-1.933241	22127.062363
HLA B*0802	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.363478	2.429816	-1.933662	23092.855761
HLA A*2601	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.015477	2.081726	-1.933750	10362.788235
HLA A*0216	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.309094	2.374610	-1.934484	20374.835618
HLA A*0201	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.384708	2.449598	-1.935110	24249.768078
HLA A*0211	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.342560	2.407316	-1.935244	22006.966278
HLA B*0702	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.310083	2.374610	-1.935473	20421.293482
HLA B*1501	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.381788	1.445980	-1.935808	2408.727248
HLA A*6901	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.809558	1.873374	-1.936184	6449.979879
HLA B*5701	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.375220	2.438231	-1.936989	23725.772895
HLA B*4501	1:345-353	9	VVTIAINTF	1.511825	1.191327	-4.640209	2.703152	-1.937057	43672.633838
HLA A*6802	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.065154	2.127896	-1.937258	11618.608936
HLA A*0250	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.546792	1.609050	-1.937742	3522.021131
HLA B*5401	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.378658	2.439993	-1.938665	23914.299585
HLA A*0202	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.464416	2.525575	-1.938841	29135.080179
HLA A*2601	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.379085	2.439993	-1.939092	23937.857195
HLA B*4601	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.336205	2.397104	-1.939101	21687.266739
HLA A*2601	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.389108	2.449598	-1.939510	24496.733348
HLA A*2403	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.048017	2.106921	-1.941096	11169.069431
HLA B*0702	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.371212	2.429816	-1.941396	23507.808682
HLA A*0202	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.495918	2.554318	-1.941601	31326.949898
HLA A*0219	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.353739	2.411682	-1.942057	22580.784579
HLA B*0803	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.354063	2.411682	-1.942381	22597.648890
HLA B*3901	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.442989	2.500470	-1.942519	27732.493149
HLA A*6901	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.370752	2.428102	-1.942650	23482.895664
HLA B*3901	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.481271	2.538391	-1.942881	30288.057633
HLA A*6802	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.432475	2.489515	-1.942960	27069.171835
HLA B*5801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.340117	2.397104	-1.943012	21883.496484
HLA A*0203	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.340182	2.397104	-1.943078	21886.811579
HLA B*1517	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.511897	1.568231	-1.943667	3250.105106
HLA B*4402	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.374208	2.429816	-1.944392	23670.516851
HLA B*3501	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.982231	2.037813	-1.944418	9599.119773
HLA B*1503	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-2.842929	0.898050	-1.944878	696.511901
HLA A*0201	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.352672	2.407316	-1.945356	22525.392200
HLA B*1503	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.126619	1.181170	-1.945449	1338.503334
HLA B*4001	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.375542	2.429816	-1.945726	23743.363883

HLA A*2402	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.343000	2.397104	-1.945895	22029.240874
HLA A*2403	1:427-435	9	REIPDVSTL	1.524929	0.472437	-3.943399	1.997366	-1.946033	8778.071672
HLA B*5701	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.343448	2.397104	-1.946344	22052.015207
HLA B*3801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.409267	2.462765	-1.946501	25660.597001
HLA A*2601	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.262725	2.316186	-1.946539	18311.531888
HLA B*3801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.984445	2.037813	-1.946632	9648.162855
HLA A*0301	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.358577	2.411682	-1.946894	22833.717163
HLA B*3901	1:23-31	9	SEVHLARDL	1.447686	0.429685	-3.824346	1.877371	-1.946975	6673.382505
HLA B*3501	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.344513	2.397104	-1.947408	22106.123909
HLA A*2602	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.473102	2.525575	-1.947527	29723.658546
HLA A*2501	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.387743	2.439993	-1.947750	24419.857428
HLA A*3001	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.264670	2.316186	-1.948484	18393.740332
HLA A*6802	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-2.966455	1.017549	-1.948906	925.667604
HLA A*0212	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.438626	2.489515	-1.949111	27455.282753
HLA B*4001	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.377617	2.428102	-1.949515	23857.055654
HLA A*0219	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.258857	2.309312	-1.949546	18149.197442
HLA B*1517	1:58-66	9	REAQNAAAL	1.509434	0.528379	-3.987386	2.037813	-1.949573	9713.733420
HLA A*3002	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.399479	2.449598	-1.949881	25088.737157
HLA A*0219	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.266308	2.316186	-1.950122	18463.228402
HLA B*3801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.362291	2.411682	-1.950609	23029.852318
HLA A*2402	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.413388	2.462765	-1.950622	25905.247913
HLA A*3301	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.571806	2.621122	-1.950684	37308.387432
HLA A*1101	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.400388	2.449598	-1.950790	25141.318641
HLA A*0211	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.505586	2.554318	-1.951269	32032.161342
HLA A*2403	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.348575	2.397104	-1.951471	22313.867996
HLA B*0702	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.389815	2.438231	-1.951584	24536.655751
HLA A*0202	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.226315	2.274057	-1.952258	16838.938412
HLA B*5101	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.359667	2.407316	-1.952350	22891.106097
HLA B*4801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.359770	2.407316	-1.952454	22896.555633
HLA B*5801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.250099	2.297586	-1.952512	17786.829629
HLA A*2603	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.415307	2.462765	-1.952542	26019.999392
HLA A*6901	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.364335	2.411682	-1.952653	23138.500184
HLA A*6901	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.772770	1.819741	-1.953029	5926.115665
HLA B*0803	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.311751	2.358694	-1.953057	20499.882940
HLA A*6901	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.328334	2.374610	-1.953724	21297.765763
HLA B*0702	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.403574	2.449598	-1.953976	25326.428705
HLA B*4801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.351105	2.397104	-1.954001	22444.258133
HLA A*2501	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.443931	2.489515	-1.954416	27792.720368
HLA A*1101	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.417269	2.462765	-1.954504	26137.804305
HLA A*0206	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-2.950493	0.995952	-1.954541	892.262547
HLA B*4801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.313699	2.358694	-1.955005	20592.027246
HLA B*1517	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.252732	2.297586	-1.955146	17895.025347
HLA A*2402	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.850266	1.894713	-1.955552	7083.787700
HLA A*0203	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.418420	2.462765	-1.955655	26207.183507
HLA B*3801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.481337	2.525575	-1.955762	30292.645921
HLA B*0702	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.352943	2.397104	-1.955838	22539.410445
HLA B*4403	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.577664	2.621122	-1.956542	37814.968607
HLA B*1503	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.266103	2.309312	-1.956791	18454.540537
HLA A*0201	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.368724	2.411682	-1.957042	23373.515794
HLA A*2402	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.397101	2.439993	-1.957108	24951.756456
HLA B*0803	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.447986	2.490827	-1.957159	28053.449404
HLA B*3801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.331851	2.374610	-1.957241	21470.948257
HLA A*0219	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.446859	2.489515	-1.957343	27980.696201
HLA A*6802	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.512095	1.554751	-1.957343	3251.582389
HLA A*3101	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.395659	2.438231	-1.957427	24869.012408
HLA B*4501	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.420262	2.462765	-1.957497	26318.573481
HLA B*0801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.316253	2.358694	-1.957559	20713.476426
HLA A*0216	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.420338	2.462765	-1.957572	26323.130053
HLA B*0702	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.447098	2.489515	-1.957583	27996.140453
HLA B*1801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.387527	2.429816	-1.957711	24407.706449
HLA A*2602	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.332340	2.374610	-1.957730	21495.122189
HLA A*0219	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.365515	2.407316	-1.958198	23201.424303
HLA A*1101	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.388131	2.429816	-1.958315	24441.665098
HLA A*0211	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.450329	2.490827	-1.959502	28205.168951
HLA B*0802	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.388126	2.428102	-1.960024	24441.400646

HLA B*5801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.269754	2.309312	-1.960442	18610.341252
HLA A*2602	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.390377	2.429816	-1.960561	24568.401270
HLA B*1501	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.293362	1.332686	-1.960677	1964.999336
HLA B*4002	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.461150	2.500470	-1.960680	28916.813463
HLA A*6802	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.151167	1.190001	-1.961165	1416.337900
HLA B*0802	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.320005	2.358694	-1.961311	20893.207715
HLA A*3301	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-3.061407	1.099547	-1.961860	1151.879772
HLA A*0212	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.320837	2.358694	-1.962142	20933.258652
HLA B*1503	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.188552	1.226371	-1.962181	1543.660822
HLA B*1509	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.260136	2.297586	-1.962549	18202.688835
HLA A*2301	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.581799	1.618772	-1.963027	3817.677899
HLA B*0803	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.412777	2.449598	-1.963179	25868.835952
HLA A*2301	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.083236	2.120022	-1.963214	12112.555244
HLA A*0250	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.584710	2.621122	-1.963588	38433.492373
HLA B*4402	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.371081	2.407316	-1.963764	23500.687981
HLA A*6802	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.393781	2.429816	-1.963965	24761.748058
HLA B*4001	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.280266	2.316186	-1.964080	19066.278507
HLA A*0201	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.392219	2.428102	-1.964117	24672.825829
HLA A*0203	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.413872	2.449598	-1.964274	25934.133777
HLA A*2402	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.323482	2.358694	-1.964788	21061.163506
HLA A*8001	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.377013	2.411682	-1.965331	23823.909247
HLA B*1801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.785100	1.819741	-1.965359	6096.775747
HLA B*1509	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.100833	2.135178	-1.965656	12613.436162
HLA B*3801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.275116	2.309312	-1.965804	18841.516782
HLA A*6802	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-2.863186	0.897363	-1.965823	729.769655
HLA A*2902	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.363539	2.397104	-1.966434	23096.104163
HLA A*0206	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.034148	1.067242	-1.966907	1081.803611
HLA A*2602	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.552865	2.585626	-1.967239	35716.173994
HLA A*3002	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.430158	2.462765	-1.967393	26925.165211
HLA B*4801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.395870	2.428102	-1.967768	24881.123830
HLA A*0212	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.417452	2.449598	-1.967854	26148.836037
HLA A*0301	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.365096	2.397104	-1.967992	23179.093007
HLA B*1509	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.365139	2.397104	-1.968034	23181.350250
HLA A*3002	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.326852	2.358694	-1.968157	21225.186807
HLA A*3001	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.277564	2.309312	-1.968252	18948.028307
HLA A*0203	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.277792	2.309312	-1.968480	18957.974069
HLA A*0216	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.458075	2.489515	-1.968560	28712.761106
HLA A*2601	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.396817	2.428102	-1.968715	24935.428466
HLA A*0203	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.235442	2.266682	-1.968760	17196.594782
HLA A*2601	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.366217	2.397104	-1.969113	23238.984295
HLA B*4001	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.366290	2.397104	-1.969186	23242.881952
HLA A*3002	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.458888	2.489515	-1.969373	28766.556606
HLA A*0301	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.344698	2.374610	-1.970088	22115.573671
HLA A*2603	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-2.999343	1.028753	-1.970590	998.488704
HLA A*2902	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.237559	2.266682	-1.970877	17280.620937
HLA A*6901	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.300651	1.329751	-1.970900	1998.253169
HLA A*3001	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.277579	1.306673	-1.970905	1894.866281
HLA B*1509	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.345570	2.374610	-1.970960	22160.005725
HLA B*5401	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-2.523554	0.552387	-1.971167	333.851742
HLA A*3002	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.497126	2.525575	-1.971550	31414.181442
HLA A*8001	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.368731	2.397104	-1.971627	23373.895141
HLA A*0206	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.510732	2.538765	-1.971966	32413.924443
HLA A*0201	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.238955	2.266682	-1.972273	17336.241085
HLA A*0216	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.229522	1.257069	-1.972453	1696.376320
HLA A*2301	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.526797	2.554318	-1.972480	33635.461735
HLA A*2403	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.034146	2.061629	-1.972517	10817.966475
HLA B*3501	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.239225	2.266682	-1.972543	17347.029962
HLA A*2603	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.331402	2.358694	-1.972708	21448.774024
HLA B*1503	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-3.781872	1.809098	-1.972775	6051.625282
HLA B*4002	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-2.215630	0.242669	-1.972961	164.297193
HLA A*6802	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.331701	2.358694	-1.973006	21463.515595
HLA B*3801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.370336	2.397104	-1.973231	23460.420370
HLA B*3901	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.541694	1.568231	-1.973463	3480.916253
HLA B*1501	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.401640	2.428102	-1.973539	25213.917520
HLA A*0101	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.283034	2.309312	-1.973722	19188.173024

HLA A*3002	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.290023	2.316186	-1.973837	19499.494090
HLA B*0702	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.402362	2.428102	-1.974260	25255.828495
HLA A*0211	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.287211	1.312789	-1.974422	1937.365030
HLA B*1503	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.003257	1.028753	-1.974504	1007.528634
HLA A*0203	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.056480	2.081726	-1.974754	11388.849021
HLA A*2603	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.241443	2.266682	-1.974761	17435.846720
HLA A*3301	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.845792	1.870848	-1.974944	7011.196153
HLA B*1502	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.464534	2.489515	-1.975018	29142.962123
HLA B*2705	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.291398	2.316186	-1.975212	19561.303554
HLA A*2301	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.870020	1.894713	-1.975307	7413.443925
HLA A*0101	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.403541	2.428102	-1.975439	25324.510593
HLA A*2902	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.350093	2.374610	-1.975483	22391.986668
HLA B*3501	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.250244	2.274057	-1.976187	17792.796565
HLA B*1517	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.242944	2.266682	-1.976262	17496.225334
HLA B*4601	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.405150	2.428102	-1.977049	25418.531611
HLA B*1509	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.335808	2.358694	-1.977113	21667.447755
HLA B*0801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.058933	2.081726	-1.977206	11453.354366
HLA B*5101	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.389395	2.411682	-1.977712	24512.906687
HLA B*1502	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.851102	1.873374	-1.977728	7097.443659
HLA A*0219	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.427588	2.449598	-1.977990	26766.281443
HLA B*1509	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.468041	2.489515	-1.978526	29379.301963
HLA B*5301	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.547079	1.568231	-1.978848	3524.346455
HLA A*6802	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.428542	2.449598	-1.978944	26825.135916
HLA A*3301	1:194-202	9	DARSDVYSL	1.476461	0.343280	-3.798995	1.819741	-1.979254	6294.990446
HLA A*0250	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.470177	2.490827	-1.979350	29524.133120
HLA B*5801	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.547633	1.568231	-1.979402	3528.848981
HLA A*6802	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.442204	2.462765	-1.979439	27682.428470
HLA B*5701	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.407554	2.428102	-1.979452	25559.595799
HLA A*3001	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.277228	2.297586	-1.979642	18933.375513
HLA B*4002	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.601278	2.621122	-1.980156	39928.079166
HLA B*3501	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.278238	2.297586	-1.980652	18977.470590
HLA A*0206	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.430523	2.449598	-1.980925	26947.752315
HLA A*0202	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.471798	2.490827	-1.980971	29634.547448
HLA B*0702	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.392938	2.411682	-1.981255	24713.703694
HLA A*0216	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.388721	2.407316	-1.981404	24474.876543
HLA B*1502	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.255639	2.274057	-1.981582	18015.181039
HLA A*6901	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.379257	2.397104	-1.982152	23947.312647
HLA A*0216	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.231740	1.249564	-1.982177	1705.061764
HLA A*1101	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-3.220904	1.238694	-1.982210	1663.046109
HLA B*4403	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.567876	2.585626	-1.982250	36972.242225
HLA B*5101	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.471796	2.489515	-1.982281	29634.387129
HLA A*3001	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.295618	1.312789	-1.982828	1975.231094
HLA B*0801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.103150	2.120022	-1.983128	12680.897896
HLA A*6802	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.421595	2.438231	-1.983363	26399.427203
HLA B*4403	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.522526	2.538765	-1.983761	33306.272438
HLA A*2301	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.522733	2.538765	-1.983967	33322.132338
HLA A*0219	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.381371	2.397104	-1.984267	24064.194034
HLA A*0212	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.381385	2.397104	-1.984281	24064.975154
HLA A*1101	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.422560	2.438231	-1.984329	26458.190696
HLA A*3101	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.381639	2.397104	-1.984535	24079.039658
HLA B*5101	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.414638	2.429816	-1.984822	25979.912190
HLA A*6801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-3.347993	1.363134	-1.984859	2228.397350
HLA B*5701	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.359507	2.374610	-1.984897	22882.686638
HLA A*0216	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.670234	1.685171	-1.985063	4679.871186
HLA A*6802	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.014433	2.028437	-1.985996	10337.926784
HLA A*6901	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.001115	1.014988	-1.986127	1002.569913
HLA A*0216	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.247742	2.261413	-1.986329	17690.577551
HLA A*0212	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.394472	2.407316	-1.987156	24801.163139
HLA A*6802	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.303615	2.316186	-1.987429	20119.404146
HLA A*0202	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.437118	2.449598	-1.987520	27360.091872
HLA A*3101	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.107755	2.120022	-1.987733	12816.073704
HLA B*3801	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.426608	2.438231	-1.988377	26705.966811
HLA B*5101	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.451186	2.462765	-1.988421	28260.918170
HLA A*2603	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.428603	2.439993	-1.988610	26828.909328
HLA A*3101	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-3.606577	1.616917	-1.989659	4041.819851

HLA B*0702	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.256463	2.266682	-1.989781	18049.422045
HLA A*0219	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.072499	2.081726	-1.990772	11816.765696
HLA A*6802	1:289-297	9	TDAERTSLL	1.288079	0.301720	-3.580587	1.589799	-1.990788	3807.035701
HLA A*3201	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.529734	2.538765	-1.990969	33863.687688
HLA B*2705	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-3.813510	1.822112	-1.991398	6508.938882
HLA A*0211	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.403163	2.411682	-1.991480	25302.462747
HLA B*5101	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.390570	1.398961	-1.991609	2457.932774
HLA B*4402	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.419767	2.428102	-1.991665	26288.548322
HLA A*1101	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.431829	2.439993	-1.991836	27028.930441
HLA B*1801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.053698	2.061629	-1.992069	11316.133059
HLA A*0211	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.517750	2.525575	-1.992174	32941.966951
HLA A*0219	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.366992	2.374610	-1.992383	23280.509059
HLA A*0212	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.259210	2.266682	-1.992528	18163.931191
HLA B*0801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.420746	2.428102	-1.992645	26347.920227
HLA B*1509	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.399965	2.407316	-1.992649	25116.848442
HLA A*3301	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.578437	2.585626	-1.992811	37882.333644
HLA B*1501	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.302140	2.309312	-1.992828	20051.166256
HLA A*0203	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.309209	2.316186	-1.993023	20380.237389
HLA A*2301	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.351787	2.358694	-1.993092	22479.497844
HLA A*0202	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.031030	2.037813	-1.993217	10740.641330
HLA A*2501	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.022237	1.028753	-1.993483	1052.534979
HLA A*3101	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-2.744001	0.750403	-1.993598	554.627151
HLA B*5401	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.494123	2.500470	-1.993653	31197.737960
HLA B*3901	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.423967	2.429816	-1.994151	26544.068156
HLA A*0301	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-3.232882	1.238694	-1.994188	1709.550621
HLA A*2402	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.613780	1.618772	-1.995008	4109.419464
HLA A*6901	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.412336	1.417212	-1.995124	2584.256573
HLA B*5401	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.549693	2.554318	-1.995376	35456.276479
HLA B*1503	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.123609	2.127896	-1.995713	13292.581175
HLA B*1509	1:25-33	9	VHLARDLRL	1.381366	0.381622	-3.758762	1.762988	-1.995775	5738.025767
HLA A*2601	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.370566	2.374610	-1.995956	23472.861659
HLA A*0216	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.408412	2.411682	-1.996729	25610.115883
HLA A*0203	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.355842	2.358694	-1.997147	22690.382483
HLA B*3901	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.447803	2.449598	-1.998205	28041.614149
HLA A*8001	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.295876	2.297586	-1.998290	19764.048501
HLA A*0101	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.395567	2.397104	-1.998463	24863.765956
HLA A*0250	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.436756	2.438231	-1.998525	27337.307045
HLA A*6802	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.296207	2.297586	-1.998621	19779.130157
HLA A*0101	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.373254	2.374610	-1.998644	23618.583627
HLA A*6901	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.649079	1.650328	-1.998751	4457.374624
HLA A*2602	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.567030	1.568231	-1.998800	3690.034452
HLA A*0201	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.396208	2.397104	-1.999104	24900.514375
HLA B*3901	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.396323	2.397104	-1.999219	24907.115992
HLA B*1509	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.000910	2.001388	-1.999522	10020.971255
HLA B*1509	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.462671	2.462765	-1.999905	29018.205386
HLA A*0250	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.585542	2.585626	-1.999916	38507.166908
HLA B*7301	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.621045	2.621122	-1.999923	41787.331200
HLA A*0212	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.428493	2.428102	-2.000391	26822.088548
HLA B*3501	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.895376	1.894713	-2.000662	7859.151289
HLA B*5301	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.463871	2.462765	-2.001106	29098.535845
HLA B*4601	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.359902	2.358694	-2.001207	22903.493282
HLA A*0202	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.586994	2.585626	-2.001368	38636.123813
HLA A*8001	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.360118	2.358694	-2.001423	22914.895412
HLA B*3901	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.268356	2.266682	-2.001674	18550.533031
HLA A*6901	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.360686	2.358694	-2.001992	22944.915083
HLA A*2603	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.556899	2.554318	-2.002581	36049.479267
HLA B*0802	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.300359	2.297586	-2.002772	19969.110876
HLA A*0301	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.361485	2.358694	-2.002791	22987.157933
HLA B*4601	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.319068	2.316186	-2.002882	20848.157409
HLA B*4801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.312588	2.309312	-2.003276	20539.402129
HLA B*3901	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.431401	2.428102	-2.003300	27002.330858
HLA A*2601	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.362395	2.358694	-2.003700	23035.334885
HLA A*0211	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.493486	2.489515	-2.003971	31152.033093
HLA A*2402	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.542821	2.538765	-2.004055	34899.634736
HLA B*4601	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.301656	2.297586	-2.004069	20028.832938

HLA A*1101	1:254-262	9	ALAKNPENR	1.033268	0.766480	-3.804436	1.799748	-2.004688	6374.358465
HLA A*2501	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.454642	2.449598	-2.005044	28486.714302
HLA A*0203	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.020056	1.014988	-2.005068	1047.264098
HLA B*3501	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.604110	1.598716	-2.005394	4018.925849
HLA B*0801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-2.804388	0.798696	-2.005691	637.364087
HLA A*0101	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.364533	2.358694	-2.005838	23149.017418
HLA B*4403	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-3.871237	1.865170	-2.006067	7434.247922
HLA A*3101	1:350-358	9	INTFGGITR	1.090401	0.639154	-3.735648	1.729555	-2.006094	5440.618334
HLA B*1503	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.446892	1.440103	-2.006788	2798.284423
HLA A*0212	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.004331	1.997366	-2.006964	10100.216116
HLA A*3001	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.268420	2.261413	-2.007007	18553.242849
HLA B*5101	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.445294	2.438231	-2.007063	27880.063538
HLA B*0803	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.382034	2.374610	-2.007424	24100.934115
HLA A*0216	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.083173	1.075727	-2.007446	1211.079856
HLA A*3301	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.546068	2.538391	-2.007677	35161.538534
HLA A*0211	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.546690	2.538765	-2.007925	35211.982991
HLA A*0203	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.436135	2.428102	-2.008034	27298.291477
HLA B*4601	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.274963	2.266682	-2.008281	18834.892463
HLA A*0219	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.269907	2.261413	-2.008494	18616.886595
HLA B*5701	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.617596	1.609050	-2.008546	4145.682490
HLA B*1503	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-2.991021	0.982334	-2.008688	979.537981
HLA B*1509	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.438729	2.429816	-2.008913	27461.818853
HLA A*2501	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.421073	2.411682	-2.009391	26367.740645
HLA B*3901	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.417074	2.407316	-2.009758	26126.070522
HLA A*2501	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.368595	2.358694	-2.009900	23366.562181
HLA A*3101	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.368889	2.358694	-2.010194	23382.368839
HLA A*0206	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-2.384098	0.373369	-2.010728	242.157328
HLA B*0801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.049685	2.037813	-2.011872	11212.052561
HLA A*2301	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.502809	2.490827	-2.011982	31827.985535
HLA A*2301	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.409932	2.397104	-2.012827	25699.913429
HLA B*4501	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-2.255689	0.242669	-2.013020	180.172648
HLA B*1509	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.462819	2.449598	-2.013221	29028.097144
HLA A*0206	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.599026	1.585464	-2.013561	3972.150617
HLA A*3001	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.864705	1.851066	-2.013640	7323.277175
HLA A*8001	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.388321	2.374610	-2.013711	24452.377808
HLA A*2603	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.463399	2.449598	-2.013801	29066.911651
HLA B*0801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.042031	2.028058	-2.013973	11016.166794
HLA A*2402	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.568945	2.554318	-2.014627	37063.361482
HLA A*6802	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.442782	2.428102	-2.014681	27719.293677
HLA B*5801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-3.936792	1.922093	-2.014699	8645.544901
HLA A*0201	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.373416	2.358694	-2.014722	23627.401673
HLA B*5801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.331442	2.316186	-2.015256	21450.746718
HLA A*6802	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.427196	2.411682	-2.015513	26742.110327
HLA B*3801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.445681	2.429816	-2.015865	27904.961277
HLA A*6802	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-3.118800	1.102823	-2.015978	1314.620412
HLA A*0219	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.886856	1.870848	-2.016009	7706.486402
HLA A*6901	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.645395	1.629324	-2.016071	4419.723940
HLA B*0801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.290352	2.274057	-2.016295	19514.268298
HLA B*1801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.313934	2.297586	-2.016348	20603.170319
HLA B*1509	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.444549	2.428102	-2.016447	27832.292019
HLA A*0211	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.516918	2.500470	-2.016447	32878.940136
HLA A*2601	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.314472	2.297586	-2.016886	20628.710674
HLA A*2402	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.014523	1.997366	-2.017156	10340.052230
HLA A*6901	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.145065	2.127896	-2.017169	13965.767837
HLA A*2603	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.507602	2.489515	-2.018087	32181.190146
HLA B*4402	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.392708	2.374610	-2.018098	24700.604724
HLA B*1503	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.883302	0.865145	-2.018157	764.367286
HLA B*5401	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.557071	2.538391	-2.018680	36063.718808
HLA A*6802	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.422509	1.403484	-2.019025	2645.506906
HLA A*6802	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.892707	1.873374	-2.019333	7810.999933
HLA B*4001	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.293489	2.274057	-2.019432	19655.714447
HLA A*8001	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.447636	2.428102	-2.019535	28030.845374
HLA A*3101	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.065070	2.044529	-2.020541	11616.346362
HLA A*0216	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.470663	2.449598	-2.021066	29557.214152
HLA A*2403	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.330695	2.309312	-2.021383	21413.875763

HLA B*7301	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.522073	2.500470	-2.021602	33271.515220
HLA A*0216	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.295669	2.274057	-2.021612	19754.641665
HLA A*0202	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-2.435786	0.414162	-2.021624	272.763519
HLA A*0202	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-3.343482	1.321448	-2.022033	2205.370810
HLA A*3001	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.707332	1.685171	-2.022161	5097.206960
HLA B*5701	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.157818	2.135178	-2.022640	14381.951596
HLA A*2603	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.561471	2.538765	-2.022706	36431.000095
HLA A*0211	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.284370	2.261413	-2.022958	19247.329577
HLA B*3501	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.671756	1.648439	-2.023318	4696.305770
HLA A*0211	1:517-525	9	FTKFSQASV	0.794238	0.070907	-2.888560	0.865145	-2.023415	773.677985
HLA A*0202	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.021064	1.997366	-2.023697	10496.963781
HLA A*0250	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.578669	2.554318	-2.024352	37902.628062
HLA A*1101	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.436563	2.411682	-2.024881	27325.182606
HLA B*1517	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.053402	2.028437	-2.024965	11308.422090
HLA A*6802	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.422506	2.397104	-2.025402	26454.898776
HLA B*5701	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.384940	2.358694	-2.026246	24262.759224
HLA A*2603	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.064623	2.038259	-2.026364	11604.412299
HLA B*3501	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.454938	2.428102	-2.026837	28506.138778
HLA B*5401	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.517759	2.490827	-2.026932	32942.679808
HLA B*1801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.071639	2.044529	-2.027110	11793.391419
HLA B*1801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.293952	2.266682	-2.027269	19676.673655
HLA A*0211	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.024785	1.997366	-2.027419	10587.301551
HLA A*2602	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.490721	2.462765	-2.027956	30954.304587
HLA B*4001	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-2.570586	0.542619	-2.027966	372.036575
HLA B*3801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.456339	2.428102	-2.028237	28598.199283
HLA B*1502	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.163969	2.135178	-2.028791	14587.093762
HLA A*0202	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.567667	2.538765	-2.028901	36954.445110
HLA A*0211	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.491877	2.462765	-2.029112	31036.804335
HLA B*1517	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.458463	2.428102	-2.030361	28738.402470
HLA B*1509	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.346646	2.316186	-2.030460	22214.980296
HLA B*4501	1:374-382	9	IATLQNRGF	1.437491	1.183631	-4.651654	2.621122	-2.030532	44838.773633
HLA B*1801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.663463	1.632662	-2.030801	4607.471775
HLA B*5701	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.461313	1.430389	-2.030924	2892.763932
HLA B*3501	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.166567	2.135178	-2.031390	14674.634898
HLA B*7301	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.617098	2.585626	-2.031472	41409.262947
HLA A*3002	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.093813	2.061629	-2.032184	12411.182231
HLA B*1502	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.075614	2.043325	-2.032289	11901.838188
HLA B*3901	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.665563	1.632662	-2.032901	4629.809514
HLA B*5801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.294396	2.261413	-2.032983	19696.802734
HLA A*0219	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.461569	2.428102	-2.033467	28944.672617
HLA B*5301	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.445235	2.411682	-2.033553	27876.293091
HLA B*5101	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.483189	2.449598	-2.033591	30422.058895
HLA A*0250	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.408362	2.374610	-2.033752	25607.206542
HLA B*3801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.031495	1.997366	-2.034129	10752.152418
HLA B*2705	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.099222	2.064862	-2.034359	12566.712134
HLA B*4801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.301606	2.266682	-2.034924	20026.557638
HLA B*3801	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.442246	2.407316	-2.034930	27685.124261
HLA A*0202	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.525301	2.489515	-2.035786	33519.750083
HLA A*2603	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.465619	2.429816	-2.035803	29215.892234
HLA B*1501	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.352322	2.316186	-2.036136	22507.242394
HLA A*0211	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.273443	1.236758	-2.036685	1876.910112
HLA B*4002	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.448374	2.411682	-2.036692	28078.501982
HLA A*1101	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.395774	2.358694	-2.037079	24875.605673
HLA B*1503	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-2.769615	0.732333	-2.037282	588.322166
HLA A*0203	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-2.953622	0.916314	-2.037308	898.715388
HLA A*0202	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-2.811182	0.773768	-2.037414	647.414318
HLA B*1801	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.466371	2.428102	-2.038269	29266.513555
HLA B*5301	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.528101	2.489515	-2.038586	33736.603584
HLA B*5701	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.347990	2.309312	-2.038678	22283.830060
HLA A*2602	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.593553	2.554318	-2.039236	39224.129245
HLA B*4001	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.397968	2.358694	-2.039274	25001.616127
HLA B*0802	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.414067	2.374610	-2.039457	25945.781357
HLA B*7301	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.593964	2.554318	-2.039647	39261.281512
HLA A*0206	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.398419	2.358694	-2.039725	25027.598765
HLA A*2501	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.436871	2.397104	-2.039767	27344.554703

HLA A*6801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.101482	2.061629	-2.039853	12632.283721
HLA A*2602	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.934715	1.894713	-2.040002	8604.297656
HLA B*4801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.078518	2.038259	-2.040259	11981.687958
HLA B*1503	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.173318	1.133041	-2.040277	1490.451407
HLA A*6901	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.302022	2.261413	-2.040610	20045.743260
HLA A*0203	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.116404	1.075727	-2.040677	1307.386200
HLA B*7301	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.248945	2.208172	-2.040773	17739.645957
HLA B*0801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.249020	2.208172	-2.040849	17742.717247
HLA A*0301	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.112059	2.070592	-2.041467	12943.724268
HLA A*0206	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-2.815402	0.773768	-2.041634	653.735358
HLA A*0212	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.123370	2.081726	-2.041643	13285.248236
HLA B*5401	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.567495	2.525575	-2.041920	36939.853871
HLA A*6901	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.316551	2.274057	-2.042494	20727.712632
HLA B*1517	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-3.915896	1.873374	-2.042522	8239.408801
HLA A*0211	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.170693	2.127896	-2.042797	14814.704748
HLA A*3101	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.178738	2.135178	-2.043560	15091.681712
HLA B*2705	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-3.795447	1.751118	-2.044330	6243.776559
HLA A*2602	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.042806	1.997366	-2.045440	11035.851119
HLA A*2602	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.535483	2.489515	-2.045968	34314.955493
HLA A*0219	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-2.844827	0.798791	-2.046036	699.563151
HLA A*0202	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.580220	1.534036	-2.046184	3803.824136
HLA B*1503	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.449965	1.403484	-2.046481	2818.155684
HLA B*1517	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.362989	2.316186	-2.046803	23066.884979
HLA B*4501	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.537631	2.490827	-2.046804	34485.050733
HLA A*1101	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.182036	2.135178	-2.046859	15206.746778
HLA B*4601	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.356284	2.309312	-2.046972	22713.471684
HLA A*6801	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.487432	2.439993	-2.047439	30720.747069
HLA A*6802	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-3.192640	1.144551	-2.048089	1558.260227
HLA A*2402	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.539200	2.490827	-2.048373	34609.898466
HLA A*1101	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.423169	2.374610	-2.048559	26495.288873
HLA A*2403	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.890376	1.840969	-2.049407	7769.193622
HLA B*5301	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.499048	2.449598	-2.049450	31553.506332
HLA A*0216	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.477703	2.428102	-2.049601	30040.181706
HLA B*4002	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.635299	2.585626	-2.049673	43181.622933
HLA B*1509	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.311145	2.261413	-2.049733	20471.290159
HLA B*5701	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.347478	2.297586	-2.049891	22257.564986
HLA A*2603	1:575-583	9	EPRLRALGW	1.410483	0.250517	-3.711477	1.661000	-2.050477	5146.082673
HLA B*1801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.121462	2.070592	-2.050870	13227.016394
HLA A*0301	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.360289	2.309312	-2.050977	22923.946793
HLA B*4403	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.449069	2.397104	-2.051965	28123.500870
HLA B*3901	1:136-144	9	HRDVKPANI	1.262411	0.208757	-3.523217	1.471168	-2.052049	3335.932272
HLA B*1517	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-3.919312	1.866969	-2.052343	8304.475387
HLA A*2602	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.349938	2.297586	-2.052351	22383.992976
HLA A*0301	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.368592	2.316186	-2.052406	23366.435771
HLA B*4002	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.326767	2.274057	-2.052710	21221.053477
HLA A*0216	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.180796	2.127896	-2.052900	15163.371878
HLA A*0206	1:459-467	9	STPELVGKV	0.780846	0.079303	-2.913563	0.860149	-2.053415	819.527362
HLA B*0702	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.412690	2.358694	-2.053996	25863.658411
HLA A*3301	1:218-226	9	GDSPVSVAY	1.493899	1.060419	-4.608999	2.554318	-2.054681	40644.223014
HLA A*3001	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.183244	2.127896	-2.055348	15249.090766
HLA A*0211	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.505001	2.449598	-2.055403	31989.041071
HLA B*1509	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.083964	2.028437	-2.055527	12132.885838
HLA B*4001	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.263841	2.208172	-2.055669	18358.647493
HLA A*1101	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.365165	2.309312	-2.055853	23182.729785
HLA B*4403	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.896983	1.840969	-2.056013	7888.286884
HLA A*0216	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.453136	2.397104	-2.056032	28388.100895
HLA A*2402	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.897274	1.840969	-2.056305	7893.580329
HLA B*1503	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-3.916032	1.859413	-2.056619	8241.994515
HLA B*0801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.675741	1.618772	-2.056969	4739.593466
HLA A*1101	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.454325	2.397104	-2.057221	28465.917052
HLA A*2602	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.085379	2.028058	-2.057321	12172.464067
HLA A*6802	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.456539	1.398961	-2.057578	2861.138230
HLA A*1101	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.319242	2.261413	-2.057829	20856.505261
HLA A*0250	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.596612	2.538765	-2.057847	39501.386599
HLA A*6802	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.319336	2.261413	-2.057923	20861.019004

HLA A*0250	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.402003	1.343697	-2.058306	2523.495848
HLA A*3001	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.266592	2.208172	-2.058420	18475.318324
HLA A*0301	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.357024	2.297586	-2.059437	22752.211052
HLA B*4601	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.166520	2.106921	-2.059599	14673.047221
HLA B*0802	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.369091	2.309312	-2.059779	23393.250028
HLA A*2603	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.434547	2.374610	-2.059937	27198.641628
HLA B*7301	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-3.454791	1.394783	-2.060008	2849.645415
HLA A*3002	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.492556	1.431809	-2.060747	3108.539895
HLA B*0803	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.359049	2.297586	-2.061463	22858.559771
HLA B*1503	1:366-374	9	RGQSSADAI	1.357283	0.227759	-3.646523	1.585042	-2.061481	4431.215758
HLA B*0702	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.063087	2.001388	-2.061698	11563.427651
HLA B*0801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.378113	2.316186	-2.061927	23884.303712
HLA A*0219	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.063627	2.001388	-2.062239	11577.824684
HLA A*0203	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.323696	2.261413	-2.062284	21071.534468
HLA A*1101	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.360104	2.297586	-2.062517	22914.151622
HLA A*3101	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.371849	2.309312	-2.062537	23542.298286
HLA A*6901	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.360322	2.297586	-2.062736	22925.683083
HLA A*0250	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.588429	2.525575	-2.062854	38764.044590
HLA B*1501	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.957820	1.894713	-2.063107	9074.448943
HLA B*1503	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-3.872337	1.809179	-2.063158	7453.094007
HLA B*7301	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.602214	2.538765	-2.063448	40014.142366
HLA A*2501	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.379995	2.316186	-2.063808	23988.026642
HLA A*3101	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.337925	2.274057	-2.063868	21773.319431
HLA B*5801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.330620	2.266682	-2.063938	21410.168990
HLA A*0201	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.662819	1.598716	-2.064103	4600.647135
HLA A*0101	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.362380	2.297586	-2.064794	23034.587185
HLA A*0219	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.332321	2.266682	-2.065639	21494.191919
HLA A*3002	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.504087	2.438231	-2.065856	31921.792619
HLA B*3901	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.128144	2.061629	-2.066515	13432.097241
HLA B*4601	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.068091	2.001388	-2.066703	11697.444425
HLA A*3301	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.605526	2.538765	-2.066761	40320.535078
HLA B*1503	1:579-587	9	RALGWTGML	1.320466	0.574247	-3.961664	1.894713	-2.066951	9155.119531
HLA B*5101	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.376506	2.309312	-2.067194	23796.086409
HLA A*2601	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.334151	2.266682	-2.067469	21584.966111
HLA B*4501	1:429-437	9	IPDVSTLTY	1.587135	0.998491	-4.653303	2.585626	-2.067677	45009.383496
HLA B*1502	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.517562	2.449598	-2.067964	32927.713045
HLA B*5801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.342210	2.274057	-2.068153	21989.234193
HLA A*2501	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.496271	2.428102	-2.068169	31352.381515
HLA A*3001	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.557289	1.488986	-2.068303	3608.190479
HLA A*3002	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.508403	2.439993	-2.068410	32240.611904
HLA B*5401	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.476500	2.407316	-2.069183	29957.089641
HLA B*7301	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.608670	2.538391	-2.070279	40613.451365
HLA A*2601	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.380117	2.309312	-2.070805	23994.775764
HLA A*0216	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.679876	1.609050	-2.070827	4784.936577
HLA B*0801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.332300	2.261413	-2.070887	21493.145414
HLA B*5101	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.468530	2.397104	-2.071426	29412.379833
HLA A*0101	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.387875	2.316186	-2.071689	24427.256637
HLA B*0801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.178677	2.106921	-2.071755	15089.559108
HLA A*3101	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.369485	2.297586	-2.071899	23414.520914
HLA A*3301	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.563943	2.490827	-2.073116	36638.927443
HLA A*0212	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.379838	1.306673	-2.073164	2397.935808
HLA B*3801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.924768	1.851066	-2.073702	8409.452201
HLA A*0250	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.481060	2.407316	-2.073744	30273.314269
HLA A*0202	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-3.883187	1.809098	-2.074089	7641.639063
HLA A*3001	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-1.697686	-0.376448	-2.074134	49.852412
HLA A*0202	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.537088	2.462765	-2.074323	34441.982220
HLA B*1501	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.683899	1.609050	-2.074849	4829.459229
HLA A*3301	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.575721	2.500470	-2.075250	37646.163155
HLA B*4002	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.434131	2.358694	-2.075437	27172.610024
HLA A*2602	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.391702	2.316186	-2.075516	24643.478301
HLA A*3201	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.373465	2.297586	-2.075879	23630.086080
HLA B*0803	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.385250	2.309312	-2.075938	24280.091578
HLA B*5101	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.393563	2.316186	-2.077377	24749.293069
HLA B*5701	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.344320	2.266682	-2.077638	22096.319566
HLA B*4402	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.386975	2.309312	-2.077663	24376.696064

HLA B*1503	1:25-33	9	VHLARDLRL	1.381366	0.381622	-3.840731	1.762988	-2.077743	6929.969558
HLA A*0201	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.352099	2.274057	-2.078042	22495.678006
HLA B*4001	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.185034	2.106921	-2.078113	15312.082382
HLA A*0250	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.206664	2.127896	-2.078768	16093.985880
HLA B*5401	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.568480	2.489515	-2.078964	37023.682019
HLA B*1503	1:254-262	9	ALAKNPENR	1.033268	0.766480	-3.878910	1.799748	-2.079162	7566.768690
HLA A*3301	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.486497	2.407316	-2.079180	30654.672285
HLA B*7301	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.604915	2.525575	-2.079340	40263.861243
HLA B*3801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-3.936567	1.857104	-2.079463	8641.056009
HLA B*0803	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.354000	2.274057	-2.079943	22594.348360
HLA A*2603	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.377563	2.297586	-2.079976	23854.087366
HLA B*0803	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.396659	2.316186	-2.080473	24926.391945
HLA A*0250	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.581075	2.500470	-2.080605	38113.180918
HLA B*4601	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.342046	2.261413	-2.080633	21980.908618
HLA B*0801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.124225	2.043325	-2.080900	13311.435318
HLA A*2602	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.124295	2.043325	-2.080970	13313.595895
HLA A*3101	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.397158	2.316186	-2.080971	24954.996336
HLA A*0212	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.355069	2.274057	-2.081012	22650.032844
HLA B*5101	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.355644	2.274057	-2.081587	22680.073619
HLA B*2705	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.391244	2.309312	-2.081932	24617.494904
HLA A*0206	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-3.011180	0.929186	-2.081994	1026.076784
HLA A*6801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-3.607813	1.525646	-2.082166	4053.337640
HLA A*3002	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.218256	2.135178	-2.083078	16529.357583
HLA A*3201	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.570475	1.487180	-2.083295	3719.416095
HLA B*1502	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.350250	2.266682	-2.083568	22400.104396
HLA B*4001	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.218989	2.135178	-2.083811	16557.280804
HLA A*6802	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-2.972545	0.888375	-2.084170	938.739149
HLA A*0202	1:143-151	9	NIMISATNA	0.971550	-0.064300	-2.991430	0.907250	-2.084180	980.460474
HLA A*0203	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.381928	2.297586	-2.084342	24095.067577
HLA A*0202	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.112835	2.028437	-2.084397	12966.852864
HLA A*0201	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.382227	2.297586	-2.084640	24111.627924
HLA B*0802	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.346399	2.261413	-2.084987	22202.364919
HLA B*5101	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.513349	2.428102	-2.085247	32609.860558
HLA A*2501	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.460056	2.374610	-2.085446	28844.005748
HLA A*1101	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.206231	2.120022	-2.086209	16077.973581
HLA B*1502	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.705053	1.618772	-2.086281	5070.528954
HLA B*4403	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.624757	2.538391	-2.086366	42146.044520
HLA A*6802	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.353135	2.266682	-2.086453	22549.411392
HLA A*3002	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.353337	2.266682	-2.086655	22559.904957
HLA A*2402	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.221949	2.135178	-2.086772	16670.528386
HLA A*0101	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.353763	2.266682	-2.087080	22582.006208
HLA B*5801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.185145	1.097502	-2.087643	1531.599193
HLA A*0203	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.216179	2.127896	-2.088283	16450.497261
HLA B*2705	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.362559	2.274057	-2.088502	23044.059839
HLA B*4501	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-3.954193	1.865170	-2.089023	8998.966945
HLA B*3801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.386648	2.297586	-2.089062	24358.372298
HLA B*5301	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.930054	1.840969	-2.089085	8512.439684
HLA B*1503	1:239-247	9	RHEGLSADL	1.161744	0.529922	-3.781285	1.691666	-2.089619	6043.446159
HLA B*5301	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.448538	2.358694	-2.089844	28089.137107
HLA A*0301	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.364380	2.274057	-2.090323	23140.878664
HLA A*2602	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.487902	2.397104	-2.090797	30754.004224
HLA B*0802	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.407103	2.316186	-2.090917	25533.060863
HLA B*5301	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.520839	2.429816	-2.091023	33177.151804
HLA B*4002	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.629942	2.538765	-2.091177	42652.268550
HLA B*1517	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.352729	2.261413	-2.091316	22528.317026
HLA B*5701	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.407617	2.316186	-2.091431	25563.329485
HLA B*4501	1:3-11	9	TPSHLSDRY	1.408193	1.130572	-4.630243	2.538765	-2.091477	42681.814016
HLA A*0250	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.189196	1.097502	-2.091693	1545.950702
HLA B*3501	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.212504	2.120022	-2.092482	16311.895693
HLA B*1801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.402047	2.309312	-2.092735	25237.526544
HLA A*0250	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.678786	1.585464	-2.093322	4772.940546
HLA A*0216	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.452058	2.358694	-2.093363	28317.696739
HLA B*3901	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.510709	1.417212	-2.093497	3241.220422
HLA A*8001	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.403172	2.309312	-2.093860	25303.010287
HLA A*2603	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.693259	1.598716	-2.094543	4934.678376

HLA B*4402	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.410794	2.316186	-2.094608	25750.989478
HLA A*3101	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-3.959991	1.865170	-2.094821	9119.923294
HLA A*3101	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.055357	1.960098	-2.095259	11359.436334
HLA B*1509	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-3.905041	1.809179	-2.095863	8036.027797
HLA A*2301	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.202848	2.106921	-2.095927	15953.208907
HLA A*6802	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.370035	2.274057	-2.095978	23444.180455
HLA B*1501	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.694800	1.598716	-2.096084	4952.222105
HLA A*0250	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.585922	2.489515	-2.096407	38540.929460
HLA A*2602	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.114256	1.017549	-2.096708	1300.937604
HLA B*1501	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.948469	1.851066	-2.097403	8881.152166
HLA A*6801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-3.733299	1.635751	-2.097548	5411.264663
HLA A*0219	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.371642	2.274057	-2.097585	23531.093165
HLA B*1801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-3.957083	1.859413	-2.097669	9059.047214
HLA B*4001	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.359091	2.261413	-2.097679	22860.785800
HLA A*6802	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-3.133062	1.034768	-2.098293	1358.506577
HLA B*0802	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.372385	2.274057	-2.098327	23571.354561
HLA A*0211	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.526511	2.428102	-2.098409	33613.269437
HLA A*2601	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.372582	2.274057	-2.098525	23582.068542
HLA A*8001	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.415197	2.316186	-2.099011	26013.384264
HLA A*0211	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.457819	2.358694	-2.099124	28695.834816
HLA B*4801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.396899	2.297586	-2.099313	24940.150340
HLA B*4501	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.549073	2.449598	-2.099475	35405.673588
HLA A*2501	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.397616	2.297586	-2.100029	24981.335961
HLA B*4002	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.639042	2.538391	-2.100651	43555.368294
HLA B*5101	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.475579	2.374610	-2.100969	29893.627659
HLA A*0219	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.566537	1.465019	-2.101518	3685.844671
HLA B*5101	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.221602	2.120022	-2.101579	16657.186243
HLA B*5401	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.564415	2.462765	-2.101650	36678.789832
HLA A*2602	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.368637	2.266682	-2.101955	23368.837681
HLA B*1509	1:239-247	9	RHEGLSADL	1.161744	0.529922	-3.793695	1.691666	-2.102029	6218.628847
HLA A*0202	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.500088	2.397104	-2.102984	31629.217550
HLA B*3801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.419372	2.316186	-2.103186	26264.666530
HLA B*2705	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.223528	2.120022	-2.103506	16731.243480
HLA A*2501	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.238781	2.135178	-2.103604	17329.302225
HLA B*5301	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.165590	2.061629	-2.103961	14641.646563
HLA A*0301	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.026533	1.922093	-2.104440	10630.000864
HLA B*3901	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.402054	2.297586	-2.104468	25237.936144
HLA B*7301	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.595931	2.490827	-2.105104	39439.462731
HLA A*0101	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.379348	2.274057	-2.105291	23952.365720
HLA A*6801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-3.425403	1.319849	-2.105554	2663.198056
HLA B*4402	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.379985	2.274057	-2.105928	23987.507557
HLA A*2403	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.372627	2.266682	-2.105944	23584.492618
HLA A*0216	1:46-54	9	LARDPSFYL	1.468873	0.401975	-3.976992	1.870848	-2.106144	9484.011219
HLA B*5701	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.380302	2.274057	-2.106245	24005.032873
HLA A*0202	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.675064	1.568231	-2.106834	4732.214701
HLA B*4601	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.150821	2.043325	-2.107496	14152.105466
HLA B*5401	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.519225	2.411682	-2.107543	33054.074662
HLA B*2705	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.405244	2.297586	-2.107658	25424.032663
HLA A*3101	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.369445	2.261413	-2.108033	23412.367624
HLA A*2301	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.382238	2.274057	-2.108181	24112.280139
HLA B*0801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.375000	2.266682	-2.108317	23713.710705
HLA A*3001	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-2.333071	0.224721	-2.108350	215.313619
HLA B*1503	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-3.949386	1.840969	-2.108416	8899.909906
HLA A*6801	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.634326	2.525575	-2.108751	43085.017530
HLA B*1503	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.860025	1.751011	-2.109015	7244.781598
HLA A*0212	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.370641	2.261413	-2.109229	23476.925549
HLA B*1503	1:27-35	9	LARDLRLHR	1.122977	0.679742	-3.912095	1.802719	-2.109375	8167.602329
HLA B*4501	1:512-520	9	LNVYGFTKF	1.369771	1.130699	-4.609964	2.500470	-2.109494	40734.694541
HLA B*1503	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.541694	1.431809	-2.109884	3480.916253
HLA A*2602	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.550010	2.439993	-2.110017	35482.180898
HLA B*1503	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.509210	1.398961	-2.110249	3230.052603
HLA B*5801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.796016	1.685171	-2.110845	6251.956222
HLA A*1101	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-3.482543	1.371517	-2.111026	3037.686425
HLA B*3501	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.528306	1.417212	-2.111095	3375.252046
HLA A*3201	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.385607	2.274057	-2.111550	24300.065385

HLA B*4402	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.373010	2.261413	-2.111597	23605.298877
HLA B*4001	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.409293	2.297586	-2.111706	25662.124078
HLA A*3201	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.508906	2.397104	-2.111802	32277.958999
HLA A*2501	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.386040	2.274057	-2.111983	24324.266189
HLA A*2602	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.179379	1.067242	-2.112138	1511.400260
HLA A*0202	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-2.522525	0.409720	-2.112805	333.061607
HLA A*3301	1:92-100	9	MEYVDGVTL	1.960528	0.479465	-4.552809	2.439993	-2.112816	35711.537002
HLA B*3801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.240903	2.127896	-2.113007	17414.165232
HLA B*0702	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.429334	2.316186	-2.113148	26874.086305
HLA A*3001	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.667964	1.554751	-2.113213	4655.478193
HLA B*2705	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.151249	2.037813	-2.113436	14166.046489
HLA A*3201	1:366-374	9	RGQSSADAI	1.357283	0.227759	-3.698573	1.585042	-2.113531	4995.435862
HLA A*0250	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.576461	2.462765	-2.113695	37710.371242
HLA B*4001	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.380410	2.266682	-2.113728	24011.007386
HLA A*0206	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.541923	2.428102	-2.113822	34827.586404
HLA A*3301	1:120-128	9	ADACQALNF	1.485501	1.040074	-4.639747	2.525575	-2.114171	43626.114602
HLA A*2501	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.382006	2.266682	-2.115323	24099.369565
HLA A*0212	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.010369	1.894713	-2.115655	10241.624364
HLA B*4501	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.605388	2.489515	-2.115872	40307.667484
HLA A*6801	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.545690	2.429816	-2.115874	35130.926443
HLA A*3301	1:615-623	9	NRDGIITLR	0.950398	0.693822	-3.760609	1.644220	-2.116389	5762.476792
HLA B*5401	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.566374	2.449598	-2.116777	36844.652833
HLA B*5701	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.378284	2.261413	-2.116871	23893.738009
HLA A*3001	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.187619	2.070592	-2.117027	15403.474378
HLA B*4501	1:86-94	9	PLPYIVMEY	1.487942	1.050449	-4.656179	2.538391	-2.117788	45308.411269
HLA B*5101	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.307873	1.190001	-2.117871	2031.761971
HLA B*1801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.434418	2.316186	-2.118232	27190.550042
HLA A*0206	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.548756	1.430389	-2.118367	3537.986135
HLA A*2902	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.428300	2.309312	-2.118988	26810.192616
HLA A*6901	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.704471	1.585464	-2.119006	5063.730627
HLA B*4801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-3.810733	1.691666	-2.119067	6467.450335
HLA A*3001	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.135014	2.015621	-2.119393	13646.262506
HLA B*5401	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.558558	2.438231	-2.120327	36187.429264
HLA A*2501	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.163955	2.043325	-2.120630	14586.620282
HLA A*2403	1:127-135	9	NFSHQNGII	1.000888	0.339659	-3.461595	1.340547	-2.121048	2894.642485
HLA B*5401	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.240132	1.118640	-2.121492	1738.331003
HLA A*0216	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.388312	2.266682	-2.121629	24451.848675
HLA A*0211	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.518741	2.397104	-2.121637	33017.258491
HLA B*4501	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.116625	0.994371	-2.122254	1308.051214
HLA B*3501	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.082620	1.960098	-2.122522	12095.399180
HLA B*7301	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.612659	2.489515	-2.123144	40988.244984
HLA A*3001	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-2.996510	0.873256	-2.123253	991.995443
HLA A*0203	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.610867	1.487180	-2.123688	4081.944656
HLA B*0702	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.421350	2.297586	-2.123764	26384.578312
HLA B*4601	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.194568	2.070592	-2.123976	15651.950551
HLA A*0206	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.012153	0.887960	-2.124193	1028.377457
HLA B*5401	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.139227	1.014988	-2.124239	1377.928852
HLA B*4601	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.422993	1.298743	-2.124250	2648.456801
HLA B*5301	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.440437	2.316186	-2.124251	27570.038569
HLA B*0802	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-3.871223	1.746933	-2.124290	7434.006615
HLA B*5101	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.483480	2.358694	-2.124785	30442.473658
HLA A*6802	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.611967	1.487180	-2.124787	4092.292533
HLA A*2602	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.552900	2.428102	-2.124799	35719.072419
HLA A*0212	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.422870	2.297586	-2.125284	26477.091380
HLA A*3301	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.555741	2.429816	-2.125925	35953.460691
HLA A*2902	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.400790	2.274057	-2.126733	25164.587411
HLA B*1503	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-3.396928	1.270153	-2.126775	2494.179509
HLA B*0802	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.394204	2.266682	-2.127522	24785.872298
HLA A*0219	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.425140	2.297586	-2.127554	26615.821596
HLA B*4801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.389061	2.261413	-2.127649	24494.082999
HLA B*7301	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.590880	2.462765	-2.128114	38983.389516
HLA A*2403	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.402249	2.274057	-2.128192	25249.271047
HLA B*3501	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.980098	1.851066	-2.129032	9552.082796
HLA A*0202	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.390957	2.261413	-2.129545	24601.252559
HLA B*4002	1:174-182	9	AAVIGTAQY	1.097758	1.393069	-4.620507	2.490827	-2.129679	41735.594408

HLA A*2301	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.265058	2.135178	-2.129880	18410.166498
HLA B*4402	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.396669	2.266682	-2.129986	24926.931347
HLA B*0801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-3.893120	1.762988	-2.130132	7818.440644
HLA B*1517	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.547393	1.417212	-2.130182	3526.902268
HLA B*4403	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.427940	2.297586	-2.130354	26788.010651
HLA A*0211	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.474151	1.343697	-2.130454	2979.549329
HLA B*1509	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.127951	1.997366	-2.130585	13426.139937
HLA B*5401	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.561060	2.429816	-2.131244	36396.526074
HLA A*2603	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.528738	2.397104	-2.131634	33786.100417
HLA B*5801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.438410	1.306673	-2.131737	2744.164957
HLA B*3501	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.339915	2.208172	-2.131743	21873.317545
HLA A*3301	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-3.884183	1.751118	-2.133065	7659.187520
HLA A*0250	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.162221	2.028437	-2.133784	14528.499328
HLA A*0206	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-3.984966	1.851066	-2.133900	9659.757215
HLA B*0803	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.401260	2.266682	-2.134577	25191.829671
HLA B*1501	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-3.943700	1.809098	-2.134602	8784.152292
HLA B*1503	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.437856	1.303070	-2.134785	2740.663624
HLA B*4403	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.129359	0.994371	-2.134988	1346.973206
HLA A*0250	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.438072	1.303070	-2.135001	2742.028019
HLA A*0301	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.255195	2.120022	-2.135172	17996.770488
HLA A*3301	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.509789	2.374610	-2.135180	32343.683010
HLA A*8001	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.409683	2.274057	-2.135626	25685.180083
HLA A*1101	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.452091	2.316186	-2.135905	28319.841559
HLA A*0211	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.173776	2.037813	-2.135962	14920.230238
HLA A*0206	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.218148	2.081726	-2.136422	16525.244683
HLA A*0250	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.403311	2.266682	-2.136628	25311.087878
HLA B*4001	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.770054	1.632662	-2.137392	5889.170379
HLA A*0216	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-2.921340	0.783751	-2.137589	834.334599
HLA B*0702	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.257986	2.120022	-2.137964	18112.807283
HLA A*0211	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.005097	1.866969	-2.138128	10118.044815
HLA B*4501	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.496846	2.358694	-2.138152	31393.964228
HLA A*0250	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.588345	2.449598	-2.138747	38756.495795
HLA B*1517	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-3.405456	1.266360	-2.139096	2543.644050
HLA A*1101	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.413341	2.274057	-2.139284	25902.445174
HLA B*4002	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.514124	2.374610	-2.139514	32668.129747
HLA A*0201	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.401102	2.261413	-2.139690	25182.700230
HLA A*0202	1:254-262	9	ALAKNPENR	1.033268	0.766480	-3.939485	1.799748	-2.139737	8699.311468
HLA A*6901	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.708004	1.568231	-2.139773	5105.099607
HLA A*8001	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.406551	2.266682	-2.139868	25500.620696
HLA A*0206	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.769345	1.629324	-2.140020	5879.556587
HLA B*1502	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.514796	2.374610	-2.140186	32718.713924
HLA B*5401	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.568320	2.428102	-2.140218	37010.064531
HLA B*2705	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.401647	2.261413	-2.140235	25214.326737
HLA A*0219	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.366812	1.226371	-2.140441	2327.083721
HLA A*6802	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.623263	1.482642	-2.140621	4200.132538
HLA B*7301	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.579001	2.438231	-2.140769	37931.551003
HLA A*2602	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.590466	2.449598	-2.140868	38946.289517
HLA B*1517	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-2.489467	0.348457	-2.141010	308.650737
HLA B*4403	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.548730	2.407316	-2.141413	35377.719677
HLA A*2402	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.248426	2.106921	-2.141504	17718.449367
HLA A*0219	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.448424	1.306673	-2.141750	2808.172093
HLA A*0202	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.827508	1.685171	-2.142337	6722.153499
HLA B*1801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.007648	1.865170	-2.142478	10177.664707
HLA A*0203	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.180392	2.037813	-2.142579	15149.268909
HLA B*0702	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.559818	1.417212	-2.142606	3629.255152
HLA A*3301	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.632278	2.489515	-2.142762	42882.245919
HLA B*4801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.350964	2.208172	-2.142793	22436.974059
HLA A*2301	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.186364	2.043325	-2.143039	15359.039791
HLA A*3001	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.225046	2.081726	-2.143320	16789.817929
HLA A*0206	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.271585	2.127896	-2.143689	18688.936376
HLA B*1801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.271812	2.127896	-2.143917	18698.746142
HLA A*1101	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-3.507654	1.363134	-2.144520	3218.505355
HLA A*3201	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.590925	1.445980	-2.144945	3898.743678
HLA A*0212	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.011072	0.865145	-2.145926	1025.821471
HLA B*5801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.216696	2.070592	-2.146104	16470.087897

HLA A*0202	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.574440	2.428102	-2.146339	37535.331068
HLA B*7301	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.596300	2.449598	-2.146702	39472.974971
HLA A*0202	1:289-297	9	TDAERTSLL	1.288079	0.301720	-3.737077	1.589799	-2.147278	5458.543147
HLA A*6901	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.356091	2.208172	-2.147919	22703.397975
HLA A*0250	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.899873	1.751011	-2.148862	7940.951862
HLA B*5801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.357162	2.208172	-2.148991	22759.474341
HLA A*6801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.193723	2.044529	-2.149194	15621.497101
HLA A*3101	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.044977	1.894713	-2.150263	11091.154551
HLA A*0250	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.562211	2.411682	-2.150529	36493.135640
HLA B*5301	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.285865	2.135178	-2.150687	19313.667721
HLA A*0301	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.257859	2.106921	-2.150938	18107.516689
HLA B*0801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.286243	2.135178	-2.151065	19330.497102
HLA B*1503	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.705908	1.554751	-2.151157	5080.523675
HLA A*2603	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.179499	2.028058	-2.151441	15118.157670
HLA A*3001	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.194940	2.043325	-2.151615	15665.334970
HLA A*2402	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.153274	2.001388	-2.151886	14232.261631
HLA A*2403	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.360456	2.208172	-2.152285	22932.753621
HLA A*0216	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.450094	2.297586	-2.152507	28189.914394
HLA B*3501	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.737547	1.584939	-2.152608	5464.452366
HLA B*1517	1:489-497	9	GSGPATKDI	1.136230	0.120187	-3.409183	1.256417	-2.152766	2565.562628
HLA B*5401	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-3.115135	0.961636	-2.153499	1303.572454
HLA B*1509	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.181590	2.028058	-2.153532	15191.124114
HLA B*1501	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.390326	1.236758	-2.153567	2456.550260
HLA A*0219	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.215775	2.061629	-2.154146	16435.197177
HLA A*2501	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.463589	2.309312	-2.154277	29079.651593
HLA A*6801	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.451917	2.297586	-2.154331	28308.506495
HLA B*1502	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.582464	2.428102	-2.154362	38235.233087
HLA B*4801	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.156117	2.001388	-2.154729	14325.731120
HLA B*5801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.115724	1.960098	-2.155627	13053.424135
HLA B*4002	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.585650	2.429816	-2.155834	38516.750798
HLA B*5101	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.453594	2.297586	-2.156008	28418.064110
HLA A*3002	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.465391	2.309312	-2.156079	29200.564947
HLA B*5701	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-3.985713	1.828833	-2.156881	9676.389630
HLA B*4403	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.586702	2.429816	-2.156886	38610.214378
HLA B*4801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.066595	0.909118	-2.157476	1165.721522
HLA A*2402	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.220046	2.061629	-2.158417	16597.637781
HLA B*7301	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.570371	2.411682	-2.158689	37185.270302
HLA A*0301	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.366971	2.208172	-2.158800	23279.375582
HLA B*1501	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.910069	1.751011	-2.159059	8129.602821
HLA B*1801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.367289	2.208172	-2.159117	23296.383535
HLA B*4402	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.024358	1.865170	-2.159188	10576.882426
HLA A*0216	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.187807	2.028437	-2.159369	15410.142308
HLA A*2501	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.279899	2.120022	-2.159877	19050.194449
HLA A*2403	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.197773	2.037813	-2.159960	15767.874865
HLA B*3501	1:575-583	9	EPRLRALGW	1.410483	0.250517	-3.821014	1.661000	-2.160015	6622.385356
HLA B*2705	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.295291	2.135178	-2.160113	19737.443018
HLA B*4001	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.161765	2.001388	-2.160377	14513.259398
HLA A*0250	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.588528	2.428102	-2.160426	38772.853377
HLA B*0803	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.296416	2.135178	-2.161239	19788.655708
HLA A*3002	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.539509	1.378166	-2.161343	3463.447060
HLA B*5301	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.558520	2.397104	-2.161416	36184.297080
HLA A*3002	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.436072	2.274057	-2.162015	27294.304389
HLA B*1503	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-3.311815	1.149326	-2.162489	2050.289857
HLA B*0802	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.370766	2.208172	-2.162594	23483.657915
HLA B*3501	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.290860	2.127896	-2.162964	19537.084752
HLA A*6801	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.601638	2.438231	-2.163407	39961.141839
HLA A*3002	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.037285	1.873374	-2.163910	10896.437776
HLA A*6801	1:48-56	9	RDPSFYLRF	1.356655	1.132860	-4.653646	2.489515	-2.164131	45044.947923
HLA B*5401	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.539167	2.374610	-2.164557	34607.277265
HLA B*5401	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.561678	2.397104	-2.164574	36448.347939
HLA A*6801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.299863	2.135178	-2.164685	19946.329408
HLA A*3001	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.229902	2.064862	-2.165040	16978.619361
HLA A*2402	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.426587	2.261413	-2.165175	26704.666556
HLA B*4601	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.285263	2.120022	-2.165241	19286.938125
HLA B*7301	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-3.974661	1.809179	-2.165483	9433.250557

HLA A*0206	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.193990	2.028437	-2.165553	15631.134277
HLA B*7301	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.562895	2.397104	-2.165791	36550.631216
HLA B*5401	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-3.667053	1.501143	-2.165909	4645.716421
HLA A*0211	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.795964	1.629324	-2.166640	6251.212174
HLA B*1517	1:366-374	9	RGQSSADAI	1.357283	0.227759	-3.751911	1.585042	-2.166869	5648.217289
HLA A*2402	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.476340	2.309312	-2.167028	29946.071279
HLA A*3101	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.248907	2.081726	-2.167181	17738.110511
HLA A*3301	1:11-19	9	YELGEILGF	1.340749	1.097482	-4.606050	2.438231	-2.167819	40369.207338
HLA A*0301	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.232820	2.064862	-2.167958	17093.084221
HLA A*3001	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.212951	2.044529	-2.168422	16328.670967
HLA B*3501	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-2.823019	0.654207	-2.168812	665.302270
HLA A*2403	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.431740	2.261413	-2.170327	27023.374519
HLA A*3301	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.633452	2.462765	-2.170687	42998.397038
HLA A*1101	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.278121	2.106921	-2.171200	18972.337984
HLA B*3901	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.428401	1.257069	-2.171333	2681.645760
HLA A*0202	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-3.046464	0.875034	-2.171430	1112.921230
HLA B*1502	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.487723	2.316186	-2.171537	30741.362266
HLA B*0801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.131861	1.960098	-2.171763	13547.548438
HLA A*2402	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.445895	2.274057	-2.171838	27918.702269
HLA A*0301	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.307146	2.135178	-2.171969	20283.663192
HLA A*3001	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.094128	1.922093	-2.172035	12420.182671
HLA B*1501	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.380420	2.208172	-2.172248	24011.526980
HLA B*5301	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.470086	2.297586	-2.172499	29517.904608
HLA A*3101	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-3.681704	1.509182	-2.172522	4805.118308
HLA B*4402	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.381425	2.208172	-2.173254	24067.188466
HLA A*3101	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.381592	2.208172	-2.173421	24076.434500
HLA B*5301	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.447674	2.274057	-2.173617	28033.271779
HLA B*0803	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.435062	2.261413	-2.173649	27230.884743
HLA B*5701	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.382013	2.208172	-2.173841	24099.760693
HLA A*0301	1:27-35	9	LARDLRLHR	1.122977	0.679742	-3.976588	1.802719	-2.173868	9475.190442
HLA B*0702	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.047979	1.873374	-2.174605	11168.102698
HLA A*0203	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-3.201592	1.026649	-2.174943	1590.711877
HLA B*0801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.236800	2.061629	-2.175172	17250.451247
HLA A*0201	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.383350	2.208172	-2.175178	24174.059521
HLA A*0219	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.203774	2.028437	-2.175337	15987.249379
HLA A*6801	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.587297	2.411682	-2.175614	38663.096435
HLA B*3501	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-2.680542	0.504447	-2.176094	479.227284
HLA B*7301	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.583533	2.407316	-2.176216	38329.465025
HLA A*0206	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.043887	1.866969	-2.176918	11063.348576
HLA A*0202	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.474874	2.297586	-2.177287	29845.150644
HLA A*2902	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.297631	2.120022	-2.177609	19844.080323
HLA A*3001	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.239291	2.061629	-2.177662	17349.657835
HLA B*0801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.037238	1.859413	-2.177824	10895.258870
HLA A*0211	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.762766	1.584939	-2.177827	5791.166036
HLA A*2902	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.221179	2.043325	-2.177854	16640.973703
HLA B*1501	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.712186	1.534036	-2.178150	5154.497145
HLA B*5301	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.606323	2.428102	-2.178221	40394.548869
HLA A*0212	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.776948	1.598716	-2.178231	5983.392711
HLA B*1801	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.179978	2.001388	-2.178590	15134.851541
HLA B*3801	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.440287	2.261413	-2.178874	27560.494567
HLA B*1509	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.030053	1.851066	-2.178987	10716.496546
HLA A*0101	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.387454	2.208172	-2.179283	24403.613460
HLA A*0250	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.177159	1.997366	-2.179792	15036.916334
HLA B*5801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.241556	2.061629	-2.179927	17440.374956
HLA B*0702	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.441377	2.261413	-2.179965	27629.763508
HLA B*4402	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.315802	2.135178	-2.180624	20691.972534
HLA A*3002	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.478212	2.297586	-2.180626	30075.467964
HLA B*5301	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.555315	2.374610	-2.180705	35918.272655
HLA B*3801	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.182196	2.001388	-2.180808	15212.341951
HLA B*5701	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.287869	2.106921	-2.180948	19402.999214
HLA B*1517	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-2.878946	0.697848	-2.181098	756.739052
HLA B*3801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.316305	2.135178	-2.181127	20715.941840
HLA B*1509	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.288332	2.106921	-2.181411	19423.688948
HLA B*2705	1:450-458	9	GRFKQANSP	0.757924	0.058749	-2.998272	0.816673	-2.181599	996.028558
HLA A*3002	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.225619	2.043325	-2.182294	16811.995340

HLA A*3301	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.632306	2.449598	-2.182708	42885.029868
HLA B*2705	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.227513	2.044529	-2.182984	16885.461925
HLA B*7301	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.612840	2.429816	-2.183024	41005.322665
HLA B*4601	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.391479	2.208172	-2.183307	24630.816299
HLA B*3901	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.444937	2.261413	-2.183524	27857.147097
HLA A*0212	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.391883	2.208172	-2.183711	24653.745963
HLA B*4002	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.391970	2.208172	-2.183798	24658.681296
HLA A*0101	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.769420	1.585464	-2.183955	5880.574523
HLA A*0202	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-2.285447	0.100651	-2.184796	192.951180
HLA B*7301	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.612904	2.428102	-2.184802	41011.312627
HLA B*4801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.249857	2.064862	-2.184994	17776.921237
HLA A*0250	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.036105	1.851066	-2.185039	10866.885765
HLA B*0803	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.393943	2.208172	-2.185772	24770.992907
HLA B*4801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.306033	2.120022	-2.186011	20231.716680
HLA B*0702	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.248170	2.061629	-2.186541	17708.004269
HLA B*7301	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.545342	2.358694	-2.186647	35102.809647
HLA B*0702	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.268441	2.081726	-2.186715	18554.146210
HLA A*3101	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.314709	2.127896	-2.186814	20639.985257
HLA B*5401	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.835299	1.648439	-2.186861	6843.831645
HLA B*1801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.015735	1.828833	-2.186902	10368.956839
HLA A*0202	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.669642	1.482642	-2.187000	4673.495502
HLA B*1503	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.796101	1.609050	-2.187051	6253.173947
HLA A*2601	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.395372	2.208172	-2.187200	24852.604114
HLA B*1517	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.674392	1.487180	-2.187213	4724.898546
HLA B*1509	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.454236	2.266682	-2.187554	28460.065750
HLA B*0702	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.107762	0.920120	-2.187642	1281.629487
HLA A*0250	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.584759	2.397104	-2.187655	38437.858961
HLA A*2601	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.307691	2.120022	-2.187669	20309.137084
HLA A*3001	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.216625	2.028437	-2.188188	16467.415074
HLA B*3901	1:460-468	9	TPELVGKVI	1.597950	0.050489	-3.836742	1.648439	-2.188303	6866.602406
HLA A*0211	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.450595	1.262230	-2.188364	2822.244552
HLA B*3501	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.227193	2.038259	-2.188934	16873.043101
HLA B*4002	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.596434	2.407316	-2.189117	39485.148880
HLA A*0203	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.818867	1.629324	-2.189543	6589.720877
HLA B*0801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.317611	2.127896	-2.189715	20778.347095
HLA B*5401	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.506319	2.316186	-2.190133	32086.273615
HLA A*0216	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.333557	1.143250	-2.190307	2155.546507
HLA B*4801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.325978	2.135178	-2.190800	21182.514522
HLA A*3201	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.319352	2.127896	-2.191456	20861.809010
HLA A*0202	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.230130	2.038259	-2.191871	16987.531387
HLA B*0702	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.401318	2.208172	-2.193147	25195.237027
HLA A*3101	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.944414	1.751011	-2.193403	8798.610650
HLA B*1517	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.944715	1.751011	-2.193704	8804.705497
HLA A*0206	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.491318	2.297586	-2.193732	30996.868500
HLA A*0203	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.401922	2.208172	-2.193751	25230.291374
HLA A*3001	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.231681	2.037813	-2.193868	17048.294236
HLA B*3901	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.222419	2.028437	-2.193982	16688.575290
HLA B*1517	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.402176	2.208172	-2.194004	25245.036934
HLA A*2603	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.622576	2.428102	-2.194475	41934.985723
HLA A*0219	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.402658	2.208172	-2.194486	25273.049899
HLA A*0211	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.451567	1.257069	-2.194499	2828.572600
HLA A*0203	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.223087	2.028437	-2.194649	16714.235466
HLA B*5801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.192055	1.997366	-2.194688	15561.609686
HLA A*2902	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.322679	2.127896	-2.194783	21022.232545
HLA A*0211	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.763184	1.568231	-2.194954	5796.745384
HLA A*0216	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.403428	2.208172	-2.195257	25317.935313
HLA A*2902	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.303086	2.106921	-2.196165	20094.929202
HLA A*0206	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.138860	0.942253	-2.196607	1376.766450
HLA A*0212	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.234446	2.037813	-2.196633	17157.194559
HLA B*5401	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.555471	2.358694	-2.196776	35931.099660
HLA A*3002	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.054379	1.857104	-2.197276	11333.900510
HLA B*1501	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.162778	0.965301	-2.197477	1454.715384
HLA B*1503	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-2.783613	0.586005	-2.197609	607.593953
HLA A*0203	1:38-46	9	AVKVLRADL	1.192397	0.558614	-3.949367	1.751011	-2.198356	8899.524734
HLA B*5401	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.216520	1.017549	-2.198971	1646.342356

HLA A*2603	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.319892	2.120022	-2.199870	20887.782983
HLA A*0212	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.885151	1.685171	-2.199979	7676.277926
HLA A*0250	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-2.774610	0.574537	-2.200073	595.127771
HLA B*1501	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.244692	2.044529	-2.200164	17566.788810
HLA B*4002	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.597489	2.397104	-2.200384	39581.176475
HLA B*7301	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.575953	2.374610	-2.201343	37666.331050
HLA A*2603	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-3.333520	1.132158	-2.201362	2155.359935
HLA A*2301	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.198760	1.997366	-2.201394	15803.742630
HLA A*3101	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.202890	2.001388	-2.201502	15954.762474
HLA A*2601	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.244904	2.043325	-2.201579	17575.343987
HLA B*4601	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.263899	2.061629	-2.202270	18361.130617
HLA A*2602	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.643713	1.440103	-2.203609	4402.637339
HLA A*2602	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.071127	1.866969	-2.204158	11779.491012
HLA A*3001	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.743185	1.538857	-2.204329	5535.863953
HLA B*5701	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.324706	2.120022	-2.204684	21120.609232
HLA B*4403	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.339992	2.135178	-2.204815	21877.222857
HLA A*6801	1:44-52	9	ADLARDPSF	1.368587	1.094178	-4.667682	2.462765	-2.204916	46524.521223
HLA A*3002	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.325515	2.120022	-2.205492	21159.951322
HLA A*6901	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.645686	1.440103	-2.205583	4422.689802
HLA B*4601	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.341120	2.135178	-2.205942	21934.106289
HLA B*1503	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.838753	1.632662	-2.206091	6898.474456
HLA A*3301	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.618218	2.411682	-2.206536	41516.258251
HLA A*2602	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.480945	2.274057	-2.206888	30265.290344
HLA B*4501	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.635019	2.428102	-2.206918	43153.832552
HLA A*0202	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.415180	2.208172	-2.207009	26012.399176
HLA B*5101	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.468587	2.261413	-2.207174	29416.198906
HLA A*6801	1:616-624	9	RDGIITLRF	1.386647	1.062951	-4.656935	2.449598	-2.207337	45387.406595
HLA A*8001	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.415744	2.208172	-2.207573	26046.194918
HLA B*2705	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.314608	2.106921	-2.207687	20635.184434
HLA A*0201	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.336816	2.127896	-2.208920	21717.792887
HLA B*4002	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.638137	2.428102	-2.210036	43464.745262
HLA B*3501	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.207477	1.997366	-2.210110	16124.139163
HLA A*3301	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.526931	2.316186	-2.210745	33645.835289
HLA B*0702	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.208440	1.997366	-2.211074	16159.943076
HLA B*4501	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.608256	2.397104	-2.211152	40574.800057
HLA A*6901	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-3.830121	1.618772	-2.211349	6762.714489
HLA B*3501	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.496038	1.284672	-2.211367	3133.562651
HLA B*1509	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.254896	2.043325	-2.211571	17984.409947
HLA A*3201	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.473034	2.261413	-2.211622	29718.995662
HLA A*2501	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.293526	2.081726	-2.211800	19657.415885
HLA A*6802	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.240477	2.028058	-2.212420	17397.121802
HLA A*0201	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.294314	2.081726	-2.212587	19693.073574
HLA A*2601	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.340511	2.127896	-2.212616	21903.394589
HLA A*0206	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.545335	1.332686	-2.212649	3510.227599
HLA A*2603	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.214666	2.001388	-2.213278	16393.283967
HLA A*6801	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.572196	2.358694	-2.213502	37341.906964
HLA B*4403	1:262-270	9	RYQTAAEMR	1.515713	0.912389	-4.642138	2.428102	-2.214037	43867.038076
HLA B*5801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.295970	2.081726	-2.214244	19768.325816
HLA B*1801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.334452	2.120022	-2.214430	21599.918138
HLA B*4403	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.589115	2.374610	-2.214505	38825.328064
HLA A*0203	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.282329	1.067242	-2.215088	1915.707619
HLA B*4501	1:444-452	9	LTAAGFGRF	1.264045	1.143271	-4.622405	2.407316	-2.215089	41918.427948
HLA B*1503	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-3.832076	1.616917	-2.215158	6793.222261
HLA B*3901	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-3.609951	1.394783	-2.215168	4073.341417
HLA B*0702	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.066545	1.851066	-2.215479	11655.878974
HLA A*3001	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.865894	1.650328	-2.215567	7343.351405
HLA A*0212	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.244192	2.028437	-2.215755	17546.558146
HLA B*5101	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.483315	2.266682	-2.216633	30430.947512
HLA A*6802	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.425243	2.208172	-2.217072	26622.157850
HLA B*5801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.345180	2.127896	-2.217284	22140.114051
HLA A*8001	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.353109	2.135178	-2.217932	22548.069544
HLA A*0203	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.752301	1.534036	-2.218265	5653.291901
HLA A*0212	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.786688	1.568231	-2.218458	6119.112994
HLA B*3801	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.486168	2.266682	-2.219485	30631.463702
HLA A*2902	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-3.746790	1.525910	-2.220880	5581.995969

HLA B*5401	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.531038	2.309312	-2.221726	33965.515812
HLA A*3201	1:239-247	9	RHEGLSADL	1.161744	0.529922	-3.913443	1.691666	-2.221777	8193.004412
HLA A*3201	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.807655	1.585464	-2.222191	6421.777838
HLA B*4001	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.342349	2.120022	-2.222327	21996.253913
HLA A*3301	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.619550	2.397104	-2.222446	41643.801031
HLA A*2301	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.531844	2.309312	-2.222532	34028.600462
HLA B*5401	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.490587	2.266682	-2.223905	30944.760875
HLA A*2602	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.909271	1.685171	-2.224099	8114.663279
HLA B*4501	1:553-561	9	LQVSKGNQF	1.316494	1.095188	-4.635917	2.411682	-2.224234	43243.105511
HLA B*7301	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.540885	2.316186	-2.224699	34744.407176
HLA B*1517	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.353044	2.127896	-2.225148	22544.654291
HLA A*0201	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.274895	1.049687	-2.225208	1883.195709
HLA B*1503	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.910431	1.685171	-2.225260	8136.378601
HLA A*8001	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.332702	2.106921	-2.225781	21513.037730
HLA A*0202	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.690876	1.465019	-2.225858	4907.682680
HLA A*0203	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-2.958265	0.732039	-2.226226	908.374136
HLA B*0803	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.346326	2.120022	-2.226304	22198.641749
HLA A*0250	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.585086	2.358694	-2.226391	38466.774124
HLA B*4002	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.091638	1.865170	-2.226468	12349.163176
HLA A*0250	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.605036	1.378166	-2.226870	4027.501311
HLA A*2602	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.020124	1.793234	-2.226890	10474.273377
HLA B*4501	1:562-570	9	VMPDLSGMF	1.302537	1.127279	-4.656813	2.429816	-2.226997	45374.640267
HLA B*2705	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.225549	1.997366	-2.228182	16809.267030
HLA B*4501	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.602949	2.374610	-2.228339	40081.955523
HLA A*0101	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.363527	2.135178	-2.228349	23095.479435
HLA A*0206	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.436542	2.208172	-2.228370	27323.852203
HLA B*2705	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.290467	2.061629	-2.228838	19519.441915
HLA A*0201	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.257716	2.028437	-2.229278	18101.542136
HLA A*0219	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.357291	2.127896	-2.229396	22766.247291
HLA A*0212	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.357432	2.127896	-2.229537	22773.638263
HLA B*4001	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.357881	2.127896	-2.229985	22797.182171
HLA B*1503	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.295077	2.064862	-2.230215	19727.728668
HLA B*5101	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.439288	2.208172	-2.231117	27497.200190
HLA B*0801	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.233264	2.001388	-2.231876	17110.570308
HLA A*3002	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.073241	1.840969	-2.232272	11836.984029
HLA B*5301	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.052575	1.819741	-2.232834	11286.908168
HLA A*0211	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.530634	2.297586	-2.233048	33933.925567
HLA B*0702	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.918297	1.685171	-2.233126	8285.089890
HLA B*3501	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.866703	1.632662	-2.234041	7357.030120
HLA B*1503	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.429120	1.194908	-2.234213	2686.088703
HLA B*4601	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.362521	2.127896	-2.234626	23042.065273
HLA B*5301	1:235-243	9	PPSARHEGL	1.512930	0.077910	-3.825469	1.590840	-2.234629	6690.661717
HLA B*4801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.362709	2.127896	-2.234814	23052.039832
HLA A*2403	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.236222	2.001388	-2.234834	17227.509051
HLA A*0211	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.443362	2.208172	-2.235191	27756.358136
HLA A*3001	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.803520	1.568231	-2.235289	6360.923659
HLA A*0202	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.284989	1.049687	-2.235302	1927.475398
HLA A*0301	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.363215	2.127896	-2.235319	23078.867862
HLA B*3501	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-3.958647	1.723131	-2.235516	9091.745707
HLA A*3201	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.820615	1.584939	-2.235676	6616.297673
HLA B*1501	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-3.920868	1.685171	-2.235696	8334.269912
HLA B*5801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.279366	2.043325	-2.236041	19026.814315
HLA A*0212	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.550001	1.312789	-2.237212	3548.144952
HLA A*0250	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.233460	0.995952	-2.237508	1711.827261
HLA B*2705	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.365827	2.127896	-2.237931	23218.124089
HLA A*0202	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.637181	1.398961	-2.238221	4336.919332
HLA B*1503	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.727392	1.488986	-2.238406	5338.167174
HLA A*2402	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.505234	2.266682	-2.238551	32006.178320
HLA B*4402	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.359350	2.120022	-2.239327	22874.394023
HLA A*3201	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.722205	1.482642	-2.239563	5274.781902
HLA A*2501	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.448000	2.208172	-2.239829	28054.360015
HLA B*7301	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.513901	2.274057	-2.239844	32651.344619
HLA A*3201	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.694852	1.454961	-2.239891	4952.811542
HLA A*2602	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.048316	0.807959	-2.240357	1117.675732
HLA A*2602	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.550295	2.309312	-2.240983	35505.415016

HLA A*6901	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.279164	2.037813	-2.241351	19017.964139
HLA B*3501	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.269999	2.028437	-2.241562	18620.814905
HLA A*6801	1:441-449	9	VKKLTAAGF	1.183095	1.214009	-4.639467	2.397104	-2.242363	43598.038160
HLA B*1801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.349308	2.106921	-2.242387	22351.563052
HLA B*5801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.827880	1.585464	-2.242415	6727.901800
HLA A*3001	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.064191	1.819741	-2.244450	11592.866786
HLA B*0702	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-3.968257	1.723131	-2.245126	9295.155805
HLA A*2301	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.205245	1.960098	-2.245147	16041.483430
HLA B*4801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.288630	2.043325	-2.245305	19437.038694
HLA A*0216	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.307205	2.061629	-2.245576	20286.406687
HLA B*5801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.283464	2.037813	-2.245651	19207.178908
HLA B*1502	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.352616	2.106921	-2.245695	22522.467752
HLA B*3901	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.055272	1.809179	-2.246093	11357.224231
HLA B*1501	1:147-155	9	SATNAVKVM	1.243941	0.165923	-3.656259	1.409864	-2.246395	4531.679243
HLA A*3201	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.875720	1.629324	-2.246396	7511.382146
HLA A*6901	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.284721	2.038259	-2.246461	19262.850594
HLA B*5101	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.381710	2.135178	-2.246532	24082.947923
HLA A*2902	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.455152	2.208172	-2.246981	28520.175802
HLA B*1503	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.553751	1.306673	-2.247078	3578.912922
HLA B*1509	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-3.501325	1.254080	-2.247244	3171.938246
HLA B*4002	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-3.350666	1.103143	-2.247523	2242.158692
HLA A*0101	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.367613	2.120022	-2.247591	23313.782287
HLA B*4402	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.107774	1.859413	-2.248360	12816.628384
HLA B*2705	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-3.473272	1.224706	-2.248566	2973.526906
HLA A*3301	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.522716	2.274057	-2.248659	33320.870478
HLA B*0801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.105941	1.857104	-2.248837	12762.659830
HLA A*2603	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.565028	2.316186	-2.248842	36730.616169
HLA B*0802	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.377100	2.127896	-2.249204	23828.678458
HLA B*1502	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.558729	2.309312	-2.249417	36201.723295
HLA B*1501	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.377410	2.127896	-2.249514	23845.700722
HLA B*4002	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.565846	2.316186	-2.249660	36799.831882
HLA A*2402	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.265516	2.015621	-2.249895	18429.598153
HLA A*0206	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.210850	1.960098	-2.250753	16249.888981
HLA A*6801	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.560132	2.309312	-2.250820	36318.833152
HLA B*0801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.716105	1.465019	-2.251087	5201.220246
HLA A*2301	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.517956	2.266682	-2.251274	32957.653375
HLA B*5701	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.322303	2.070592	-2.251711	21004.043946
HLA A*6801	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.567899	2.316186	-2.251713	36974.242436
HLA A*0212	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.313408	2.061629	-2.251779	20578.218206
HLA A*0301	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.194789	1.942822	-2.251967	15659.912055
HLA A*1101	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-3.639827	1.386802	-2.253025	4363.418457
HLA A*2402	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.903712	1.650328	-2.253384	8011.459136
HLA A*0211	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.282014	2.028437	-2.253577	19143.174115
HLA A*0202	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.321157	1.067242	-2.253915	2094.868737
HLA B*1502	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.382095	2.127896	-2.254199	24104.324321
HLA A*6802	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.149054	1.894713	-2.254341	14094.648306
HLA A*0216	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.251731	1.997366	-2.254365	17853.831729
HLA A*3301	1:509-517	9	QKNLNVYGF	1.205828	1.152866	-4.613129	2.358694	-2.254435	41032.617357
HLA B*4402	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.325303	2.070592	-2.254711	21149.651260
HLA A*6801	1:331-339	9	RWVAVVAVL	1.724622	0.649988	-4.629322	2.374610	-2.254712	42591.395602
HLA B*4801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.336543	2.081726	-2.254817	21704.168223
HLA B*5701	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.382856	2.127896	-2.254960	24146.611529
HLA A*1101	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.463944	2.208172	-2.255772	29103.416270
HLA A*3201	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-3.376158	1.120342	-2.255816	2377.706579
HLA A*0301	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.337654	2.081726	-2.255928	21759.777651
HLA A*1101	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.300685	2.044529	-2.256157	19984.132787
HLA A*3001	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.294781	2.038259	-2.256522	19714.285922
HLA B*1801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.123520	1.866969	-2.256551	13289.848823
HLA A*6802	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.216762	1.960098	-2.256664	16472.582924
HLA B*4002	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.554296	2.297586	-2.256709	35834.039358
HLA A*0101	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.363661	2.106921	-2.256740	23102.602340
HLA A*2301	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.518194	2.261413	-2.256781	32975.666318
HLA A*3301	1:40-48	9	KVLRADLAR	0.915954	0.778633	-3.951824	1.694587	-2.257238	8950.027623
HLA A*0216	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.066517	1.809098	-2.257419	11655.122314
HLA B*0802	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.392825	2.135178	-2.257648	24707.287004

HLA B*4001	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.319277	2.061629	-2.257648	20858.197800
HLA B*1501	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.079895	1.822112	-2.257782	12019.732518
HLA A*8001	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.377878	2.120022	-2.257855	23871.386063
HLA B*4801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.319526	2.061629	-2.257897	20870.162327
HLA A*3101	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-3.524378	1.266360	-2.258018	3344.859425
HLA B*5301	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.519676	2.261413	-2.258263	33088.425724
HLA A*3201	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-2.990425	0.732039	-2.258386	978.192910
HLA A*0250	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-2.676980	0.418508	-2.258472	475.313026
HLA A*2501	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.051847	1.793234	-2.258612	11267.995146
HLA A*0250	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.797778	1.538857	-2.258921	6277.374546
HLA A*6801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.365881	2.106921	-2.258960	23221.013240
HLA A*0211	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.714033	1.454961	-2.259072	5176.461623
HLA A*2403	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.132594	1.873374	-2.259220	13570.434456
HLA B*1503	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.288165	2.028058	-2.260107	19416.229700
HLA A*2301	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.322162	2.061629	-2.260533	20997.227279
HLA B*5301	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.379203	1.118640	-2.260563	2394.435772
HLA B*4001	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.299059	2.038259	-2.260800	19909.459186
HLA B*4402	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.388847	2.127896	-2.260952	24482.027532
HLA A*3001	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.258449	1.997366	-2.261082	18132.121265
HLA B*7301	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-2.878998	0.617889	-2.261109	756.829122
HLA A*6801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.252800	1.991397	-2.261404	17897.833060
HLA B*1801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.304811	2.043325	-2.261486	20174.881961
HLA A*2902	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.343267	2.081726	-2.261541	22042.831100
HLA A*2403	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.221935	1.960098	-2.261838	16669.987281
HLA A*1101	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.263554	2.001388	-2.262166	18346.534664
HLA A*3001	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.640489	1.378166	-2.262324	4370.080319
HLA A*2902	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.157183	1.894713	-2.262470	14360.959645
HLA A*0301	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.307059	2.044529	-2.262531	20279.603501
HLA A*0219	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.662001	1.398961	-2.263041	4591.993914
HLA A*6901	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.693470	1.430389	-2.263081	4937.081607
HLA B*5101	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.307020	2.043325	-2.263695	20277.738510
HLA A*0250	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.130775	1.866969	-2.263806	13513.730397
HLA B*1501	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.129044	0.865145	-2.263899	1345.997105
HLA B*0802	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.346561	2.081726	-2.264835	22210.654217
HLA B*3801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.142931	1.877371	-2.265561	13897.333698
HLA A*3001	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.293736	2.028058	-2.265678	19666.882819
HLA A*0101	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.347659	2.081726	-2.265932	22266.838561
HLA A*2301	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.028925	1.762988	-2.265937	10688.704618
HLA B*3501	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.456243	1.190001	-2.266241	2859.188611
HLA A*6801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-3.680116	1.413806	-2.266310	4787.577675
HLA A*0203	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.226681	1.960098	-2.266583	16853.155509
HLA A*3002	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.304513	2.037813	-2.266700	20161.025449
HLA A*6802	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.328661	2.061629	-2.267032	21313.787165
HLA A*2603	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.645221	1.378166	-2.267055	4417.954938
HLA B*0801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.076436	1.809098	-2.267339	11924.395206
HLA B*1502	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.305662	2.037813	-2.267848	20214.430757
HLA B*0801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.141451	1.873374	-2.268077	13850.049011
HLA B*0802	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.388441	2.120022	-2.268419	24459.125256
HLA B*1501	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-3.001082	0.732333	-2.268749	1002.493983
HLA B*1503	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.646960	1.378166	-2.268794	4435.676866
HLA A*3101	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.021209	1.752221	-2.268989	10500.485191
HLA B*4601	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.350722	2.081726	-2.268996	22424.475242
HLA A*2402	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.313076	2.043325	-2.269752	20562.527242
HLA A*3301	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.334741	2.064862	-2.269879	21614.295860
HLA B*5401	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.567653	2.297586	-2.270066	36953.245612
HLA A*1101	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.335126	2.064862	-2.270264	21633.481045
HLA B*4402	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.377274	2.106921	-2.270353	23838.219745
HLA A*3001	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.143740	1.873374	-2.270366	13923.220743
HLA B*3501	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.144083	1.873374	-2.270709	13934.222257
HLA B*1501	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.921709	1.650328	-2.271381	8350.426869
HLA A*0206	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.533045	2.261413	-2.271632	34122.801087
HLA A*0203	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.091623	1.819741	-2.271882	12348.762337
HLA A*0201	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.671113	1.398961	-2.272152	4689.349548
HLA A*2403	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.315560	2.043325	-2.272235	20680.445794
HLA B*5401	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.546803	2.274057	-2.272746	35221.127839

HLA A*3001	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.233084	1.960098	-2.272986	17103.444188
HLA A*0202	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.510135	1.236758	-2.273377	3236.944791
HLA A*0201	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.603306	1.329751	-2.273556	4011.496979
HLA B*3801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.037045	1.762988	-2.274057	10890.426686
HLA A*2501	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.302356	2.028058	-2.274298	20061.148401
HLA A*6801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-3.980582	1.706161	-2.274421	9562.733926
HLA B*1503	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.194675	0.920120	-2.274554	1565.577748
HLA B*1503	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.021844	1.746933	-2.274911	10515.834143
HLA A*2602	1:147-155	9	SATNAVKVM	1.243941	0.165923	-3.684975	1.409864	-2.275111	4841.440157
HLA B*5301	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.456379	1.181170	-2.275209	2860.085890
HLA B*5101	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.356998	2.081726	-2.275272	22750.857136
HLA A*2602	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.502452	1.226371	-2.276081	3180.185670
HLA A*0202	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.133238	1.857104	-2.276134	13590.564958
HLA A*2603	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.484375	2.208172	-2.276204	30505.285414
HLA B*0802	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.278069	2.001388	-2.276681	18970.080077
HLA B*4402	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.342147	2.064862	-2.277284	21986.022526
HLA B*0803	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.405468	2.127896	-2.277572	25437.102435
HLA A*8001	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.339332	2.061629	-2.277703	21843.990831
HLA A*2403	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.887199	1.609050	-2.278150	7712.575727
HLA B*4001	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.321950	2.043325	-2.278626	20987.006427
HLA B*0801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.276091	1.997366	-2.278725	18883.865467
HLA B*5101	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.385678	2.106921	-2.278757	24304.009525
HLA A*2403	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.360924	2.081726	-2.279197	22957.455583
HLA B*0802	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.150337	1.870848	-2.279489	14136.342619
HLA B*1501	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.188829	0.909118	-2.279711	1544.646559
HLA A*6802	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.146761	1.866969	-2.279792	14020.423960
HLA A*2603	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.408050	2.127896	-2.280154	25588.788393
HLA B*5801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.309313	2.028437	-2.280875	20385.089178
HLA A*3001	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.890446	1.609050	-2.281397	7770.454638
HLA A*2603	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.591197	2.309312	-2.281885	39011.870850
HLA B*4601	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.319885	2.037813	-2.282072	20887.443984
HLA A*2603	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.279688	1.997366	-2.282322	19040.921357
HLA B*5701	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.364695	2.081726	-2.282968	23157.660151
HLA A*2301	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.298867	2.015621	-2.283246	19900.629091
HLA A*0211	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.083161	1.799748	-2.283412	12110.458543
HLA A*0301	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.105955	1.822112	-2.283843	12763.074104
HLA B*2705	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.354585	2.070592	-2.283993	22624.804866
HLA A*2602	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-3.397910	1.113773	-2.284137	2499.826063
HLA B*4002	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.593492	2.309312	-2.284180	39218.612480
HLA A*0101	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.412084	2.127896	-2.284188	25827.584355
HLA B*0803	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.322204	2.037813	-2.284391	20999.272047
HLA A*3301	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.013978	1.729555	-2.284423	10327.082630
HLA A*3201	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.200774	0.916314	-2.284459	1587.719954
HLA A*3201	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.591160	1.306673	-2.284486	3900.853425
HLA A*0212	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.628183	1.343697	-2.284486	4247.983456
HLA B*1509	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.355407	2.070592	-2.284815	22667.684639
HLA A*3301	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.107421	1.822112	-2.285309	12806.232122
HLA A*3201	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.601666	2.316186	-2.285480	39963.736148
HLA A*3001	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.126668	1.840969	-2.285699	13386.540326
HLA A*0216	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.356474	2.070592	-2.285882	22723.426931
HLA B*1517	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.593453	1.306673	-2.286779	3921.504605
HLA B*0702	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.357432	2.070592	-2.286840	22773.638263
HLA B*5801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.352407	2.064862	-2.287544	22511.626242
HLA A*0301	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.303528	2.015621	-2.287907	20115.377331
HLA B*3801	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.394911	2.106921	-2.287990	24826.265913
HLA A*0250	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.586171	2.297586	-2.288585	38563.037027
HLA A*3101	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.359521	2.070592	-2.288929	22883.429407
HLA A*3001	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.280416	1.991397	-2.289019	19072.881023
HLA A*6802	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.327420	2.038259	-2.289161	21252.992874
HLA B*4001	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.370895	2.081726	-2.289169	23490.646374
HLA B*0801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.318097	2.028437	-2.289660	20801.628699
HLA A*8001	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.417579	2.127896	-2.289683	26156.476118
HLA A*3201	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.539776	1.249564	-2.290213	3465.583722
HLA A*2902	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.305922	2.015621	-2.290301	20226.573121
HLA A*0211	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.352038	2.061629	-2.290409	22492.514051

HLA B*1801	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.425683	2.135178	-2.290505	26649.103764
HLA A*0211	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.668796	1.378166	-2.290630	4664.402446
HLA A*6802	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.233561	1.942822	-2.290738	17122.237637
HLA A*6801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.721147	1.430389	-2.290758	5261.956327
HLA B*0702	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.418679	2.127896	-2.290783	26222.783724
HLA B*4601	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.161821	1.870848	-2.290974	14515.143884
HLA B*3801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.319441	2.028437	-2.291004	20866.098133
HLA B*0802	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.361720	2.070592	-2.291128	22999.597095
HLA A*3201	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.168687	1.877371	-2.291316	14746.418006
HLA A*0301	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.353015	2.061629	-2.291386	22543.190769
HLA A*3001	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-3.663030	1.371517	-2.291513	4602.887689
HLA A*0202	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.180277	0.887960	-2.292317	1514.526916
HLA A*0216	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.330263	2.037813	-2.292450	21392.570577
HLA A*0219	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.330425	2.037813	-2.292612	21400.557537
HLA B*0803	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.399535	2.106921	-2.292614	25091.994823
HLA B*4801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.363569	2.070592	-2.292977	23097.728536
HLA A*2301	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.501503	2.208172	-2.293331	31732.394027
HLA B*5801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.923438	1.629324	-2.294114	8383.741864
HLA B*3501	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.041058	1.746933	-2.294125	10991.521559
HLA A*0250	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.103719	1.809098	-2.294621	12697.510514
HLA B*0801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.333378	2.038259	-2.295119	21546.582202
HLA A*0203	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.154731	1.859413	-2.295317	14280.078652
HLA B*4001	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.366151	2.070592	-2.295559	23235.464392
HLA A*2402	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.504017	2.208172	-2.295845	31916.612239
HLA B*7301	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.593643	2.297586	-2.296056	39232.193605
HLA A*3201	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.726509	1.430389	-2.296119	5327.319747
HLA A*3101	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.357813	2.061629	-2.296184	22793.605875
HLA B*1502	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.504503	2.208172	-2.296332	31952.373983
HLA B*1509	1:136-144	9	HRDVKPANI	1.262411	0.208757	-3.767813	1.471168	-2.296645	5858.854467
HLA B*3901	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.364773	1.067242	-2.297531	2316.181856
HLA B*5301	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.564326	2.266682	-2.297643	36671.250336
HLA B*4501	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.534551	1.236758	-2.297793	3424.137062
HLA A*0250	1:146-154	9	ISATNAVKV	1.443784	0.185540	-3.927141	1.629324	-2.297816	8455.527109
HLA B*4501	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.564540	2.266682	-2.297857	36689.308034
HLA A*6901	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.362970	2.064862	-2.298108	23065.886686
HLA A*3101	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.289593	1.991397	-2.298197	19480.198954
HLA B*5301	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.368872	2.070592	-2.298280	23381.483384
HLA B*0802	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.336437	2.037813	-2.298624	21698.885095
HLA A*6802	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.884206	1.585464	-2.298742	7659.601885
HLA A*0301	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.342565	2.043325	-2.299240	22007.204390
HLA A*3001	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-2.457049	0.157255	-2.299794	286.450197
HLA A*3002	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.428457	2.127896	-2.300562	26819.912068
HLA B*4501	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.610167	2.309312	-2.300855	40753.650786
HLA B*7301	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.610394	2.309312	-2.301082	40775.042254
HLA B*5401	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.562862	2.261413	-2.301449	36547.863033
HLA B*0803	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.048750	1.746933	-2.301817	11187.937459
HLA A*2602	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.900911	1.598716	-2.302195	7959.962756
HLA B*4001	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.196937	1.894713	-2.302223	15737.536416
HLA A*6802	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.564667	1.262230	-2.302436	3670.006548
HLA B*0801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.373103	2.070592	-2.302511	23610.407512
HLA B*4403	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.618806	2.316186	-2.302620	41572.445828
HLA B*0802	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.409626	2.106921	-2.302705	25681.845405
HLA B*0803	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.364749	2.061629	-2.303120	23160.541778
HLA B*3501	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.112647	1.809098	-2.303549	12961.242140
HLA B*3801	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.374156	2.070592	-2.303564	23667.699811
HLA B*4001	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.368449	2.064862	-2.303587	23358.726044
HLA B*5801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.348631	2.044529	-2.304103	22316.765358
HLA B*0803	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.385852	2.081726	-2.304126	24313.741141
HLA A*0101	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.369041	2.064862	-2.304179	23390.592526
HLA A*2403	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.375086	2.070592	-2.304494	23718.457856
HLA B*5101	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.432466	2.127896	-2.304570	27068.586076
HLA B*1502	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.342854	2.038259	-2.304595	22021.853217
HLA B*1517	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.265201	1.960098	-2.305103	18416.242915
HLA B*0802	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.349893	2.044529	-2.305364	22381.692291
HLA B*0801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.350551	2.044529	-2.306022	22415.621074

HLA A*1101	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.321690	2.015621	-2.306069	20974.407562
HLA B*1503	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.334511	2.028437	-2.306074	21602.839665
HLA A*0201	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.368036	2.061629	-2.306407	23336.495840
HLA A*2602	1:372-380	9	DAIATLQNR	1.011737	0.626562	-3.944856	1.638299	-2.306557	8807.563909
HLA A*0206	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.184978	1.877371	-2.307607	15310.094431
HLA B*4403	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.582311	2.274057	-2.308254	38221.790306
HLA B*4601	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.907053	1.598716	-2.308336	8073.327857
HLA B*3901	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.352877	2.044529	-2.308348	22535.996504
HLA B*5801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.346935	2.038259	-2.308676	22229.767427
HLA B*1509	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.371334	2.061629	-2.309705	23514.422694
HLA A*0101	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.353842	2.043325	-2.310517	22586.160239
HLA A*3301	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.619900	2.309312	-2.310589	41677.382528
HLA A*2501	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.308479	1.997366	-2.311112	20345.976967
HLA A*2603	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.348998	2.037813	-2.311185	22335.607379
HLA B*5701	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.309021	1.997366	-2.311655	20371.418911
HLA A*2402	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.393997	2.081726	-2.312271	24774.075290
HLA A*8001	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.350457	2.037813	-2.312644	22410.770958
HLA B*0702	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.132566	1.819741	-2.312824	13569.553510
HLA B*1503	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.007756	1.694587	-2.313169	10180.197784
HLA A*2402	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.351030	2.037813	-2.313217	22440.372999
HLA A*3001	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.135357	1.822112	-2.313244	13657.045180
HLA A*0101	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.375446	2.061629	-2.313817	23738.098060
HLA B*4402	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.375897	2.061629	-2.314268	23762.767602
HLA B*0802	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.376536	2.061629	-2.314907	23797.760012
HLA B*1801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.343291	2.028058	-2.315233	22044.023625
HLA A*1101	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.137363	1.822112	-2.315251	13720.287326
HLA B*5701	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.377008	2.061629	-2.315379	23823.651478
HLA B*4001	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.166727	1.851066	-2.315661	14680.034286
HLA B*0801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.961077	1.645104	-2.315973	9142.745855
HLA A*0201	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.387012	2.070592	-2.316420	24378.806159
HLA A*3301	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.614102	2.297586	-2.316516	41124.620860
HLA A*0101	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.317942	2.001388	-2.316554	20794.202747
HLA A*0206	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.176130	1.859413	-2.316716	15001.328068
HLA B*4403	1:244-252	9	SADLDAVVL	1.902706	0.406606	-4.626075	2.309312	-2.316763	42274.149863
HLA B*0803	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.360099	2.043325	-2.316774	22913.903697
HLA B*4501	1:149-157	9	TNAVKVMDF	1.199005	1.098581	-4.614699	2.297586	-2.317112	41181.169532
HLA B*3801	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.378895	2.061629	-2.317266	23927.369900
HLA A*0202	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.967646	1.650328	-2.317318	9282.090698
HLA B*2705	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.318882	2.001388	-2.317494	20839.249202
HLA A*0203	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.388244	2.070592	-2.317652	24448.012804
HLA B*7301	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.584350	2.266682	-2.317668	38401.693632
HLA A*0301	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.346223	2.028437	-2.317786	22193.358321
HLA B*0801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.215242	0.897363	-2.317879	1641.504326
HLA B*3901	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.917367	1.598716	-2.318651	8267.359608
HLA B*4403	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.147889	1.828833	-2.319056	14056.878762
HLA B*0702	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-2.829612	0.510481	-2.319131	675.478702
HLA A*1101	1:24-32	9	EVHLARDLR	0.880960	0.651501	-3.851675	1.532461	-2.319215	7106.818562
HLA A*3101	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.362728	2.043325	-2.319403	23053.037526
HLA B*3901	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.279676	1.960098	-2.319578	19040.406317
HLA B*5401	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.604693	1.284672	-2.320021	4024.321470
HLA A*8001	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.401779	2.081726	-2.320053	25221.966670
HLA B*4402	1:116-124	9	IEVIADACQ	1.170936	0.004468	-3.495747	1.175404	-2.320343	3131.461280
HLA A*0250	1:266-274	9	AAEMRADLV	0.998847	0.162308	-3.481819	1.161155	-2.320664	3032.629107
HLA B*4002	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.587407	2.266682	-2.320725	38672.928349
HLA B*4601	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.318158	1.997366	-2.320792	20804.554802
HLA A*0250	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.529004	2.208172	-2.320832	33806.760764
HLA A*2501	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.930115	1.609050	-2.321066	8513.637103
HLA A*0301	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.359202	2.037813	-2.321389	22866.599232
HLA A*3101	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.359364	2.037813	-2.321551	22875.136523
HLA A*2601	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.386775	2.064862	-2.321913	24365.489247
HLA B*1501	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-3.220021	0.898050	-2.321971	1659.666715
HLA A*0101	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.360271	2.038259	-2.322011	22922.954687
HLA B*3801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.360381	2.038259	-2.322122	22928.783928
HLA B*4801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.199648	1.877371	-2.322277	15836.093371
HLA A*2902	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.193173	1.870848	-2.322325	15601.734140

HLA B*5301	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.531017	2.208172	-2.322846	33963.862105
HLA A*3001	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.265854	1.942822	-2.323032	18443.960846
HLA B*3501	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.932455	1.609050	-2.323406	8559.634516
HLA B*1501	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.167656	0.844164	-2.323491	1471.145279
HLA B*1503	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.074693	1.751118	-2.323575	11876.624983
HLA B*1517	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.126363	1.802719	-2.323643	13377.129074
HLA A*3201	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.561988	1.238104	-2.323885	3647.442265
HLA A*2301	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.325541	2.001388	-2.324152	21161.210562
HLA A*3002	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.532326	2.208172	-2.324154	34066.360042
HLA B*5301	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.219017	1.894713	-2.324304	16558.355715
HLA A*0101	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.369199	2.044529	-2.324670	23399.072278
HLA B*4403	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.586143	2.261413	-2.324730	38560.533647
HLA B*2705	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.520163	1.195398	-2.324765	3312.553447
HLA A*3201	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.533200	2.208172	-2.325028	34134.986900
HLA B*5701	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.247479	1.922093	-2.325386	17679.861943
HLA A*0206	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.134647	1.809098	-2.325550	13634.750701
HLA B*5801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.354303	2.028058	-2.326245	22610.121910
HLA B*1517	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.135394	1.809098	-2.326297	13658.227361
HLA B*5701	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.391187	2.064862	-2.326325	24614.298842
HLA B*1501	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.243112	0.916314	-2.326797	1750.296494
HLA B*5101	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.287180	1.960098	-2.327083	19372.267930
HLA B*0802	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.365573	2.038259	-2.327314	23204.562443
HLA A*8001	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.370738	2.043325	-2.327413	23482.133437
HLA A*0219	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.398882	2.070592	-2.328290	25054.286101
HLA A*0201	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.393161	2.064862	-2.328299	24726.408306
HLA A*2501	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.356854	2.028437	-2.328417	22743.350518
HLA A*2601	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.356608	2.028058	-2.328550	22730.435091
HLA B*3501	1:477-485	9	TSAITNVVI	1.425064	0.225264	-3.979003	1.650328	-2.328675	9528.032245
HLA B*4402	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.410543	2.081726	-2.328816	25736.087621
HLA A*0250	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.128792	1.799748	-2.329044	13452.168080
HLA B*5101	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.390913	2.061629	-2.329284	24598.723978
HLA A*0301	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.367636	2.038259	-2.329377	23315.043571
HLA A*2402	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.400386	2.070592	-2.329794	25141.182629
HLA B*1509	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.290073	1.960098	-2.329975	19501.709508
HLA B*1501	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.394886	2.064862	-2.330023	24824.788576
HLA B*3901	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.395177	2.064862	-2.330314	24841.447283
HLA A*3001	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-3.028355	0.697848	-2.330506	1067.467341
HLA A*6801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.152630	1.822112	-2.330518	14211.180641
HLA B*1509	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.450636	2.120022	-2.330614	28225.164912
HLA B*4801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.358790	2.028058	-2.330733	22844.960967
HLA A*0201	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.368780	2.037813	-2.330967	23376.550746
HLA B*4001	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.359474	2.028058	-2.331416	22880.953604
HLA A*0202	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.191681	0.860149	-2.331533	1554.824574
HLA B*1509	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-3.967383	1.635751	-2.331631	9276.468312
HLA A*0201	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.329051	1.997366	-2.331684	21332.936430
HLA B*0802	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.083038	1.751011	-2.332028	12107.052178
HLA B*3901	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.402662	2.070592	-2.332070	25273.323349
HLA A*0101	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.360905	2.028437	-2.332468	22956.462026
HLA A*2602	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.370914	2.038259	-2.332655	23491.663050
HLA B*4801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.203543	1.870848	-2.332696	15978.775679
HLA B*1502	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.203581	1.870848	-2.332733	15980.158833
HLA A*0206	1:143-151	9	NIMISATNA	0.971550	-0.064300	-3.240161	0.907250	-2.332911	1738.443856
HLA B*7301	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.324565	1.991397	-2.333169	21113.754735
HLA B*1503	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.918687	1.585464	-2.333223	8292.533588
HLA B*4001	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.362077	2.028437	-2.333640	23018.517514
HLA A*0216	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.372098	2.038259	-2.333839	23555.802447
HLA B*4601	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.372119	2.038259	-2.333860	23556.949383
HLA B*3801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.362298	2.028058	-2.334240	23030.226088
HLA B*4801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.294440	1.960098	-2.334343	19698.827431
HLA B*5301	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.441321	2.106921	-2.334400	27626.176366
HLA A*0212	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.372782	2.038259	-2.334522	23592.915027
HLA A*6901	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.379076	2.044529	-2.334547	23937.339196
HLA A*0219	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.332147	1.997366	-2.334781	21485.588833
HLA B*0802	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.332429	1.997366	-2.335063	21499.541520
HLA A*0206	1:289-297	9	TDAERTSLL	1.288079	0.301720	-3.924989	1.589799	-2.335190	8413.729744

HLA B*1501	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.257504	1.922093	-2.335411	18092.730821
HLA A*3101	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.824604	1.488986	-2.335618	6677.354935
HLA B*1501	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.364178	2.028437	-2.335741	23130.114863
HLA A*0216	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.186937	1.851066	-2.335871	15379.327309
HLA A*1101	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.397515	2.061629	-2.335886	24975.525348
HLA B*4501	1:570-578	9	FWVDAEPRL	1.784497	0.531689	-4.652657	2.316186	-2.336471	44942.471943
HLA B*5401	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.364533	2.028058	-2.336475	23149.017418
HLA A*0202	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.921864	1.584939	-2.336925	8353.408944
HLA A*2501	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.178197	1.840969	-2.337228	15072.915195
HLA B*7301	1:450-458	9	GRFKQANSP	0.757924	0.058749	-3.154099	0.816673	-2.337426	1425.932718
HLA B*3901	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.210930	1.873374	-2.337556	16252.878199
HLA A*3201	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.088917	1.751011	-2.337906	12272.041792
HLA B*5801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.353798	2.015621	-2.338177	22583.838774
HLA B*0702	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.382748	2.044529	-2.338220	24140.603274
HLA A*6901	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.971123	1.632662	-2.338461	9356.707334
HLA B*4402	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.376935	2.038259	-2.338676	23819.656431
HLA A*2301	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.179804	1.840969	-2.338835	15128.793792
HLA B*4402	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.340394	2.001388	-2.339006	21897.470644
HLA B*4601	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.404065	2.064862	-2.339203	25355.080653
HLA A*3301	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-3.975047	1.635751	-2.339295	9441.623657
HLA A*2902	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.340692	2.001388	-2.339304	21912.520600
HLA A*0301	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.340854	2.001388	-2.339466	21920.701684
HLA A*2602	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.828491	1.488986	-2.339504	6737.371731
HLA A*0212	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.410181	2.070592	-2.339589	25714.655226
HLA B*4501	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.613853	2.274057	-2.339796	41101.044779
HLA B*5701	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.383361	2.043325	-2.340036	24174.713425
HLA B*4002	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.405031	2.064862	-2.340168	25411.519495
HLA A*0301	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.368513	2.028058	-2.340455	23362.138232
HLA A*0101	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.378712	2.037813	-2.340899	23917.275365
HLA B*5401	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.549211	2.208172	-2.341040	35416.976297
HLA A*1101	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.468967	2.127896	-2.341071	29441.990623
HLA A*2601	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.379684	2.038259	-2.341425	23970.902778
HLA A*2601	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.385988	2.044529	-2.341459	24321.371347
HLA A*0203	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.379917	2.038259	-2.341658	23983.744529
HLA A*6802	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.379879	2.037813	-2.342066	23981.668629
HLA B*1501	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-3.831080	1.488986	-2.342093	6777.657873
HLA B*5101	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.910605	1.568231	-2.342374	8139.636504
HLA B*4601	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.387005	2.044529	-2.342477	24378.410502
HLA B*3901	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.264585	1.922093	-2.342492	18390.158389
HLA B*5101	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.413096	2.070592	-2.342504	25887.875820
HLA A*2501	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.380396	2.037813	-2.342583	24010.228018
HLA A*0201	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.655446	1.312789	-2.342657	4523.204681
HLA A*0101	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.303399	1.960098	-2.343301	20109.393013
HLA A*0201	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.381653	2.038259	-2.343394	24079.821260
HLA B*1509	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.203144	1.859413	-2.343731	15964.087056
HLA B*4402	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.387271	2.043325	-2.343946	24393.318006
HLA B*1517	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.067203	1.723131	-2.344072	11673.548317
HLA A*0202	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.539034	1.194908	-2.344126	3459.664281
HLA B*1502	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.464186	2.120022	-2.344164	29119.637753
HLA B*7301	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.605937	2.261413	-2.344525	40358.725838
HLA B*4801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.389465	2.044529	-2.344937	24516.885373
HLA A*0206	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.383429	2.038259	-2.345170	24178.506415
HLA A*2601	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.383002	2.037813	-2.345189	24154.711978
HLA B*1517	1:64-72	9	AALNHPAIV	1.169288	0.295731	-3.810489	1.465019	-2.345470	6463.812587
HLA A*0211	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.383747	2.038259	-2.345488	24196.171275
HLA A*3101	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.374076	2.028437	-2.345639	23663.346864
HLA B*5301	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.427377	2.081726	-2.345650	26753.252380
HLA B*1509	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.361459	2.015621	-2.345838	22985.790036
HLA A*2403	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.374450	2.028437	-2.346013	23683.710178
HLA A*6802	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.489385	1.143250	-2.346134	3085.919840
HLA B*4403	1:153-161	9	KVMDFGIAR	1.467969	0.798713	-4.612828	2.266682	-2.346146	41004.213508
HLA A*3002	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.343902	1.997366	-2.346535	22075.051930
HLA B*5101	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.385048	2.038259	-2.346789	24268.797882
HLA B*3901	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.255963	0.909118	-2.346845	1802.865407
HLA A*0202	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.098070	1.751011	-2.347060	12533.443834

HLA A*0201	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.391876	2.044529	-2.347347	24653.345844
HLA A*2601	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.376200	2.028437	-2.347763	23779.356848
HLA B*5701	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.376249	2.028437	-2.347812	23782.058518
HLA A*0201	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.916051	1.568231	-2.347820	8242.351229
HLA A*6802	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-3.669332	1.321448	-2.347883	4670.159325
HLA B*4402	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.177225	1.828833	-2.348392	15039.194252
HLA B*3901	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-3.993537	1.645104	-2.348433	9852.288769
HLA B*0802	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.376907	2.028437	-2.348470	23818.110141
HLA A*0212	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.609490	1.261014	-2.348476	4069.024586
HLA A*2602	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.556955	2.208172	-2.348784	36054.160140
HLA B*3801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.468955	2.120022	-2.348933	29441.194244
HLA A*0216	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.539067	1.190001	-2.349065	3459.926320
HLA A*2902	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.377962	2.028437	-2.349525	23876.035611
HLA B*3901	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.169269	1.819741	-2.349528	14766.215853
HLA B*3501	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.394385	2.044529	-2.349857	24796.199288
HLA B*3501	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.781722	1.431809	-2.349912	6049.530373
HLA B*4001	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.310076	1.960098	-2.349978	20420.962054
HLA A*3101	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.388246	2.038259	-2.349987	24448.145065
HLA A*0219	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.388422	2.038259	-2.350163	24458.066710
HLA A*0216	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.378996	1.028753	-2.350243	2393.296123
HLA B*0801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.415199	2.064862	-2.350337	26013.524994
HLA A*6901	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.366008	2.015621	-2.350387	23227.797879
HLA A*2301	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.000825	1.650328	-2.350498	10019.019801
HLA B*5701	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.388596	2.037813	-2.350783	24467.860012
HLA A*3002	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.432825	2.081726	-2.351099	27091.000373
HLA A*6801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-3.438053	1.086732	-2.351321	2741.909349
HLA B*1801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.311669	1.960098	-2.351571	20496.001735
HLA A*3301	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-3.102138	0.750403	-2.351735	1265.137776
HLA B*2705	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.433659	2.081726	-2.351933	27143.078920
HLA B*5401	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.219097	1.866969	-2.352128	16561.401677
HLA A*8001	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.380641	2.028437	-2.352203	24023.740657
HLA B*5301	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.950936	1.598716	-2.352220	8931.744071
HLA A*8001	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.354073	2.001388	-2.352685	22598.137899
HLA B*3501	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.752240	1.398961	-2.353280	5652.496782
HLA A*0203	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.415857	2.061629	-2.354228	26052.959333
HLA A*0101	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.382447	2.028058	-2.354390	24123.892518
HLA A*0203	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.419266	2.064862	-2.354404	26258.273306
HLA A*0211	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.211771	1.857104	-2.354668	16284.386305
HLA A*6801	1:614-622	9	VNRDGIITL	1.888708	0.385349	-4.628939	2.274057	-2.354882	42553.854556
HLA A*3101	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.352393	1.997366	-2.355026	22510.895541
HLA B*4601	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.222081	1.866969	-2.355112	16675.579551
HLA B*0702	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.383575	2.028437	-2.355138	24186.617564
HLA A*0301	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.228547	1.873374	-2.355173	16925.703130
HLA A*2301	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.437059	2.081726	-2.355333	27356.391746
HLA B*4402	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.347036	1.991397	-2.355639	22234.939234
HLA B*1501	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.393997	2.038259	-2.355738	24774.075290
HLA A*0211	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.164904	1.809098	-2.355806	14618.535594
HLA A*6901	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.299144	1.942822	-2.356322	19913.337050
HLA B*2705	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-2.974269	0.617889	-2.356381	942.474160
HLA B*0802	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.421606	2.064862	-2.356744	26400.141303
HLA B*4801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.372460	2.015621	-2.356839	23575.435503
HLA B*1503	1:137-145	9	RDVKPANIM	0.886768	0.128226	-3.372343	1.014994	-2.357349	2356.908354
HLA A*0216	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.214751	1.857104	-2.357647	16396.476969
HLA B*5701	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.402185	2.044529	-2.357657	25245.583231
HLA A*6901	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.355116	1.997366	-2.357750	22652.483660
HLA B*3801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.401196	2.043325	-2.357871	25188.150245
HLA A*8001	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.396234	2.038259	-2.357975	24901.996219
HLA B*1502	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.373653	2.015621	-2.358032	23640.315185
HLA B*1501	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.553173	1.194908	-2.358265	3574.153156
HLA A*2402	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.151592	1.793234	-2.358357	14177.239873
HLA A*0203	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.250606	0.892112	-2.358494	1780.764461
HLA A*0201	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.762127	1.403484	-2.358643	5782.650660
HLA A*6801	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.486755	2.127896	-2.358859	30672.919936
HLA A*3301	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.420934	2.061629	-2.359305	26359.325841
HLA A*2602	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.281445	1.922093	-2.359352	19118.128401

HLA A*0202	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.846572	1.487180	-2.359393	7023.800160
HLA B*0802	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.402728	2.043325	-2.359403	25277.151964
HLA B*4402	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.388128	2.028437	-2.359691	24441.532872
HLA B*4501	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.479775	2.120022	-2.359753	30183.861614
HLA A*6802	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.424682	2.064862	-2.359819	26587.758615
HLA A*2403	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.404756	2.044529	-2.360227	25395.440184
HLA A*0219	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.404946	2.044529	-2.360417	25406.570930
HLA B*1509	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-3.631275	1.270153	-2.361122	4278.334522
HLA A*2602	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.793084	1.431809	-2.361274	6209.888051
HLA A*8001	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.405949	2.044529	-2.361421	25465.328525
HLA A*0201	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.739624	1.378166	-2.361458	5490.647834
HLA B*4601	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.389569	2.028058	-2.361511	24522.721947
HLA B*3801	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.443567	2.081726	-2.361841	27769.425029
HLA B*5301	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.489875	2.127896	-2.361979	30894.077885
HLA A*6802	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.817063	1.454961	-2.362102	6562.398737
HLA A*0301	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.353791	1.991397	-2.362394	22583.472249
HLA B*0702	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.427717	2.064862	-2.362855	26774.246772
HLA B*4801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-3.995562	1.632662	-2.362901	9898.340481
HLA A*3101	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.008005	1.645104	-2.362901	10186.037274
HLA A*6801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-3.216501	0.853416	-2.363085	1646.271105
HLA A*2501	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.408170	2.044529	-2.363641	25595.849425
HLA A*0202	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.183404	1.819741	-2.363663	15254.701519
HLA B*4801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.392332	2.028437	-2.363895	24679.233569
HLA B*3901	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.223331	1.859413	-2.363917	16723.642017
HLA B*1501	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.241417	1.877371	-2.364046	17434.809165
HLA A*3002	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.049276	1.685171	-2.364105	11201.503389
HLA A*3101	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.392221	2.028058	-2.364164	24672.959306
HLA B*0803	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.402561	2.038259	-2.364302	25267.444820
HLA B*3901	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.193521	1.828833	-2.364688	15614.230883
HLA A*2403	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.819661	1.454961	-2.364700	6601.781485
HLA B*0803	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.393253	2.028437	-2.364816	24731.625775
HLA B*0803	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.362914	1.997366	-2.365547	23062.892067
HLA A*0250	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-3.497754	1.132158	-2.365595	3145.962245
HLA B*0803	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.430591	2.064862	-2.365728	26951.980392
HLA B*5801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.357432	1.991397	-2.366036	22773.638263
HLA A*2402	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.326405	1.960098	-2.366307	21203.381093
HLA A*2603	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.004852	1.638299	-2.366553	10112.353716
HLA A*2403	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.394947	2.028058	-2.366889	24828.280605
HLA A*0301	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.364831	1.997366	-2.367465	23164.927552
HLA B*3901	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.953253	1.585464	-2.367788	8979.514635
HLA A*0202	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.907165	1.538857	-2.368309	8075.424568
HLA A*3201	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.225868	1.857104	-2.368765	16821.638914
HLA B*0802	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.396934	2.028058	-2.368877	24942.174274
HLA A*0201	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.397085	2.028058	-2.369027	24950.811571
HLA A*3101	1:487-495	9	IVGSGPATK	0.962871	0.205808	-3.537958	1.168679	-2.369279	3451.102780
HLA B*1503	1:452-460	9	FKQANSPST	0.861933	-0.283110	-2.948110	0.578823	-2.369287	887.381327
HLA B*3501	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.937765	1.568231	-2.369534	8664.929977
HLA B*1501	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.397761	2.028058	-2.369704	24989.716434
HLA B*5701	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.408090	2.038259	-2.369831	25591.141854
HLA B*0801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-3.959860	1.589799	-2.370061	9117.160797
HLA B*3901	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.361518	1.991397	-2.370121	22988.899011
HLA A*2601	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.969159	1.598716	-2.370443	9314.485609
HLA B*5101	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.398978	2.028437	-2.370541	25059.843895
HLA A*2403	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.435454	2.064862	-2.370592	27255.497643
HLA A*0250	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-2.467636	0.096922	-2.370714	293.518787
HLA A*6901	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.222015	1.851066	-2.370949	16673.053778
HLA A*0211	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.103928	0.732827	-2.371101	1270.363863
HLA B*1503	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.801551	1.430389	-2.371162	6332.151761
HLA A*0212	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.436403	2.064862	-2.371541	27315.132273
HLA B*2705	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.387330	2.015621	-2.371709	24396.617358
HLA B*5401	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.491816	2.120022	-2.371794	31032.439094
HLA A*2902	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.314655	1.942822	-2.371833	20637.417236
HLA B*0801	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.266745	1.894713	-2.372031	18481.816179
HLA A*0203	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.957576	1.584939	-2.372637	9069.344835
HLA A*2902	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.437559	2.064862	-2.372697	27387.932860

HLA B*4601	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.401429	2.028437	-2.372992	25201.644103
HLA A*6801	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.493315	2.120022	-2.373293	31139.732902
HLA A*0203	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.417899	2.044529	-2.373370	26175.727693
HLA A*3002	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.819440	1.445980	-2.373460	6598.425138
HLA B*5101	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.034611	1.661000	-2.373611	10829.560435
HLA A*1101	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.125907	1.752221	-2.373686	13363.096895
HLA A*2902	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.166943	1.793234	-2.373709	14687.342501
HLA A*2402	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.401903	2.028058	-2.373846	25229.199453
HLA A*6802	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.371854	1.997366	-2.374487	23542.553009
HLA A*2902	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.412314	2.037813	-2.374501	25841.280974
HLA A*0206	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.231643	1.857104	-2.374540	17046.818630
HLA B*5401	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.279505	0.904921	-2.374584	1903.290787
HLA B*4601	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.334915	1.960098	-2.374817	21622.950483
HLA A*0219	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.403024	2.028058	-2.374966	25294.387908
HLA A*0212	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.419724	2.044529	-2.375196	26285.988520
HLA B*1517	1:79-87	9	EAETPAGPL	0.986891	0.274759	-3.637050	1.261650	-2.375400	4335.605645
HLA B*1501	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.178329	1.802719	-2.375609	15077.482283
HLA A*0211	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.473488	1.097502	-2.375986	2975.007228
HLA A*2602	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.779743	1.403484	-2.376260	6022.036662
HLA A*8001	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.373931	1.997366	-2.376564	23655.411198
HLA A*0201	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.336825	1.960098	-2.376727	21718.262855
HLA B*7301	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.128134	1.751118	-2.377017	13431.806579
HLA B*4601	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.392926	2.015621	-2.377305	24713.035211
HLA B*3501	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.442293	2.064862	-2.377431	27688.119892
HLA A*3101	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-3.611140	1.233662	-2.377478	4084.507073
HLA B*5701	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.405557	2.028058	-2.377499	25442.332225
HLA A*0202	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.567655	1.190001	-2.377654	3695.348347
HLA B*1509	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.422241	2.044529	-2.377712	26438.731376
HLA A*1101	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.421223	2.043325	-2.377898	26376.871605
HLA B*4001	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.393704	2.015621	-2.378083	24757.327828
HLA A*8001	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.443027	2.064862	-2.378164	27734.893729
HLA A*6901	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.237620	1.859413	-2.378207	17283.051750
HLA A*0211	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.963863	1.585464	-2.378399	9201.595479
HLA B*1503	1:136-144	9	HRDVKPANI	1.262411	0.208757	-3.849692	1.471168	-2.378524	7074.443178
HLA A*1101	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.460688	2.081726	-2.378961	28886.011839
HLA A*2601	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.172272	1.793234	-2.379038	14868.660818
HLA B*3501	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.064285	1.685171	-2.379114	11595.375703
HLA B*0801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.250150	1.870848	-2.379303	17788.946700
HLA A*0203	1:392-400	9	STIPPDHVI	1.394582	0.214468	-3.988725	1.609050	-2.379676	9743.733277
HLA A*0206	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-3.502438	1.122659	-2.379779	3180.082445
HLA B*0803	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.381251	2.001388	-2.379863	24057.555534
HLA B*5301	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.377605	1.997366	-2.380239	23856.410342
HLA A*3101	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-3.942107	1.561867	-2.380240	8751.991874
HLA B*0803	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.395971	2.015621	-2.380350	24886.912480
HLA A*3301	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.451139	2.070592	-2.380547	28257.860567
HLA B*1501	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.200409	1.819741	-2.380668	15863.875281
HLA B*4402	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.408773	2.028058	-2.380716	25631.461148
HLA A*0203	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.376708	0.995952	-2.380756	2380.718457
HLA A*2601	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.396401	2.015621	-2.380780	24911.562965
HLA B*0803	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.451539	2.070592	-2.380947	28283.860743
HLA A*0101	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.372737	1.991397	-2.381340	23590.490086
HLA A*0206	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.014344	1.632662	-2.381683	10335.801775
HLA B*4002	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.488792	2.106921	-2.381871	30817.125323
HLA A*0250	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.419990	2.037813	-2.382177	26302.062517
HLA A*6901	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.400118	1.017549	-2.382570	2512.570795
HLA A*3001	1:162-170	9	AIADSGNSV	1.093291	0.318474	-3.794512	1.411765	-2.382747	6230.347322
HLA A*0206	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.453442	2.070592	-2.382850	28408.072860
HLA B*4403	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.591049	2.208172	-2.382877	38998.576972
HLA A*0101	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.398997	2.015621	-2.383376	25060.928486
HLA A*0201	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.399004	2.015621	-2.383383	25061.335220
HLA B*1502	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.385119	2.001388	-2.383731	24272.736946
HLA A*3101	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.690754	1.306673	-2.384081	4906.302273
HLA A*0250	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.871284	1.487180	-2.384104	7435.052335
HLA A*0211	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.017046	1.632662	-2.384384	10400.305089
HLA B*1503	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.276592	0.892112	-2.384480	1890.565742

HLA A*2402	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.147781	1.762988	-2.384793	14053.381074
HLA B*4001	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.076577	1.691666	-2.384911	11928.266413
HLA B*4601	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.376325	1.991397	-2.384928	23786.175940
HLA B*1517	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.450141	2.064862	-2.385278	28192.964645
HLA A*2902	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.258681	1.873374	-2.385307	18141.835049
HLA A*6901	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.376870	1.991397	-2.385473	23816.048576
HLA A*6802	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-3.459109	1.073598	-2.385511	2878.121852
HLA A*6801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.256400	1.870848	-2.385552	18046.785813
HLA A*2403	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-3.984299	1.598716	-2.385583	9644.927277
HLA A*6901	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-3.341668	0.956046	-2.385622	2196.179431
HLA B*5401	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.492589	2.106921	-2.385668	31087.721473
HLA A*0203	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.816165	1.430389	-2.385776	6548.851034
HLA B*4801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.236998	1.851066	-2.385932	17258.292163
HLA B*4402	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.401560	2.015621	-2.385939	25209.280193
HLA B*4002	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.647897	2.261413	-2.386484	44452.572542
HLA A*3201	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.415007	2.028437	-2.386569	26001.987669
HLA A*2403	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.237667	1.851066	-2.386602	17284.921839
HLA A*6802	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.246198	1.859413	-2.386785	17627.811592
HLA A*0301	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.282178	1.894713	-2.387465	19150.424860
HLA A*2601	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.384952	1.997366	-2.387586	24263.415527
HLA A*0101	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.384957	1.997366	-2.387590	24263.678053
HLA B*0803	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.258763	1.870848	-2.387916	18145.270461
HLA B*2705	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.431429	2.043325	-2.388105	27004.083870
HLA B*4402	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.239364	1.851066	-2.388298	17352.567730
HLA B*5801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.787422	1.398961	-2.388461	6129.450077
HLA B*4001	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.247958	1.859413	-2.388545	17699.384517
HLA A*3301	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.433123	2.044529	-2.388595	27109.619801
HLA B*3501	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.521864	1.133041	-2.388823	3325.553365
HLA A*2902	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.433652	2.044529	-2.389123	27142.638401
HLA A*0211	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.459910	2.070592	-2.389318	28834.332712
HLA A*0211	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.240773	1.851066	-2.389708	17408.984524
HLA A*0203	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.241241	1.851066	-2.390175	17427.736571
HLA B*5701	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.210315	1.819741	-2.390574	16229.857835
HLA B*4501	1:45-53	9	DLARDPSFY	1.045970	1.215443	-4.652626	2.261413	-2.391214	44939.311315
HLA A*6901	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.534471	1.143250	-2.391221	3423.507297
HLA A*2902	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.429620	2.038259	-2.391361	26891.829230
HLA A*8001	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.419447	2.028058	-2.391389	26269.213769
HLA B*1501	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.250850	1.859413	-2.391437	17817.648225
HLA A*2602	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.429602	2.037813	-2.391789	26890.665401
HLA A*0219	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.457351	2.064862	-2.392489	28664.958424
HLA B*5401	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.139887	1.746933	-2.392954	13800.237265
HLA A*3002	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.143975	1.751011	-2.392964	13930.755089
HLA A*3301	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.520905	2.127896	-2.393009	33182.177757
HLA B*3901	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.408651	2.015621	-2.393030	25624.251667
HLA A*0250	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.810244	1.417212	-2.393033	6460.176885
HLA A*6802	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-3.038993	0.645932	-2.393061	1093.938897
HLA A*6802	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.437968	2.044529	-2.393439	27413.725826
HLA B*2705	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.315600	1.922093	-2.393507	20682.347824
HLA B*1801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.458430	2.064862	-2.393567	28736.225950
HLA A*0206	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.237792	0.844164	-2.393628	1728.989631
HLA A*6901	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.353732	1.960098	-2.393634	22580.418104
HLA A*2301	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.431707	2.037813	-2.393894	27021.327888
HLA B*5801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-3.548968	1.154939	-2.394028	3539.709165
HLA B*0702	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.432318	2.038259	-2.394058	27059.362051
HLA B*0802	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.213900	1.819741	-2.394159	16364.397860
HLA B*0801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.979356	1.584939	-2.394417	9535.767222
HLA A*0216	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.024203	1.629324	-2.394878	10573.106596
HLA B*4402	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.027652	1.632662	-2.394990	10657.409531
HLA B*1509	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.337849	1.942822	-2.395027	21769.550438
HLA B*5701	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.355240	1.960098	-2.395143	22658.979605
HLA B*3501	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.411022	2.015621	-2.395401	25764.506094
HLA B*1501	1:63-71	9	AAALNHPAI	1.199473	0.385466	-3.980352	1.584939	-2.395413	9557.665404
HLA A*0203	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.424083	2.028058	-2.396025	26551.105512
HLA A*0101	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.318128	1.922093	-2.396035	20803.091699
HLA B*2705	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.424524	2.028437	-2.396087	26578.123294

HLA B*1501	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.387499	1.991397	-2.396102	24406.121985
HLA A*0212	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.424303	2.028058	-2.396246	26564.610968
HLA A*2403	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.434735	2.038259	-2.396476	27210.415507
HLA A*3301	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.503451	2.106921	-2.396529	31875.027008
HLA A*0203	1:288-296	9	LTDAERTSL	1.232510	0.352954	-3.982053	1.585464	-2.396588	9595.173891
HLA A*2501	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.634700	1.238104	-2.396597	4312.213830
HLA A*0219	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.740380	1.343697	-2.396684	5500.220792
HLA B*1501	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.413345	2.015621	-2.397724	25902.725434
HLA A*2603	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.006910	1.609050	-2.397861	10160.390531
HLA B*5801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.272499	1.873374	-2.399124	18728.307663
HLA A*3301	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.519192	2.120022	-2.399170	33051.571292
HLA B*4402	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.240271	1.840969	-2.399301	17388.841522
HLA A*2902	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.321542	1.922093	-2.399449	20967.260219
HLA A*0202	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.008809	1.609050	-2.399759	10204.900743
HLA A*2403	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.270628	1.870848	-2.399781	18647.831880
HLA B*1509	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.277273	1.877371	-2.399902	18935.321735
HLA A*1101	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.438022	2.037813	-2.400209	27417.137058
HLA A*3001	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.257579	1.857104	-2.400476	18095.863241
HLA A*2403	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.193887	1.793234	-2.400653	15627.413961
HLA A*6901	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.744506	1.343697	-2.400809	5552.720572
HLA A*0212	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.258185	1.857104	-2.401082	18121.138202
HLA B*1501	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-3.383550	0.982334	-2.401216	2418.520313
HLA B*0803	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.445999	2.044529	-2.401470	27925.348692
HLA B*1502	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.399032	1.997366	-2.401666	25062.962221
HLA B*1501	1:366-374	9	RGQSSADAI	1.357283	0.227759	-3.986752	1.585042	-2.401710	9699.555218
HLA B*0801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.417422	2.015621	-2.401801	26146.997092
HLA B*3501	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.261306	1.859413	-2.401892	18251.795270
HLA B*5101	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.403722	2.001388	-2.402334	25335.062006
HLA A*0219	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.957393	1.554751	-2.402641	9065.518639
HLA B*1517	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.447357	2.044529	-2.402828	28012.805573
HLA A*0216	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.942046	1.538857	-2.403189	8750.760930
HLA A*0301	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.363832	1.960098	-2.403735	23111.727866
HLA B*1517	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.431855	2.028058	-2.403797	27030.538948
HLA B*0702	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.419428	2.015621	-2.403807	26268.076885
HLA A*0211	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.364091	1.960098	-2.403993	23125.485466
HLA B*1503	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-3.473850	1.069720	-2.404130	2977.486807
HLA A*0201	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.599045	1.194908	-2.404137	3972.322531
HLA A*0206	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.943329	1.538857	-2.404472	8776.647136
HLA B*5801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.347410	1.942822	-2.404587	22254.073342
HLA B*5301	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.433051	2.028437	-2.404613	27105.073721
HLA A*8001	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.299478	1.894713	-2.404764	19928.640438
HLA B*5701	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.420396	2.015621	-2.404775	26326.690425
HLA A*0201	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.396201	1.991397	-2.404804	24900.110251
HLA A*0203	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.667062	1.262230	-2.404832	4645.816953
HLA A*6901	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.326943	1.922093	-2.404850	21229.665490
HLA B*0702	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-3.169310	0.764421	-2.404889	1476.758910
HLA A*2402	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.262043	1.857104	-2.404940	18282.826038
HLA B*4002	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.525317	2.120022	-2.405295	33521.019474
HLA B*5401	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.540796	2.135178	-2.405618	34737.265302
HLA A*3301	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.158161	1.752221	-2.405940	14393.315579
HLA A*0212	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.422680	2.015621	-2.407059	26465.491633
HLA A*2301	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.436681	2.028437	-2.408243	27332.574917
HLA B*4403	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.528414	2.120022	-2.408392	33760.886320
HLA A*2603	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.451851	2.043325	-2.408526	28304.218735
HLA B*3901	1:79-87	9	EAETPAGPL	0.986891	0.274759	-3.670455	1.261650	-2.408805	4682.251644
HLA B*4501	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.516070	2.106921	-2.409148	32814.791214
HLA A*0216	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.437247	2.028058	-2.409189	27368.233912
HLA A*3001	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.268667	1.859413	-2.409253	18563.784797
HLA A*0216	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.008461	1.598716	-2.409745	10196.733321
HLA B*0801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.287364	1.877371	-2.409993	19380.444197
HLA A*2603	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.438617	2.028437	-2.410179	27454.688640
HLA A*3301	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.545455	2.135178	-2.410277	35111.926142
HLA A*0206	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.438494	2.028058	-2.410437	27446.966331
HLA B*1502	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.319700	0.909118	-2.410582	2087.854043
HLA B*2705	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.267811	1.857104	-2.410708	18527.264968

HLA A*2601	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.402171	1.991397	-2.410775	25244.763789
HLA A*0201	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.020049	1.609050	-2.410999	10472.460265
HLA A*0219	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.789184	1.378166	-2.411018	6154.370333
HLA B*0802	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.426994	2.015621	-2.411373	26729.671442
HLA A*3001	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.288870	1.877371	-2.411499	19447.767180
HLA A*3201	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-2.870234	0.458556	-2.411678	741.710208
HLA A*0212	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.810733	1.398961	-2.411772	6467.450335
HLA B*2705	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.439848	2.028058	-2.411790	27532.627111
HLA A*3001	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.211616	1.799748	-2.411868	16278.572959
HLA A*0202	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-3.210952	0.798791	-2.412161	1625.368624
HLA A*1101	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.440621	2.028437	-2.412183	27581.674791
HLA B*5301	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.414382	2.001388	-2.412993	25964.596925
HLA A*0211	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-2.987624	0.574537	-2.413087	971.905242
HLA A*3001	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-3.859414	1.445980	-2.413434	7234.598460
HLA B*0803	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.286821	1.873374	-2.413447	19356.239886
HLA A*3002	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.264656	1.851066	-2.413590	18393.143293
HLA A*0212	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.405028	1.991397	-2.413631	25411.382022
HLA A*6901	1:191-199	9	DSVDARSDV	0.837527	0.035965	-3.287338	0.873492	-2.413846	1937.931082
HLA A*0216	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.478847	2.064862	-2.413984	30119.430399
HLA B*0801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.281022	1.866969	-2.414054	19099.520610
HLA A*0216	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.374170	1.960098	-2.414072	23668.468061
HLA B*4801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.406236	1.991397	-2.414839	25482.141354
HLA B*0801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.280779	0.865145	-2.415633	1908.879730
HLA A*6801	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.458961	2.043325	-2.415636	28771.381351
HLA B*4601	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.266982	1.851066	-2.415916	18491.917381
HLA A*2902	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.024987	1.609050	-2.415938	10592.228444
HLA A*0203	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.283365	1.866969	-2.416396	19202.815238
HLA B*7301	1:340-348	9	AVLTVVVTI	1.737080	0.382942	-4.536773	2.120022	-2.416751	34417.023408
HLA B*4501	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.625086	2.208172	-2.416914	42177.977371
HLA B*1501	1:521-529	9	SQASVDSPR	0.518283	0.661153	-3.596357	1.179436	-2.416920	3947.814091
HLA A*3001	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.284366	1.866969	-2.417397	19247.121326
HLA B*4402	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.274543	1.857104	-2.417439	18816.662144
HLA B*1517	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.455930	2.038259	-2.417671	28571.291872
HLA A*0203	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.409412	1.991397	-2.418016	25669.205346
HLA A*6802	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.036843	1.618772	-2.418071	10885.361088
HLA B*1509	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.483111	2.064862	-2.418249	30416.628241
HLA B*5801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.269402	1.851066	-2.418336	18595.245395
HLA B*4801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.228053	1.809098	-2.418956	16906.485152
HLA A*2902	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.276302	1.857104	-2.419199	18893.062072
HLA A*3002	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.447831	2.028437	-2.419394	28043.434633
HLA B*5401	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.018122	1.598716	-2.419406	10426.106180
HLA A*0203	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.219280	1.799748	-2.419532	16568.391588
HLA A*3301	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.627839	2.208172	-2.419668	42446.251783
HLA B*0801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.411654	1.991397	-2.420257	25802.027449
HLA B*3501	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.277609	1.857104	-2.420505	18949.976035
HLA A*2501	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.485874	2.064862	-2.421012	30610.756602
HLA B*0801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.825328	1.403484	-2.421844	6688.490325
HLA B*4801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.279047	1.857104	-2.421943	19012.820581
HLA B*3801	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.486905	2.064862	-2.422043	30683.541749
HLA A*3001	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.007221	1.585042	-2.422179	10167.648711
HLA A*3001	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.287437	1.865170	-2.422267	19383.694698
HLA B*0801	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.990628	1.568231	-2.422398	9786.524102
HLA B*0802	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.317261	1.894713	-2.422547	20761.604969
HLA A*0216	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.289673	1.866969	-2.422704	19483.782398
HLA A*6901	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.683847	1.261014	-2.422832	4828.884472
HLA A*2902	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.420340	1.997366	-2.422974	26323.272459
HLA B*1502	1:162-170	9	AIADSGNSV	1.093291	0.318474	-3.835172	1.411765	-2.423408	6841.832621
HLA A*2301	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.488308	2.064862	-2.423446	30782.800703
HLA A*0201	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.315805	0.892112	-2.423692	2069.210572
HLA A*3101	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.265098	1.840969	-2.424128	18411.859724
HLA B*1801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.452610	2.028437	-2.424173	28353.720600
HLA B*1517	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.500563	1.075727	-2.424836	3166.383329
HLA A*0212	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.291962	1.866969	-2.424993	19586.717925
HLA B*0702	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.416393	1.991397	-2.424996	26085.114306
HLA B*4001	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.416893	1.991397	-2.425496	26115.189674

HLA B*4601	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.320287	1.894713	-2.425574	20906.775712
HLA A*0216	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.368020	0.942253	-2.425767	2333.563608
HLA B*0801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.843071	1.417212	-2.425860	6967.410745
HLA A*6802	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.176877	1.751011	-2.425866	15027.157736
HLA A*0250	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.487530	2.061629	-2.425902	30727.728087
HLA B*1502	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.454097	2.028058	-2.426040	28450.983218
HLA B*5401	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.507811	2.081726	-2.426085	32196.688480
HLA B*0803	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.454177	2.028058	-2.426119	28456.216866
HLA B*5701	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.417798	1.991397	-2.426401	26169.639267
HLA B*4501	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.561943	2.135178	-2.426766	36470.636263
HLA A*2501	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.465333	2.038259	-2.427073	29196.615918
HLA A*8001	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.387198	1.960098	-2.427100	24389.227430
HLA B*5401	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.555160	2.127896	-2.427265	35905.450229
HLA A*0202	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.369641	0.942253	-2.427388	2342.290668
HLA B*1501	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.294457	1.866969	-2.427488	19699.573424
HLA A*6802	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.443177	2.015621	-2.427556	27744.498124
HLA A*6802	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.344421	0.916314	-2.428107	2210.148302
HLA B*4002	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.018094	1.589799	-2.428295	10425.429353
HLA A*2402	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.456863	2.028437	-2.428425	28632.721121
HLA B*0802	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.419938	1.991397	-2.428541	26298.932296
HLA B*5801	1:479-487	9	AITNVVIII	1.197409	0.357342	-3.983453	1.554751	-2.428702	9626.161481
HLA A*2601	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.323750	1.894713	-2.429037	21074.156508
HLA A*0202	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-3.955067	1.525910	-2.429157	9017.095411
HLA A*0101	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.372124	1.942822	-2.429302	23557.204266
HLA B*5401	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.061973	1.632662	-2.429311	11533.813684
HLA A*2601	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.372173	1.942822	-2.429351	23559.880697
HLA A*2402	1:478-486	9	SAITNVVII	1.257201	0.311030	-3.997602	1.568231	-2.429371	9944.930250
HLA A*0206	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.473922	2.044529	-2.429394	29779.831350
HLA B*4001	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.372406	1.942822	-2.429584	23572.502254
HLA B*3901	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.372873	1.942822	-2.430051	23597.893320
HLA B*3501	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.352184	1.922093	-2.430091	22500.059601
HLA A*3002	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.301047	1.870848	-2.430199	20000.788964
HLA B*4403	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.495300	2.064862	-2.430438	31282.409581
HLA B*5101	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.029376	1.598716	-2.430660	10699.812730
HLA A*1101	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.428060	1.997366	-2.430694	26795.402599
HLA A*2403	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.422508	1.991397	-2.431112	26455.041894
HLA A*6901	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.288329	1.857104	-2.431226	19423.583868
HLA B*5101	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.469254	2.037813	-2.431441	29461.428942
HLA A*8001	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.447225	2.015621	-2.431604	28004.320273
HLA B*1501	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.374779	1.942822	-2.431956	23701.654647
HLA A*3201	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.252082	1.819741	-2.432340	17868.229031
HLA A*3201	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.398196	0.965301	-2.432895	2501.476509
HLA A*0212	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.428993	0.995952	-2.433042	2685.304120
HLA B*4601	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.717961	1.284672	-2.433290	5223.496855
HLA B*0702	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.766149	1.332686	-2.433463	5836.456795
HLA B*4001	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.290613	1.857104	-2.433509	19525.990090
HLA A*0203	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.066183	1.632662	-2.433522	11646.172238
HLA A*1101	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.236340	1.802719	-2.433620	17232.169627
HLA A*0202	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.864236	1.430389	-2.433846	7315.357836
HLA A*3002	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.449871	2.015621	-2.434249	28175.430207
HLA A*0201	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.301235	1.866969	-2.434266	20009.447001
HLA A*0301	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.305128	1.870848	-2.434281	20189.621766
HLA B*4002	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.285585	1.851066	-2.434519	19301.238031
HLA A*0203	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.450507	2.015621	-2.434886	28216.767935
HLA A*0216	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.479819	2.044529	-2.435291	30186.964309
HLA A*3002	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.080445	1.645104	-2.435341	12034.958102
HLA A*2601	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.395456	1.960098	-2.435359	24857.444779
HLA A*3201	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.473805	2.038259	-2.435546	29771.777160
HLA B*4601	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.357912	1.922093	-2.435819	22798.785520
HLA A*0216	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.451464	2.015621	-2.435842	28278.964765
HLA A*0211	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.464045	2.028058	-2.435987	29110.187246
HLA A*0219	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.427846	1.991397	-2.436450	26782.214471
HLA B*4001	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.303603	1.866969	-2.436634	20118.859935
HLA B*1501	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-2.845786	0.409024	-2.436761	701.108956
HLA B*1509	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.307767	1.870848	-2.436919	20312.653235

HLA A*2601	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.308455	1.870848	-2.437607	20344.876302
HLA A*0216	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.460679	1.022974	-2.437705	2888.541643
HLA B*1503	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.266646	1.828833	-2.437813	18477.617304
HLA B*0802	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.397935	1.960098	-2.437837	24999.722615
HLA A*0203	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.380669	1.942822	-2.437847	24025.300296
HLA B*4501	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.023061	1.584939	-2.438122	10545.344231
HLA B*5101	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.502988	2.064862	-2.438125	31841.074352
HLA A*0201	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.289220	1.851066	-2.438154	19463.449830
HLA B*1503	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-3.475137	1.036678	-2.438459	2986.327019
HLA A*2501	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.454565	2.015621	-2.438944	28481.629127
HLA B*7301	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.477216	2.037813	-2.439403	30006.560126
HLA B*5101	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.436805	1.997366	-2.439439	27340.412949
HLA A*0202	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.306409	1.866969	-2.439440	20249.236477
HLA B*5301	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.399714	1.960098	-2.439616	25102.313558
HLA B*5101	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.299464	1.859413	-2.440050	19927.993578
HLA A*0219	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.259814	1.819741	-2.440073	18189.202822
HLA A*6901	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.172129	0.732039	-2.440090	1486.377018
HLA A*1101	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.478633	2.038259	-2.440374	30104.606255
HLA A*6802	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.431932	1.991397	-2.440535	27035.365042
HLA A*0203	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.405940	0.965301	-2.440639	2546.480362
HLA A*2501	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.260967	1.819741	-2.441226	18237.582219
HLA B*4801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.308227	1.866969	-2.441258	20334.202941
HLA A*2603	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.031387	1.589799	-2.441589	10749.477025
HLA B*1501	1:268-276	9	EMRADLVRV	1.216414	0.187070	-3.845374	1.403484	-2.441890	7004.447899
HLA B*3501	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.385201	1.942822	-2.442379	24277.333330
HLA A*0219	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.458197	2.015621	-2.442576	28720.839551
HLA B*1502	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.471319	2.028437	-2.442882	29601.860287
HLA B*4403	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.549883	2.106921	-2.442962	35471.816860
HLA A*0206	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-3.837771	1.394783	-2.442988	6882.892328
HLA A*3201	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.741785	1.298743	-2.443043	5518.043445
HLA A*0201	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.300528	1.857104	-2.443424	19976.890600
HLA A*0211	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.175714	0.732039	-2.443676	1498.698581
HLA B*7301	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.578871	2.135178	-2.443694	37920.266380
HLA B*4801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.303145	1.859413	-2.443732	20097.647170
HLA B*0802	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.317247	1.873374	-2.443873	20760.931072
HLA A*1101	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.435435	1.991397	-2.444039	27254.318075
HLA A*2902	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.472212	2.028058	-2.444154	29662.777138
HLA B*1509	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.094678	1.650328	-2.444350	12435.915511
HLA B*4403	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.572532	2.127896	-2.444637	37370.806369
HLA A*0250	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-3.716039	1.270153	-2.445887	5200.432441
HLA A*0201	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.389512	1.942822	-2.446690	24519.538189
HLA B*1509	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.438527	1.991397	-2.447130	27449.045200
HLA A*2603	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.462762	2.015621	-2.447141	29024.328458
HLA B*1503	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.930435	1.482642	-2.447793	8519.903273
HLA B*3801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.315020	1.866969	-2.448051	20654.729645
HLA B*0801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.391075	1.942822	-2.448253	24607.907961
HLA A*3001	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.077611	1.629324	-2.448287	11956.693697
HLA B*4002	1:175-183	9	AVIGTAQYL	1.498806	0.636372	-4.583570	2.135178	-2.448393	38332.782899
HLA B*0702	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.289610	1.840969	-2.448641	19480.936668
HLA A*0201	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.709748	1.261014	-2.448733	5125.633365
HLA A*0206	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.513624	2.064862	-2.448761	32630.507732
HLA B*3801	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.493343	2.044529	-2.448815	31141.754517
HLA B*0801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.371031	1.922093	-2.448938	23498.018274
HLA A*6802	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.300150	1.851066	-2.449084	19959.498460
HLA B*1501	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.879587	1.430389	-2.449198	7578.567269
HLA B*3501	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-3.703399	1.254080	-2.449319	5051.254258
HLA A*0219	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.409772	1.960098	-2.449674	25690.460877
HLA A*2603	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.344416	1.894713	-2.449703	22101.221194
HLA A*2602	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.478553	2.028437	-2.450116	30099.069437
HLA A*6901	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.279025	1.828833	-2.450193	19011.894888
HLA A*2902	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.301261	1.851066	-2.450195	20010.637775
HLA B*4402	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.410728	1.960098	-2.450630	25747.089093
HLA B*4801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.393525	1.942822	-2.450703	24747.150906
HLA A*1101	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.345617	1.894713	-2.450903	22162.403518
HLA A*0203	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.360219	0.909118	-2.451101	2292.025015

HLA A*3301	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.989971	1.538857	-2.451114	9771.711001
HLA A*2301	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.318325	1.866969	-2.451356	20812.547411
HLA B*5101	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.632783	1.181170	-2.451613	4293.219648
HLA B*5801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.036707	1.585042	-2.451665	10881.946085
HLA B*4801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.374069	1.922093	-2.451976	23662.962819
HLA B*1801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.309299	1.857104	-2.452195	20384.427503
HLA B*0802	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.395339	1.942822	-2.452517	24850.721887
HLA A*0206	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.713671	1.261014	-2.452657	5172.150790
HLA B*5301	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.309956	1.857104	-2.452853	20415.328599
HLA B*1801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.395781	1.942822	-2.452959	24876.009399
HLA A*2301	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.375314	1.922093	-2.453221	23730.907602
HLA B*1801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.375514	1.922093	-2.453421	23741.822546
HLA B*0803	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.273189	1.819741	-2.453448	18758.118876
HLA A*0301	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.318781	1.865170	-2.453611	20834.402030
HLA B*5101	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.498246	2.044529	-2.453718	31495.350959
HLA A*2602	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.469672	2.015621	-2.454051	29489.812791
HLA A*0202	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.871392	1.417212	-2.454181	7436.902814
HLA A*0212	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.414323	1.960098	-2.454225	25961.085523
HLA B*4001	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.295310	1.840969	-2.454340	19738.297255
HLA A*0201	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.139591	1.685171	-2.454419	13790.833594
HLA A*3001	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.263542	1.809098	-2.454445	18346.038407
HLA B*7301	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.582607	2.127896	-2.454711	38247.852920
HLA B*4601	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.397616	1.942822	-2.454793	24981.335961
HLA B*4403	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-3.558290	1.103143	-2.455147	3616.515550
HLA A*3001	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.284032	1.828833	-2.455199	19232.341283
HLA A*2301	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.525806	2.070592	-2.455214	33558.760464
HLA B*0801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.140389	1.685171	-2.455218	13816.223276
HLA B*5801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.264372	1.809098	-2.455274	18381.107144
HLA A*0211	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.636514	1.181170	-2.455344	4330.261168
HLA B*4601	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.314803	1.859413	-2.455390	20644.452142
HLA B*1801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.471237	2.015621	-2.455616	29596.255820
HLA B*0801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.306698	1.851066	-2.455632	20262.715134
HLA A*3101	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.313046	1.857104	-2.455942	20561.081160
HLA A*3002	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.085374	1.629324	-2.456050	12172.332364
HLA A*2402	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.494795	2.038259	-2.456536	31246.045344
HLA A*0219	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.399648	1.942822	-2.456826	25098.511425
HLA B*1801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-2.999611	0.542619	-2.456992	999.104689
HLA B*4001	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.379254	1.922093	-2.457161	23947.183095
HLA A*0201	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.322637	0.865145	-2.457491	2102.020713
HLA A*2602	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.208524	1.751011	-2.457514	16163.090628
HLA B*1502	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.066865	1.609050	-2.457815	11664.457883
HLA A*0206	1:266-274	9	AAEMRADLV	0.998847	0.162308	-3.618982	1.161155	-2.457827	4158.935963
HLA A*0211	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-3.996897	1.538857	-2.458040	9928.803049
HLA A*6901	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.335925	1.877371	-2.458554	21673.309473
HLA B*5401	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.520355	2.061629	-2.458726	33140.198548
HLA B*5801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.325909	1.866969	-2.458940	21179.191526
HLA A*0212	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.368184	0.909118	-2.459066	2334.447478
HLA A*3001	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-3.441606	0.982334	-2.459272	2764.429467
HLA B*1509	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.268509	1.809098	-2.459412	18557.057339
HLA A*3001	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.509247	1.049687	-2.459560	3230.332203
HLA A*2301	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.498357	2.038259	-2.460098	31503.360136
HLA B*5401	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-3.994289	1.534036	-2.460253	9869.359473
HLA A*0203	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.050240	1.589799	-2.460441	11226.376510
HLA A*8001	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.452168	1.991397	-2.460772	28324.897848
HLA B*3501	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.051762	1.590840	-2.460922	11265.800850
HLA B*2705	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.096943	1.635751	-2.461191	12500.939874
HLA A*6801	1:34-42	9	HRDVAVKVL	1.797280	0.410892	-4.669526	2.208172	-2.461355	46722.519966
HLA B*1517	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.477005	2.015621	-2.461384	29991.953788
HLA B*0801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.046856	1.585464	-2.461392	11139.260108
HLA A*2902	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.453623	1.991397	-2.462226	28419.909033
HLA B*1801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.185640	1.723131	-2.462509	15333.469164
HLA A*6801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.840703	1.378166	-2.462537	6929.519688
HLA A*0101	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.357296	1.894713	-2.462583	22766.493618
HLA A*2601	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.384705	1.922093	-2.462612	24249.636890
HLA A*3201	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.478278	2.015621	-2.462657	30080.024047

HLA A*8001	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.340173	1.877371	-2.462802	21886.337963
HLA A*0201	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.384926	1.922093	-2.462833	24261.971684
HLA B*2705	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.303841	1.840969	-2.462871	20129.855860
HLA B*1503	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.405919	1.942822	-2.463097	25463.537648
HLA B*4001	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.333954	1.870848	-2.463106	21575.159468
HLA A*2902	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.292114	1.828833	-2.463282	19593.606665
HLA B*1501	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.031669	1.568231	-2.463439	10756.457708
HLA A*1101	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.491503	2.028058	-2.463446	31010.118812
HLA A*0212	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.841704	1.378166	-2.463538	6945.507964
HLA A*0211	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.766661	1.303070	-2.463591	5843.344115
HLA A*0203	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.946646	1.482642	-2.464004	8843.946582
HLA B*5401	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.335220	1.870848	-2.464373	21638.162941
HLA B*1517	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.227461	1.762988	-2.464473	16883.452378
HLA A*2402	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.529368	2.064862	-2.464505	33835.120731
HLA B*3501	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.457083	1.991397	-2.465687	28647.285410
HLA A*2601	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.285562	1.819741	-2.465821	19300.193883
HLA A*2902	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.425941	1.960098	-2.465843	26664.967040
HLA B*4801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.339252	1.873374	-2.465878	21839.973299
HLA B*2705	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.426143	1.960098	-2.466045	26677.375815
HLA A*0203	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.343702	1.877371	-2.466331	22064.903259
HLA B*4601	1:147-155	9	SATNAVKVM	1.243941	0.165923	-3.876505	1.409864	-2.466641	7524.966754
HLA A*2601	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.340034	1.873374	-2.466660	21879.353321
HLA B*1501	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.411241	0.944464	-2.466777	2577.749845
HLA A*0202	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.531661	2.064862	-2.466798	34014.244397
HLA A*3101	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-3.449260	0.982334	-2.466926	2813.585621
HLA B*4002	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-3.046906	0.579907	-2.466999	1114.053712
HLA A*0211	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.531870	2.064862	-2.467008	34030.625523
HLA B*1503	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.799860	1.332686	-2.467174	6307.535243
HLA B*4403	1:116-124	9	IEVIADACQ	1.170936	0.004468	-3.642637	1.175404	-2.467233	4391.742299
HLA A*0206	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.218430	1.751011	-2.467419	16535.976135
HLA B*0702	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.112736	1.645104	-2.467632	12963.906931
HLA A*6802	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.214572	1.746933	-2.467639	16389.736917
HLA B*1502	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.112853	1.645104	-2.467750	12967.414070
HLA A*0203	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.389923	1.922093	-2.467830	24542.762578
HLA A*2403	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.153138	1.685171	-2.467966	14227.796624
HLA B*2705	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.410820	1.942822	-2.467998	25752.521933
HLA A*0201	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-3.266949	0.798791	-2.468158	1849.053587
HLA B*4001	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.341613	1.873374	-2.468239	21959.039277
HLA B*0803	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.459832	1.991397	-2.468436	28829.185484
HLA A*0216	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.411414	1.942822	-2.468592	25787.793593
HLA B*4002	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.596866	2.127896	-2.468970	39524.472740
HLA A*0202	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.909383	1.440103	-2.469280	8116.770726
HLA A*2601	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.900169	1.430389	-2.469779	7946.366626
HLA A*2301	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.263103	1.793234	-2.469869	18327.488036
HLA A*6802	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.799686	1.329751	-2.469935	6305.010641
HLA B*5801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.347579	1.877371	-2.470208	22262.743260
HLA B*5701	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.413038	1.942822	-2.470216	25884.374793
HLA B*7301	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.515454	2.044529	-2.470926	32768.312772
HLA A*0203	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.312153	1.840969	-2.471184	20518.855973
HLA A*2301	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.516319	2.044529	-2.471790	32833.614195
HLA A*3001	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.281290	1.809179	-2.472111	19111.303440
HLA B*3801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.345579	1.873374	-2.472205	22160.485263
HLA A*3101	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.345746	1.873374	-2.472372	22168.998787
HLA A*0101	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.301294	1.828833	-2.472461	20012.153407
HLA A*3301	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.515947	2.043325	-2.472623	32805.561244
HLA A*0101	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.224872	1.752221	-2.472651	16783.097776
HLA A*0216	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.464198	1.991397	-2.472801	29120.425434
HLA A*0201	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.102126	1.629324	-2.472801	12651.022562
HLA B*7301	1:334-342	9	AVVAVLAVL	1.513669	0.593252	-4.580119	2.106921	-2.473198	38029.354687
HLA B*1517	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.464924	1.991397	-2.473527	29169.145470
HLA B*1503	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.109381	1.635751	-2.473630	12864.142432
HLA B*4801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.058698	1.585042	-2.473656	11447.159904
HLA A*2403	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.236749	1.762988	-2.473761	17248.398262
HLA A*3201	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.538782	2.064862	-2.473920	34576.586550
HLA A*0212	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.417067	1.942822	-2.474245	26125.646508

HLA B*0801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.807458	1.332686	-2.474772	6418.860248
HLA B*3801	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.490505	2.015621	-2.474884	30938.902159
HLA A*0301	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-3.458996	0.984065	-2.474931	2877.374574
HLA B*0801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.277978	1.802719	-2.475258	18966.078084
HLA A*0219	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.342398	1.866969	-2.475429	21998.752999
HLA A*6802	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.397526	1.922093	-2.475433	24976.200931
HLA B*3501	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.906113	1.430389	-2.475723	8055.876423
HLA A*1101	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.436004	1.960098	-2.475906	27290.022609
HLA A*2301	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.504221	2.028058	-2.476163	31931.637658
HLA B*4403	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.546773	2.070592	-2.476181	35218.650875
HLA A*6901	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.223336	1.746933	-2.476403	16723.822964
HLA B*0803	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.436563	1.960098	-2.476465	27325.182606
HLA A*0301	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.229428	1.752221	-2.477207	16960.075301
HLA A*8001	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.399321	1.922093	-2.477228	25079.645076
HLA A*6802	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.810000	1.332686	-2.477314	6456.543227
HLA B*5301	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.515804	2.038259	-2.477545	32794.737089
HLA B*4601	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.351101	1.873374	-2.477726	22444.015293
HLA A*0219	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.334854	1.857104	-2.477750	21619.909275
HLA A*0201	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.960541	1.482642	-2.477899	9131.475644
HLA A*2601	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.318948	1.840969	-2.477979	20842.406106
HLA A*0201	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.063561	1.585464	-2.478097	11576.071044
HLA B*5401	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.543100	2.064862	-2.478238	34922.109545
HLA A*3001	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.933512	1.454961	-2.478552	8580.497905
HLA B*4001	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-2.958293	0.479739	-2.478554	908.433108
HLA A*3101	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.184978	1.706161	-2.478817	15310.094431
HLA A*3001	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.225911	1.746933	-2.478978	16823.277051
HLA A*0211	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.494633	2.015621	-2.479012	31234.383924
HLA A*0216	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.494079	1.014988	-2.479091	3119.456341
HLA A*8001	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.352489	1.873374	-2.479115	22515.889135
HLA B*0802	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.401234	1.922093	-2.479141	25190.330581
HLA A*0206	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.129718	1.650328	-2.479390	13480.871907
HLA A*3001	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.209187	1.729555	-2.479632	16187.767676
HLA A*0101	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.353241	1.873374	-2.479867	22554.901602
HLA B*2705	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.353391	1.873374	-2.480017	22562.712203
HLA B*7301	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.541968	2.061629	-2.480339	34831.166442
HLA A*6901	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.290348	1.809098	-2.481250	19514.057159
HLA A*0250	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.338594	1.857104	-2.481490	21806.915829
HLA B*0801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.303899	1.822112	-2.481787	20132.578551
HLA A*1101	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.347001	1.865170	-2.481831	22233.134978
HLA B*4402	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.403966	1.922093	-2.481873	25349.320244
HLA A*0202	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.543556	2.061629	-2.481927	34958.780185
HLA B*0801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.311089	1.828833	-2.482256	20468.632394
HLA B*5301	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.133082	1.650328	-2.482755	13585.713276
HLA B*5401	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.553408	2.070592	-2.482816	35760.835840
HLA A*0211	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.913302	1.430389	-2.482913	8190.345448
HLA A*0250	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.521426	2.038259	-2.483167	33222.053340
HLA B*4601	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-3.915149	1.431809	-2.483339	8225.246363
HLA B*5101	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.499285	2.015621	-2.483664	31570.751841
HLA B*4402	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.354545	1.870848	-2.483697	22622.724201
HLA A*1101	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.354709	1.870848	-2.483862	22631.292874
HLA A*8001	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.312992	1.828833	-2.484159	20558.522956
HLA B*3901	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.128449	1.644220	-2.484229	13441.547164
HLA A*8001	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.247361	1.762988	-2.484373	17675.080285
HLA B*0702	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.444598	1.960098	-2.484501	27835.454160
HLA A*0202	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.555489	2.070592	-2.484897	35932.654760
HLA A*6901	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.939912	1.454961	-2.484952	8707.881026
HLA A*3002	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.135310	1.650328	-2.484982	13655.567598
HLA B*4403	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.486595	2.001388	-2.485207	30661.638289
HLA B*0702	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.428236	1.942822	-2.485414	26806.276817
HLA B*1503	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-3.752052	1.266360	-2.485692	5650.050960
HLA A*2902	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.326668	1.840969	-2.485699	21216.232275
HLA A*2402	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.232670	1.746933	-2.485738	17087.167057
HLA A*2403	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.428591	1.942822	-2.485769	26828.183630
HLA A*0216	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.286353	1.799748	-2.486605	19335.412791
HLA B*0702	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.343864	1.857104	-2.486760	22073.141235

HLA B*5801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.346225	1.859413	-2.486812	22193.478385
HLA B*5801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.343932	1.857104	-2.486829	22076.604491
HLA A*2902	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.771511	1.284672	-2.486839	5908.956594
HLA A*2402	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.357710	1.870848	-2.486862	22788.180842
HLA B*1509	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.306684	1.819741	-2.486942	20262.057430
HLA B*1501	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.012906	1.525910	-2.486996	10301.638050
HLA A*0250	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.557785	2.070592	-2.487193	36123.078225
HLA B*0802	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.210413	1.723131	-2.487282	16233.545926
HLA A*2402	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.531858	2.044529	-2.487330	34029.705026
HLA A*0301	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.328304	1.840969	-2.487334	21296.267975
HLA A*0203	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.584962	1.097502	-2.487459	3845.578584
HLA B*1503	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.217659	1.729555	-2.488105	16506.659995
HLA B*7301	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.569953	2.081726	-2.488226	37149.479599
HLA B*3901	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.359133	1.870848	-2.488286	22863.012046
HLA A*6802	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.073758	1.584939	-2.488819	11851.080506
HLA B*4001	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-3.286549	0.797462	-2.489087	1934.411661
HLA A*1101	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-3.473225	0.984065	-2.489160	2973.205194
HLA B*0802	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.356248	1.866969	-2.489279	22711.628598
HLA A*0201	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.366673	1.877371	-2.489302	23263.386842
HLA A*0301	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.366760	1.877371	-2.489389	23268.043845
HLA A*0216	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-3.612253	1.122659	-2.489594	4094.994364
HLA A*2301	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.362994	1.873374	-2.489620	23067.134559
HLA B*1801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.150835	1.661000	-2.489835	14152.564842
HLA A*2501	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.481236	1.991397	-2.489839	30285.599907
HLA B*5801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.355379	1.865170	-2.490209	22666.213131
HLA A*0202	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.752879	1.262230	-2.490649	5660.820496
HLA B*4601	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.310685	1.819741	-2.490944	20449.595171
HLA B*4601	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.332276	1.840969	-2.491307	21491.982690
HLA B*3801	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.386188	1.894713	-2.491474	24332.557872
HLA B*1517	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.369340	1.877371	-2.491969	23406.668694
HLA B*4001	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.357252	1.865170	-2.492081	22764.153619
HLA B*0802	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.343157	1.851066	-2.492091	22037.227097
HLA A*3001	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.255138	1.762988	-2.492150	17994.433987
HLA B*0803	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.386888	1.894713	-2.492174	24371.817169
HLA B*0702	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.414372	1.922093	-2.492279	25964.035069
HLA B*4402	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.435200	1.942822	-2.492378	27239.577778
HLA A*0201	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.301515	1.809098	-2.492417	20022.332767
HLA B*3801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.483872	1.991397	-2.492475	30469.989383
HLA B*5801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.077719	1.584939	-2.492780	11959.669549
HLA A*0211	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.537403	2.044529	-2.492874	34466.959131
HLA B*1503	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.111749	1.618772	-2.492977	12934.484384
HLA A*0206	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.308282	0.815296	-2.492986	2033.675411
HLA B*0803	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.436345	1.942822	-2.493522	27311.438227
HLA A*2501	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.353730	0.860149	-2.493581	2258.031913
HLA A*8001	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.436467	1.942822	-2.493645	27319.122404
HLA A*0219	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.344790	1.851066	-2.493724	22120.240233
HLA B*4801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.080618	1.586804	-2.493814	12039.777043
HLA A*6901	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.334797	1.840969	-2.493828	21617.102385
HLA A*3101	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.360997	1.866969	-2.494028	22961.306022
HLA B*3901	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.303281	1.809098	-2.494184	20103.954270
HLA B*1509	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.361154	1.866969	-2.494185	22969.630144
HLA A*0101	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.365169	1.870848	-2.494322	23182.980619
HLA A*2402	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.103451	1.609050	-2.494401	12689.682026
HLA A*3301	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.495944	2.001388	-2.494556	31328.814183
HLA A*3301	1:521-529	9	SQASVDSPR	0.518283	0.661153	-3.674031	1.179436	-2.494594	4720.963764
HLA B*4601	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.372077	1.877371	-2.494706	23554.655566
HLA B*1502	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.539722	2.044529	-2.495193	34651.489765
HLA A*3201	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.540197	2.044529	-2.495668	34689.377528
HLA B*0803	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.352907	1.857104	-2.495804	22537.581484
HLA B*5401	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.539221	2.043325	-2.495897	34611.583628
HLA A*2602	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.540626	2.044529	-2.496098	34723.737354
HLA A*0212	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.373566	1.877371	-2.496195	23635.583673
HLA B*0802	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.353408	1.857104	-2.496304	22563.566652
HLA B*4501	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.487718	1.991397	-2.496322	30741.029653
HLA A*0212	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.418533	1.922093	-2.496440	26213.989733

HLA A*0219	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.181792	1.685171	-2.496621	15198.193436
HLA A*0250	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-3.326547	0.829510	-2.497037	2121.028647
HLA A*0206	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.512764	2.015621	-2.497143	32565.962615
HLA A*2501	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.419555	1.922093	-2.497462	26275.751805
HLA A*6801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.106646	1.609050	-2.497596	12783.390020
HLA A*2603	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.796392	1.298743	-2.497649	6257.370147
HLA B*5701	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.371029	1.873374	-2.497655	23497.891153
HLA B*5801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.678875	1.181170	-2.497705	4773.921848
HLA B*1509	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.371217	1.873374	-2.497843	23508.063033
HLA A*6901	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.221000	1.723131	-2.497869	16634.133147
HLA B*5801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-3.980624	1.482642	-2.497983	9563.665172
HLA B*4402	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.365397	1.866969	-2.498428	23195.149295
HLA A*3001	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.291851	1.793234	-2.498617	19581.738346
HLA A*3002	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.563708	2.064862	-2.498845	36619.111550
HLA B*1501	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.689199	1.190001	-2.499197	4888.762531
HLA B*3501	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.939335	1.440103	-2.499231	8696.300001
HLA A*6802	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.356396	1.857104	-2.499293	22719.370563
HLA B*5401	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.459480	1.960098	-2.499382	28805.800569
HLA B*5101	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.373188	1.873374	-2.499814	23615.006228
HLA A*0301	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.367051	1.866969	-2.500082	23283.657896
HLA A*0211	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.492098	1.991397	-2.500701	31052.591481
HLA A*0212	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.309938	1.809098	-2.500840	20414.445061
HLA B*0801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-3.586677	1.085412	-2.501265	3860.795644
HLA B*4403	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.539736	2.038259	-2.501477	34652.614547
HLA B*5101	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.396218	1.894713	-2.501504	24901.053217
HLA A*6901	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.310844	1.809179	-2.501666	20457.119397
HLA B*4403	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.563480	2.061629	-2.501851	36599.900374
HLA B*4801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.758922	1.257069	-2.501853	5740.137017
HLA A*0202	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.379581	1.877371	-2.502210	23965.197540
HLA A*1101	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.119216	1.616917	-2.502298	13158.784790
HLA A*0250	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.322073	1.819741	-2.502332	20992.911201
HLA B*1502	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.188187	1.685171	-2.503016	15423.653708
HLA B*4002	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.585076	2.081726	-2.503350	38465.941729
HLA A*0201	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.362853	1.859413	-2.503439	23059.648335
HLA A*0212	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.323224	1.819741	-2.503483	21048.633993
HLA A*3101	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.122303	1.618772	-2.503531	13252.658513
HLA B*4601	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.693743	1.190001	-2.503741	4940.180831
HLA A*3101	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.354947	1.851066	-2.503881	22643.661964
HLA A*0203	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.348176	0.844164	-2.504012	2229.337868
HLA A*8001	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.361687	1.857104	-2.504584	22997.855207
HLA A*0250	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.072875	1.568231	-2.504644	11826.998507
HLA A*0301	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.298164	1.793234	-2.504930	19868.464713
HLA B*1801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.066869	1.561867	-2.505003	11664.584091
HLA B*4002	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.543319	2.038259	-2.505060	34939.683967
HLA A*0301	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.364584	1.859413	-2.505171	23151.772721
HLA B*0702	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.364589	1.859413	-2.505176	23152.023220
HLA B*4402	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.400071	1.894713	-2.505357	25122.963758
HLA A*2501	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.448327	1.942822	-2.505505	28075.464115
HLA A*3301	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.543822	2.038259	-2.505563	34980.157632
HLA B*5401	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.365017	1.859413	-2.505603	23174.829924
HLA A*3201	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.031636	1.525910	-2.505726	10755.643062
HLA B*5301	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.543563	2.037813	-2.505750	34959.347559
HLA A*3001	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.700791	1.194908	-2.505883	5021.012484
HLA A*2403	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.427999	1.922093	-2.505906	26791.633900
HLA A*2601	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.383573	1.877371	-2.506202	24186.486717
HLA B*1502	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.400964	1.894713	-2.506250	25174.663612
HLA A*0101	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.373409	1.866969	-2.506440	23627.018211
HLA A*0212	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-3.994148	1.487180	-2.506968	9866.156465
HLA A*2601	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.373980	1.866969	-2.507011	23658.098787
HLA B*3901	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.116157	1.609050	-2.507107	13066.424239
HLA B*5401	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.545544	2.037813	-2.507731	35119.145046
HLA A*6901	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.373035	1.865170	-2.507865	23606.703641
HLA A*0301	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.365085	1.857104	-2.507981	23178.466034
HLA B*3501	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.349249	1.840969	-2.508280	22348.540270
HLA A*0301	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.359657	1.851066	-2.508592	22890.610749

HLA B*5401	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.546979	2.038259	-2.508720	35235.421418
HLA A*0203	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.366816	1.857104	-2.509712	23271.065102
HLA B*0801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.418839	0.909118	-2.509721	2623.245907
HLA A*6801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.108676	1.598716	-2.509960	12843.281290
HLA B*2705	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-3.520896	1.010656	-2.510240	3318.149379
HLA A*3101	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.369718	1.859413	-2.510305	23427.064599
HLA A*1101	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.351338	1.840969	-2.510369	22456.282027
HLA B*1501	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-2.883918	0.373369	-2.510548	765.451462
HLA B*4501	1:436-444	9	TYAEAVKKL	1.577697	0.550199	-4.638511	2.127896	-2.510615	43502.148520
HLA A*2603	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.381477	1.870848	-2.510629	24070.053055
HLA A*2601	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.370171	1.859413	-2.510758	23451.537773
HLA B*1501	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.310560	1.799748	-2.510812	20443.732619
HLA A*2403	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.129878	1.618772	-2.511106	13485.832061
HLA B*4801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.330876	1.819741	-2.511135	21422.797817
HLA B*1509	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.433344	1.922093	-2.511251	27123.409350
HLA B*2705	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.205869	1.694587	-2.511283	16064.584231
HLA A*6802	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.320430	1.809098	-2.511333	20913.676154
HLA B*4601	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.540199	1.028753	-2.511446	3468.960081
HLA A*0101	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.370890	1.859413	-2.511477	23490.392212
HLA A*3002	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.556044	2.044529	-2.511515	35978.560495
HLA B*1501	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.368686	1.857104	-2.511583	23371.492711
HLA A*0216	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.889925	1.378166	-2.511759	7761.127960
HLA A*0203	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-2.608812	0.096922	-2.511890	406.267198
HLA B*7301	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.576794	2.064862	-2.511932	37739.351640
HLA A*2403	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.379647	1.866969	-2.512678	23968.827989
HLA B*4402	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.230805	1.718039	-2.512765	17013.927363
HLA B*2705	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.204803	1.691666	-2.513137	16025.176586
HLA B*4801	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.354723	1.840969	-2.513754	22632.027482
HLA A*2301	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.954193	1.440103	-2.514089	8998.966945
HLA B*5101	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.505586	1.991397	-2.514189	32032.161342
HLA B*0802	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.391789	1.877371	-2.514418	24648.411579
HLA A*3201	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.847498	1.332686	-2.514812	7038.787331
HLA B*5801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.954973	1.440103	-2.514869	9015.144362
HLA A*0202	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-3.298832	0.783751	-2.515081	1989.903469
HLA A*2402	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.200588	1.685171	-2.515417	15870.399080
HLA A*8001	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.356399	1.840969	-2.515429	22719.493473
HLA B*3901	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.100660	1.584939	-2.515721	12608.387613
HLA B*1509	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.380920	1.865170	-2.515750	24039.211563
HLA A*2403	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.207430	1.691666	-2.515764	16122.394661
HLA B*4001	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-3.620223	1.104337	-2.515886	4170.832620
HLA B*0803	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.393556	1.877371	-2.516185	24748.891399
HLA B*5401	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.560938	2.044529	-2.516409	36386.288653
HLA A*0211	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.375909	1.859413	-2.516495	23763.410380
HLA A*0216	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.394035	1.877371	-2.516664	24776.219783
HLA B*4501	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.578401	2.061629	-2.516773	37879.259681
HLA A*0101	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.374034	1.857104	-2.516930	23661.042687
HLA B*3801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.326121	1.809179	-2.516942	21189.505974
HLA B*1801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.387816	1.870848	-2.516968	24423.953141
HLA A*0101	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-3.672113	1.154939	-2.517174	4700.169146
HLA B*1503	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.046885	1.529572	-2.517312	11139.983277
HLA A*2403	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.346202	1.828833	-2.517369	22192.277775
HLA A*0206	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.508831	1.991397	-2.517434	32272.371637
HLA A*0206	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-3.957670	1.440103	-2.517566	9071.307614
HLA B*3501	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.395052	1.877371	-2.517681	24834.325661
HLA A*0101	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.395189	1.877371	-2.517818	24842.119239
HLA B*1801	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.509294	1.991397	-2.517897	32306.784192
HLA A*6802	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.395774	1.877371	-2.518403	24875.605673
HLA B*4601	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.163645	1.645104	-2.518541	14576.207617
HLA A*0212	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.775773	1.257069	-2.518704	5967.229835
HLA A*0219	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.440816	1.922093	-2.518723	27594.062317
HLA A*2501	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.413491	1.894713	-2.518778	25911.415006
HLA B*0801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.167235	1.648439	-2.518796	14697.198461
HLA A*3301	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.510405	1.991397	-2.519008	32389.559158
HLA B*1502	1:521-529	9	SQASVDSPR	0.518283	0.661153	-3.698790	1.179436	-2.519353	4997.922759
HLA A*6801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.136297	1.616917	-2.519379	13686.630419

HLA A*0203	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.328738	1.809179	-2.519559	21317.592577
HLA B*2705	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.045616	1.525910	-2.519706	11107.487086
HLA B*1503	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.058858	1.538857	-2.520001	11451.371774
HLA A*3101	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.339922	1.819741	-2.520181	21873.672544
HLA B*2705	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.283231	1.762988	-2.520243	19196.894700
HLA A*2501	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.391115	1.870848	-2.520267	24610.171208
HLA B*5301	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.563828	2.043325	-2.520503	36629.216316
HLA B*1509	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.415234	1.894713	-2.520521	26015.636034
HLA A*3101	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.397923	1.877371	-2.520553	24999.046396
HLA A*0206	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.105983	1.585042	-2.520942	12763.902693
HLA A*3002	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.559218	2.038259	-2.520959	36242.482463
HLA A*2402	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.394648	1.873374	-2.521274	24811.228046
HLA A*0212	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.372439	1.851066	-2.521373	23574.287667
HLA A*1101	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.372516	1.851066	-2.521450	23578.496674
HLA B*4801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.284772	1.762988	-2.521784	19265.143348
HLA A*0203	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.330916	1.809098	-2.521819	21424.768122
HLA A*8001	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.392703	1.870848	-2.521855	24700.337470
HLA B*1501	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.820671	1.298743	-2.521929	6617.156771
HLA A*2501	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.482063	1.960098	-2.521965	30343.327146
HLA A*0212	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.381731	1.859413	-2.522317	24084.120526
HLA A*2902	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-3.792802	1.270418	-2.522384	6205.857983
HLA A*2902	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.285559	1.762988	-2.522571	19300.089472
HLA A*3301	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.387809	1.865170	-2.522639	24423.556752
HLA A*6901	1:456-464	9	NSPSTPELV	0.868149	0.229670	-3.620566	1.097819	-2.522747	4174.128227
HLA A*3001	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-3.677780	1.154698	-2.523083	4761.901909
HLA A*3002	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.342894	1.819741	-2.523153	22023.878618
HLA B*4002	1:208-216	9	EVLTGEPPF	1.005134	1.056495	-4.584954	2.061629	-2.523325	38455.122234
HLA B*4601	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.380666	1.857104	-2.523563	24025.170323
HLA B*3901	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.902189	1.378166	-2.524023	7983.423270
HLA B*0802	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.389345	1.865170	-2.524175	24510.121991
HLA B*3901	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.058317	1.534036	-2.524281	11437.131985
HLA B*7301	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.595005	2.070592	-2.524413	39355.487190
HLA B*5701	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.401932	1.877371	-2.524561	25230.837352
HLA A*0203	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.346768	1.822112	-2.524656	22221.230566
HLA A*0101	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.365938	1.840969	-2.524968	23224.028391
HLA A*0250	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.553471	2.028058	-2.525413	35766.059699
HLA A*0202	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.441732	0.916314	-2.525418	2765.237169
HLA A*0211	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-3.638455	1.112976	-2.525479	4349.654535
HLA A*2301	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.124277	1.598716	-2.525560	13313.019706
HLA A*6901	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-3.395570	0.869990	-2.525580	2486.392600
HLA B*5701	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.385138	1.859413	-2.525724	24273.787472
HLA A*2603	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.590645	2.064862	-2.525782	38962.305638
HLA A*0250	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.485956	1.960098	-2.525859	30616.553178
HLA A*0216	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.094236	1.568231	-2.526005	12423.273879
HLA B*7301	1:578-586	9	LRALGWTGM	0.993924	0.288236	-3.808276	1.282160	-2.526116	6430.956042
HLA B*0702	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.554992	1.028753	-2.526239	3589.150420
HLA A*1101	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.383754	1.857104	-2.526650	24196.563974
HLA B*1503	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.943986	1.417212	-2.526775	8789.951803
HLA B*5301	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.591693	2.064862	-2.526830	39056.427804
HLA B*4501	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.591695	2.064862	-2.526832	39056.639095
HLA A*0202	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.469714	1.942822	-2.526892	29492.684590
HLA B*5701	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.329737	1.802719	-2.527017	21366.662437
HLA A*2402	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.449123	1.922093	-2.527030	28127.000423
HLA A*0201	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.717045	1.190001	-2.527044	5212.487643
HLA B*2705	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.397945	1.870848	-2.527097	25000.263604
HLA B*2705	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.066038	1.538857	-2.527181	11642.266614
HLA A*2301	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.336550	1.809098	-2.527453	21704.520478
HLA B*0803	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.188587	1.661000	-2.527587	15437.845077
HLA A*3001	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.146432	1.618772	-2.527660	14009.809128
HLA A*2902	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.392839	1.865170	-2.527669	24708.088999
HLA A*0201	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-3.367677	0.839877	-2.527800	2331.721185
HLA A*0202	1:421-429	9	STGPEQREI	1.260733	0.194228	-3.983068	1.454961	-2.528107	9617.624728
HLA A*0216	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.450343	1.922093	-2.528250	28206.084487
HLA A*3301	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.105875	1.577554	-2.528321	12760.726728
HLA B*4002	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-3.654911	1.126330	-2.528581	4517.628953

HLA B*2705	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.406013	1.877371	-2.528642	25469.048441
HLA A*2501	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.127495	1.598716	-2.528779	13412.056347
HLA A*0250	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.593915	2.064862	-2.529053	39256.821383
HLA A*2902	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.396053	1.866969	-2.529084	24891.625167
HLA A*2301	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.276199	1.746933	-2.529266	18888.565395
HLA A*3301	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.329241	1.799748	-2.529493	21342.286593
HLA A*2501	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.358344	1.828833	-2.529511	22821.491177
HLA B*0801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.162296	1.632662	-2.529634	14531.014668
HLA B*4801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.351803	1.822112	-2.529691	22480.349141
HLA A*0211	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.349468	1.819741	-2.529727	22359.787089
HLA A*3001	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.281965	1.752221	-2.529744	19140.999428
HLA B*5801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.349496	1.819741	-2.529755	22361.238704
HLA B*2705	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.832861	1.303070	-2.529790	6805.508051
HLA A*2602	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.595116	2.064862	-2.530253	39365.495177
HLA B*5401	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.558710	2.028437	-2.530273	36200.156550
HLA A*3301	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.253458	1.723131	-2.530327	17924.964686
HLA B*2705	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.333383	1.802719	-2.530664	21546.815332
HLA A*2601	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.396063	1.865170	-2.530893	24892.163816
HLA B*4402	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.404272	1.873374	-2.530898	25367.154326
HLA B*1517	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.473802	1.942822	-2.530980	29771.616099
HLA A*2902	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.333876	1.802719	-2.531157	21571.308078
HLA B*0802	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.360099	1.828833	-2.531266	22913.903697
HLA B*1501	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.018475	1.487180	-2.531295	10434.570226
HLA A*2602	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.474218	1.942822	-2.531396	29800.137574
HLA A*0101	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.396746	1.865170	-2.531576	24931.381858
HLA A*3101	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.130357	1.598716	-2.531641	13500.723476
HLA A*0301	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-3.492998	0.960920	-2.532078	3111.703072
HLA A*2301	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.962585	1.430389	-2.532196	9174.555179
HLA B*2705	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.331987	1.799748	-2.532239	21477.686330
HLA A*3001	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-3.982391	1.449604	-2.532787	9602.651674
HLA A*2601	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.383906	1.851066	-2.532841	24205.074018
HLA B*4601	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.398147	1.865170	-2.532977	25011.897694
HLA A*2603	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.326255	1.793234	-2.533020	21196.041056
HLA A*3001	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.059139	1.525910	-2.533229	11458.808266
HLA B*5801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.355501	1.822112	-2.533389	22672.590356
HLA B*5101	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.166055	1.632662	-2.533393	14657.338483
HLA A*2402	1:127-135	9	NFSHQNGII	1.000888	0.339659	-3.874080	1.340547	-2.533533	7483.071881
HLA A*0101	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.342748	1.809098	-2.533651	22016.492759
HLA B*4601	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.342877	1.809098	-2.533780	22023.044607
HLA A*2403	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.393222	1.859413	-2.533809	24729.886496
HLA A*0201	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.399058	1.865170	-2.533888	25064.453732
HLA B*0803	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.400982	1.866969	-2.534014	25175.753172
HLA A*2403	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.411417	1.877371	-2.534046	25787.933103
HLA A*0202	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.578716	2.044529	-2.534188	37906.729264
HLA B*7301	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.531569	1.997366	-2.534203	34007.068635
HLA A*0301	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.363036	1.828833	-2.534203	23069.380900
HLA A*8001	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.385572	1.851066	-2.534506	24298.093555
HLA B*4402	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.356948	1.822112	-2.534836	22748.272611
HLA A*3201	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.408722	1.873374	-2.535348	25628.410735
HLA A*0212	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.865180	1.329751	-2.535429	7331.284409
HLA B*5401	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.536900	2.001388	-2.535512	34427.079260
HLA A*2902	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.412939	1.877371	-2.535568	25878.494134
HLA A*2402	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.227428	1.691666	-2.535762	16882.173700
HLA A*6901	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.338853	1.802719	-2.536133	21819.896721
HLA B*1501	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.401309	1.865170	-2.536139	25194.691819
HLA A*6801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.165599	1.629324	-2.536275	14641.963405
HLA A*8001	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.403252	1.866969	-2.536283	25307.664855
HLA B*0803	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.458552	1.922093	-2.536459	28744.310997
HLA A*0203	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.062377	1.525910	-2.536467	11544.550903
HLA B*3801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.496578	1.960098	-2.536481	31374.608681
HLA B*5801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.299717	1.762988	-2.536729	19939.640269
HLA B*3901	1:578-586	9	LRALGWTGM	0.993924	0.288236	-3.819078	1.282160	-2.536919	6592.930128
HLA B*4001	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.346301	1.809098	-2.537203	22197.320774
HLA A*3001	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.288482	1.751118	-2.537364	19430.415232
HLA B*5301	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.346474	1.809098	-2.537377	22206.208846

HLA A*0101	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.388662	1.851066	-2.537596	24471.566608
HLA A*6901	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.092483	1.554751	-2.537732	12373.237348
HLA B*2705	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.389120	1.851066	-2.538054	24497.395980
HLA A*0219	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.867835	1.329751	-2.538084	7376.239099
HLA A*2403	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.285179	1.746933	-2.538246	19283.182244
HLA B*5701	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.405273	1.866969	-2.538304	25425.683211
HLA A*2501	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.405317	1.866969	-2.538348	25428.296798
HLA A*0202	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.566661	2.028058	-2.538603	36868.978569
HLA B*0702	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.341435	1.802719	-2.538715	21950.012639
HLA B*1517	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.671977	1.133041	-2.538937	4698.694588
HLA B*3901	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.765440	1.226371	-2.539069	5826.929056
HLA B*5101	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.358931	1.819741	-2.539190	22852.377493
HLA A*3301	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-3.902424	1.363134	-2.539290	7987.743382
HLA A*6801	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.568003	2.028437	-2.539566	36983.044652
HLA B*1801	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.434416	1.894713	-2.539702	27190.402945
HLA A*6901	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.129732	1.589799	-2.539933	13481.309495
HLA A*3001	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.185232	1.645104	-2.540128	15319.042243
HLA A*3201	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.340039	1.799748	-2.540291	21879.590052
HLA A*0203	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.957689	1.417212	-2.540477	9071.700220
HLA B*1801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.362608	1.822112	-2.540496	23046.677970
HLA A*2601	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.397611	1.857104	-2.540507	24981.065670
HLA A*2602	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.411574	1.870848	-2.540726	25797.281957
HLA B*4001	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.369939	1.828833	-2.541106	23438.980984
HLA A*0216	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.400632	1.859413	-2.541219	25155.467842
HLA A*0101	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.919533	1.378166	-2.541367	8308.699532
HLA A*3301	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.569932	2.028437	-2.541494	37147.670872
HLA B*0702	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.419095	1.877371	-2.541724	26247.905386
HLA B*2705	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.294029	1.752221	-2.541808	19680.186773
HLA B*0801	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.382917	1.840969	-2.541948	24150.008161
HLA B*5401	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.557597	2.015621	-2.541976	36107.447860
HLA B*1501	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.462126	0.920120	-2.542006	2898.183741
HLA B*5101	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.464174	1.922093	-2.542081	29118.850094
HLA B*4002	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.612758	2.070592	-2.542166	40997.559201
HLA A*3001	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-3.750502	1.208137	-2.542364	5629.913274
HLA A*2501	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.972810	1.430389	-2.542421	9393.122274
HLA A*3101	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-3.767592	1.224706	-2.542886	5855.875824
HLA A*3001	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-3.051412	0.508438	-2.542975	1125.673500
HLA B*5701	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.400148	1.857104	-2.543045	25127.449269
HLA B*5701	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.394336	1.851066	-2.543270	24793.382410
HLA A*0201	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.363172	1.819741	-2.543431	23076.620598
HLA A*3001	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.235191	1.691666	-2.543525	17186.643274
HLA A*6802	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.508867	0.965301	-2.543566	3227.502373
HLA B*1517	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.403175	1.859413	-2.543761	25303.147173
HLA A*0301	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.364002	1.819741	-2.544260	23120.731915
HLA A*1101	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.411353	1.866969	-2.544384	25784.166611
HLA A*8001	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.404025	1.859413	-2.544612	25352.748901
HLA A*3201	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.572699	2.028058	-2.544642	37385.163332
HLA A*0250	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.589254	2.044529	-2.544725	38837.722444
HLA B*4403	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.626871	2.081726	-2.545145	42351.749778
HLA A*3001	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.268298	1.723131	-2.545167	18548.024292
HLA B*5701	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.174607	1.629324	-2.545283	14948.831360
HLA A*0203	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.268638	1.723131	-2.545507	18562.579700
HLA A*0201	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.386545	1.840969	-2.545576	24352.574840
HLA B*5801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.348309	1.802719	-2.545590	22300.231308
HLA A*6802	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-2.967832	0.421976	-2.545856	928.606807
HLA A*2403	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.131085	1.585042	-2.546043	13523.384071
HLA B*1502	1:35-43	9	RDVAVKVLR	1.424674	0.640188	-4.610968	2.064862	-2.546105	40828.901377
HLA B*4002	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.403226	1.857104	-2.546122	25306.158871
HLA B*5101	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.488959	1.942822	-2.546137	30828.964520
HLA B*1501	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.796180	1.249564	-2.546617	6254.324238
HLA A*2501	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.845458	1.298743	-2.546716	7005.812190
HLA B*5301	1:265-273	9	TAAEMRADL	1.001324	0.415888	-3.964004	1.417212	-2.546793	9204.582740
HLA A*2301	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.538284	1.991397	-2.546887	34536.953516
HLA B*4801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.412258	1.865170	-2.547088	25837.926028
HLA B*5801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.356267	1.809179	-2.547088	22712.611559

HLA B*4001	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.369347	1.822112	-2.547234	23407.048579
HLA B*0802	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.349975	1.802719	-2.547256	22385.930579
HLA A*3101	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.356486	1.809098	-2.547388	22724.041596
HLA A*2601	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.376379	1.828833	-2.547546	23789.135778
HLA B*1509	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.376771	1.828833	-2.547938	23810.637819
HLA B*4402	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.209286	1.661000	-2.548286	16191.446203
HLA A*8001	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.413634	1.865170	-2.548464	25919.967268
HLA B*1502	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.370641	1.822112	-2.548529	23476.925549
HLA A*2602	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.421940	1.873374	-2.548566	26420.429796
HLA A*3001	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.691990	1.143250	-2.548740	4920.283539
HLA A*6802	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-2.823996	0.275124	-2.548873	666.801228
HLA A*0206	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.371139	1.822112	-2.549027	23503.866599
HLA A*3101	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.378395	1.828833	-2.549562	23899.814118
HLA A*0219	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.426991	1.877371	-2.549620	26729.526837
HLA A*6901	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.342894	1.793234	-2.549660	22023.878618
HLA B*4601	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.352437	1.802719	-2.549718	22513.209508
HLA B*5301	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.948812	1.398961	-2.549852	8888.169660
HLA B*5801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.349705	1.799748	-2.549957	22372.007789
HLA B*0702	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.039056	1.488986	-2.550070	10940.975735
HLA B*3901	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.135319	1.585042	-2.550277	13655.863102
HLA B*1501	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.135874	1.585464	-2.550409	13673.309139
HLA B*5301	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.595085	2.044529	-2.550557	39362.726756
HLA A*0216	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.370420	1.819741	-2.550679	23464.989873
HLA A*2501	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.424254	1.873374	-2.550880	26561.593196
HLA B*0802	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.360353	1.809098	-2.551255	22927.295470
HLA A*0202	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.473389	1.922093	-2.551296	29743.282828
HLA A*0219	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.180627	1.629324	-2.551302	15157.466713
HLA B*7301	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.594742	2.043325	-2.551417	39331.648625
HLA B*3501	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-3.526032	0.974301	-2.551731	3357.622819
HLA A*0212	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.380627	1.828833	-2.551794	24022.960875
HLA A*3001	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.836516	1.284672	-2.551845	6863.037166
HLA B*5701	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.360964	1.809098	-2.551866	22959.567034
HLA A*3001	1:433-441	9	STLTYAEAV	1.049463	0.176908	-3.778376	1.226371	-2.552005	6003.105764
HLA B*0802	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.392978	1.840969	-2.552009	24715.976671
HLA A*0250	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.569652	1.017549	-2.552104	3712.380188
HLA B*5401	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.374321	1.822112	-2.552208	23676.664283
HLA A*6802	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-2.833958	0.281512	-2.552446	682.273035
HLA A*2603	1:267-275	9	AEMRADLVR	1.301765	0.742764	-4.597007	2.044529	-2.552478	39537.304203
HLA B*4002	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.270638	1.718039	-2.552598	18648.235415
HLA A*6802	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.802251	1.249564	-2.552688	6342.368354
HLA A*2402	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.495678	1.942822	-2.552856	31309.668184
HLA B*4402	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.372603	1.819741	-2.552862	23583.216757
HLA A*0206	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-2.962607	0.409720	-2.552887	917.501131
HLA A*0216	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.007916	1.454961	-2.552955	10183.943487
HLA B*5401	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.368461	0.815296	-2.553165	2335.938188
HLA A*0216	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.650700	1.097502	-2.553198	4474.044310
HLA A*2402	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.151968	1.598716	-2.553251	14189.516753
HLA A*6801	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.591695	2.038259	-2.553436	39056.639095
HLA B*1801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.362716	1.809179	-2.553538	23052.413962
HLA A*0206	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.475736	1.922093	-2.553643	29904.464944
HLA B*3801	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.496693	1.942822	-2.553871	31382.926708
HLA B*3801	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.424799	1.870848	-2.553952	26594.951429
HLA A*0101	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.373804	1.819741	-2.554063	23648.501657
HLA B*4501	1:81-89	9	ETPAGPLPY	0.838347	1.232245	-4.624844	2.070592	-2.554252	42154.481565
HLA B*5701	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.419600	1.865170	-2.554430	26278.452773
HLA A*6801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.204831	1.650328	-2.554503	16026.216953
HLA B*1801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.348356	1.793234	-2.555122	22302.644274
HLA A*0211	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.498087	1.942822	-2.555265	31483.766818
HLA B*1501	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.384200	1.828833	-2.555367	24221.447900
HLA B*0702	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.318457	1.762988	-2.555469	20818.853606
HLA A*6801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.375653	1.819741	-2.555912	23749.401752
HLA A*3002	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.516065	1.960098	-2.555967	32814.436167
HLA A*2403	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.421235	1.865170	-2.556065	26377.585094
HLA A*3002	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-3.986639	1.430389	-2.556250	9697.036816
HLA A*0101	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.365806	1.809179	-2.556627	23216.993649

HLA A*0301	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.366356	1.809098	-2.557258	23246.402978
HLA A*0203	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.207754	1.650328	-2.557426	16134.435566
HLA B*4501	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.408494	1.851066	-2.557428	25614.965518
HLA B*1509	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.280748	1.723131	-2.557617	19087.435260
HLA A*3001	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.819915	1.262230	-2.557684	6605.639822
HLA B*4801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.366988	1.809179	-2.557809	23280.257170
HLA A*2602	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.549219	1.991397	-2.557822	35417.551108
HLA A*6901	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.308967	1.751011	-2.557957	20368.884305
HLA A*0202	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.549425	1.991397	-2.558028	35434.416364
HLA B*3501	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-3.411659	0.853416	-2.558243	2580.233312
HLA B*7301	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.415432	1.857104	-2.558328	26027.461024
HLA A*2902	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.252953	1.694587	-2.558366	17904.127811
HLA A*3201	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.608114	1.049687	-2.558426	4056.145410
HLA B*0802	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.367702	1.809179	-2.558523	23318.575529
HLA A*0212	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-3.398450	0.839877	-2.558573	2502.938468
HLA A*1101	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.432043	1.873374	-2.558669	27042.240057
HLA A*2902	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.587941	1.028753	-2.559188	3872.048937
HLA B*5401	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.556671	1.997366	-2.559305	36030.566932
HLA A*0301	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.368588	1.809179	-2.559409	23366.182953
HLA B*5101	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.024475	1.465019	-2.559457	10579.743801
HLA A*3001	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.192186	1.632662	-2.559524	15566.324849
HLA B*1503	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.809093	1.249564	-2.559530	6443.074630
HLA B*0702	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.144609	1.585042	-2.559567	13951.118194
HLA B*3901	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.306653	1.746933	-2.559720	20260.632479
HLA B*5801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.353058	1.793234	-2.559823	22545.386087
HLA A*0101	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.381968	1.822112	-2.559856	24097.283657
HLA B*0802	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.419628	1.859413	-2.560215	26280.158791
HLA A*0250	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.575836	2.015621	-2.560215	37656.143894
HLA A*6901	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.382328	1.822112	-2.560215	24117.237550
HLA A*0201	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.657768	1.097502	-2.560265	4547.445803
HLA A*0301	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.289880	1.729555	-2.560326	19493.060255
HLA B*0801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.425516	1.865170	-2.560346	26638.869752
HLA A*2902	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.312588	1.752221	-2.560367	20539.402129
HLA B*4801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.389336	1.828833	-2.560503	24509.591608
HLA A*0219	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.420096	1.859413	-2.560682	26308.466402
HLA B*4403	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.420135	1.859413	-2.560722	26310.886053
HLA B*4002	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.604187	2.043325	-2.560862	40196.392695
HLA B*5101	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.679721	1.118640	-2.561081	4783.228407
HLA A*0201	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.390064	1.828833	-2.561232	24550.730289
HLA A*2403	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.370561	1.809098	-2.561464	23472.607689
HLA A*0216	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.146987	1.585464	-2.561522	14027.707349
HLA A*6802	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-3.455599	0.894030	-2.561569	2854.953548
HLA A*2301	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.432459	1.870848	-2.561611	27068.146766
HLA A*8001	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.371074	1.809098	-2.561976	23500.306576
HLA A*2501	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-3.948869	1.386802	-2.562066	8889.323751
HLA A*1101	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.355445	1.793234	-2.562210	22669.646799
HLA A*0201	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.384553	1.822112	-2.562440	24241.111179
HLA B*4001	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.382236	1.819741	-2.562495	24112.149695
HLA B*1501	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.371687	1.809179	-2.562508	23533.512001
HLA A*0206	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.382285	1.819741	-2.562544	24114.889175
HLA B*3501	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.325818	1.762988	-2.562830	21174.723491
HLA B*2705	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.429815	1.866969	-2.562846	26903.906932
HLA B*4402	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.372034	1.809179	-2.562856	23552.361973
HLA A*0101	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-3.861646	1.298743	-2.562904	7271.875626
HLA A*0216	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.097041	1.534036	-2.563005	12503.780602
HLA A*3101	1:249-257	9	AVVLKALAK	1.021065	0.298784	-3.882952	1.319849	-2.563102	7637.506139
HLA A*2603	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.440597	1.877371	-2.563226	27580.182693
HLA B*4001	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.372554	1.809179	-2.563375	23580.537675
HLA B*3801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.286511	1.723131	-2.563380	19342.422425
HLA A*2501	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.248867	1.685171	-2.563696	17736.479246
HLA A*3002	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.592158	2.028058	-2.564100	39098.285825
HLA A*0206	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.759096	1.194908	-2.564188	5742.435436
HLA B*1502	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.507088	1.942822	-2.564265	32143.085552
HLA B*5101	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.442040	1.877371	-2.564669	27671.947334
HLA A*6802	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.097182	1.532461	-2.564722	12507.839905

HLA A*0212	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.315910	1.751011	-2.564899	20697.122474
HLA A*2501	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.422003	1.857104	-2.564900	26424.289231
HLA B*1501	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.183728	1.618772	-2.564956	15266.094393
HLA A*0206	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.481326	0.916314	-2.565011	3029.185764
HLA A*2601	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.387252	1.822112	-2.565140	24392.262308
HLA A*3001	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.964140	1.398961	-2.565180	9207.471348
HLA A*0206	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.328207	1.762988	-2.565219	21291.544870
HLA B*3801	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.430548	1.865170	-2.565378	26949.355990
HLA B*1501	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.312527	1.746933	-2.565594	20536.513319
HLA A*0101	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.368463	1.802719	-2.565744	23359.484265
HLA A*0201	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.365794	1.799748	-2.566046	23216.365650
HLA A*6802	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.407023	1.840969	-2.566054	25528.364840
HLA B*1502	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.394984	1.828833	-2.566152	24830.429789
HLA A*2601	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.289344	1.723131	-2.566213	19469.031270
HLA B*1501	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.298287	0.732039	-2.566248	1987.407519
HLA A*6901	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.318539	1.752221	-2.566318	20822.795948
HLA A*2501	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.425746	1.859413	-2.566333	26652.996603
HLA A*0219	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.366386	1.799748	-2.566638	23248.037922
HLA B*2705	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.426113	1.859413	-2.566699	26675.499700
HLA A*2501	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.289845	1.723131	-2.566714	19491.478490
HLA B*3501	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.119139	0.552387	-2.566752	1315.644932
HLA A*3002	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.558243	1.991397	-2.566846	36161.205593
HLA A*2902	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.165628	1.598716	-2.566911	14642.913973
HLA B*3901	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.184019	1.616917	-2.567102	15276.338725
HLA B*1509	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.389785	1.822112	-2.567672	24534.930184
HLA A*2301	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.510649	1.942822	-2.567827	32407.787573
HLA A*0206	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-3.550349	0.982334	-2.568015	3550.986960
HLA B*4601	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.397167	1.828833	-2.568334	24955.536357
HLA A*0202	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.584090	2.015621	-2.568469	38378.640426
HLA A*0206	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.825610	1.257069	-2.568541	6692.833814
HLA B*0803	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.146413	1.577554	-2.568859	14009.202809
HLA A*0211	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.331973	1.762988	-2.568985	21476.989190
HLA A*0212	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.378463	1.809179	-2.569284	23903.563977
HLA A*2403	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.137739	1.568231	-2.569508	13732.168505
HLA A*3001	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.287801	1.718039	-2.569761	19399.955378
HLA A*2603	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.561168	1.991397	-2.569771	36405.584655
HLA B*1503	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.435257	1.865170	-2.570087	27243.114722
HLA B*1503	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.276321	1.706161	-2.570160	18893.879764
HLA B*1517	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.427283	1.857104	-2.570179	26747.463721
HLA A*3001	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-3.165160	0.594934	-2.570226	1462.717338
HLA A*0212	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.199554	1.629324	-2.570230	15832.666882
HLA B*3501	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.264835	1.694587	-2.570248	18400.707218
HLA A*0219	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.379358	1.809098	-2.570260	23952.884044
HLA A*0212	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.392527	1.822112	-2.570414	24690.317546
HLA B*1503	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.637703	1.067242	-2.570461	4342.131081
HLA B*0803	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.421808	1.851066	-2.570742	26412.426839
HLA A*0211	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.493014	1.922093	-2.570921	31118.177166
HLA A*2501	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.436385	1.865170	-2.571214	27313.950124
HLA A*3301	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.188173	1.616917	-2.571256	15423.153075
HLA A*3101	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.322489	1.751118	-2.571371	21013.022599
HLA B*5401	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.562954	1.991397	-2.571557	36555.574922
HLA A*0201	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.380796	1.809179	-2.571617	24032.319929
HLA A*3002	1:162-170	9	AIADSGNSV	1.093291	0.318474	-3.983448	1.411765	-2.571684	9626.057329
HLA B*0702	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.380946	1.809098	-2.571849	24040.642150
HLA A*6802	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.437486	1.865170	-2.572316	27383.340109
HLA A*6802	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-3.466139	0.893801	-2.572338	2925.087326
HLA A*2602	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.810493	1.238104	-2.572390	6463.882524
HLA A*0212	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.437975	1.865170	-2.572805	27414.170745
HLA B*4501	1:198-206	9	DVYSLGCVL	1.637861	0.443865	-4.654619	2.081726	-2.572893	45145.947889
HLA B*5801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.905648	1.332686	-2.572962	8047.251926
HLA A*6901	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.055700	1.482642	-2.573058	11368.412059
HLA B*7301	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.601234	2.028058	-2.573176	39923.975254
HLA A*0250	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.565792	1.991397	-2.574395	36795.253258
HLA A*3002	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.057495	1.482642	-2.574853	11415.496709
HLA B*5101	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.425997	1.851066	-2.574932	26668.429374

HLA A*2601	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.377685	1.802719	-2.574966	23860.798804
HLA A*3002	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.160210	1.584939	-2.575271	14461.375349
HLA B*4601	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.397740	1.822112	-2.575628	24988.499740
HLA B*1503	1:145-153	9	MISATNAVK	0.938735	0.280828	-3.795325	1.219563	-2.575762	6242.020343
HLA A*0212	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.416762	1.840969	-2.575792	26107.279177
HLA A*3301	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.814102	1.238104	-2.575999	6517.818519
HLA A*0206	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.270941	1.694587	-2.576354	18661.254108
HLA B*1801	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.306284	1.729555	-2.576730	20243.431364
HLA B*1801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.323696	1.746933	-2.576764	21071.534468
HLA B*5701	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.162371	1.585464	-2.576907	14533.530444
HLA A*0301	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.328480	1.751011	-2.577469	21304.910512
HLA B*3501	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.060371	1.482642	-2.577729	11491.337573
HLA B*4501	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.210395	1.632662	-2.577733	16232.843368
HLA A*6802	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.301148	1.723131	-2.578017	20005.442193
HLA A*2301	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.187464	1.609050	-2.578414	15397.975508
HLA A*2902	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.378228	1.799748	-2.578480	23890.635911
HLA A*0216	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.341494	1.762988	-2.578506	21952.981518
HLA B*1517	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.270473	1.691666	-2.578807	18641.174810
HLA B*3901	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.419799	1.840969	-2.578830	26290.539451
HLA B*4402	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.573247	0.994371	-2.578876	3743.235564
HLA B*4501	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.622210	2.043325	-2.578885	41899.609927
HLA A*0101	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.208238	1.629324	-2.578914	16152.426403
HLA B*1801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.452389	1.873374	-2.579015	28339.305560
HLA A*2501	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.456550	1.877371	-2.579179	28612.126851
HLA A*2403	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.401422	1.822112	-2.579309	25201.235092
HLA A*2602	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.602404	1.022974	-2.579431	4003.172155
HLA B*3501	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.157024	1.577554	-2.579469	14355.677615
HLA B*0803	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.066667	1.487180	-2.579488	11659.158400
HLA A*2601	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.388674	1.809179	-2.579495	24472.228559
HLA A*0101	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.379370	1.799748	-2.579621	23953.531965
HLA B*5101	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.388798	1.809098	-2.579701	24479.246343
HLA B*7301	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.608233	2.028437	-2.579796	40572.605065
HLA B*0803	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.382823	1.802719	-2.580104	24144.782771
HLA B*1502	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.540500	1.960098	-2.580402	34713.594851
HLA A*0301	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.225605	1.645104	-2.580501	16811.449642
HLA B*1502	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-3.834764	1.254080	-2.580683	6835.395292
HLA A*3101	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.390048	1.809179	-2.580869	24549.800589
HLA A*2501	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.158471	1.577554	-2.580917	14403.597594
HLA A*1101	1:458-466	9	PSTPELVGK	1.142224	0.018975	-3.742246	1.161199	-2.581046	5523.897541
HLA A*6802	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.374316	1.793234	-2.581082	23676.408108
HLA A*0203	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.446297	1.865170	-2.581127	27944.541560
HLA A*2403	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.390454	1.809179	-2.581276	24572.787768
HLA B*1502	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.448552	1.866969	-2.581584	28090.048876
HLA A*2301	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.432757	1.851066	-2.581691	27086.750487
HLA A*2403	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.332723	1.751011	-2.581712	21514.085204
HLA A*1101	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.311298	1.729555	-2.581743	20478.490006
HLA B*0802	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.404124	1.822112	-2.582011	25358.510089
HLA A*0219	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.605069	1.022974	-2.582095	4027.806359
HLA A*2601	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.267287	1.685171	-2.582116	18504.927054
HLA A*0216	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.447326	1.865170	-2.582156	28010.835542
HLA A*3001	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.288365	1.706161	-2.582203	19425.160123
HLA A*8001	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.404591	1.822112	-2.582479	25385.824949
HLA B*1509	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.230985	1.648439	-2.582547	17021.016186
HLA A*0250	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.314771	0.732039	-2.582732	2064.290982
HLA B*1503	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.221042	1.638299	-2.582743	16635.753024
HLA B*3501	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.447932	1.865170	-2.582762	28049.959002
HLA A*0216	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.411762	1.828833	-2.582929	25808.449209
HLA B*4002	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.584397	2.001388	-2.583009	38405.848835
HLA A*0216	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.168057	1.584939	-2.583118	14725.053399
HLA B*2705	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.448336	1.865170	-2.583166	28076.071662
HLA B*2705	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.376614	1.793234	-2.583379	23802.008918
HLA B*4601	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.392686	1.809179	-2.583508	24699.402105
HLA A*6802	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.412570	1.828833	-2.583737	25856.523500
HLA A*1101	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.412617	1.828833	-2.583784	25859.321270
HLA B*4601	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.377048	1.793234	-2.583814	23825.842596

HLA A*2603	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.505946	1.922093	-2.583853	32058.685755
HLA A*6901	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.383608	1.799748	-2.583860	24188.449490
HLA B*4801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.386698	1.802719	-2.583978	24361.139753
HLA A*2603	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.307165	1.723131	-2.584034	20284.541070
HLA A*3001	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.220018	1.635751	-2.584267	16596.560320
HLA B*0802	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.245432	1.661000	-2.584433	17596.750162
HLA B*4501	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.585845	2.001388	-2.584457	38534.049503
HLA B*7301	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.600087	2.015621	-2.584466	39818.713933
HLA A*2601	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.384628	1.799748	-2.584880	24245.308077
HLA B*1501	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.766107	1.181170	-2.584937	5835.888480
HLA B*3901	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.220967	1.635751	-2.585216	16632.873351
HLA B*5801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.279949	1.694587	-2.585362	19052.358820
HLA B*5701	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.407787	1.822112	-2.585674	25573.288649
HLA A*0206	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.528564	1.942822	-2.585742	33772.577473
HLA B*5101	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.442869	1.857104	-2.585765	27724.842689
HLA B*5701	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.395207	1.809179	-2.586029	24843.194407
HLA B*4801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.337257	1.751011	-2.586247	21739.892403
HLA A*3101	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-3.994143	1.407681	-2.586463	9866.049716
HLA B*5701	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.236909	1.650328	-2.586581	17254.744640
HLA B*1503	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.379861	1.793234	-2.586626	23980.630746
HLA A*2301	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.446055	1.859413	-2.586642	27928.974680
HLA B*0801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.386399	1.799748	-2.586651	24344.408036
HLA B*4801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.338933	1.752221	-2.586712	21823.910559
HLA A*2902	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.406508	1.819741	-2.586767	25498.137618
HLA B*1501	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-3.985859	1.398961	-2.586898	9679.635763
HLA B*4403	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.578343	1.991397	-2.586946	37874.136962
HLA A*8001	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.386773	1.799748	-2.587025	24365.357432
HLA A*3001	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.119789	1.532461	-2.587328	13176.166026
HLA B*4501	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-3.384828	0.797462	-2.587366	2425.648453
HLA A*2902	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.206198	1.618772	-2.587426	16076.755907
HLA A*2601	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.396671	1.809098	-2.587574	24927.066199
HLA B*7301	1:369-377	9	SSADAIATL	1.558793	0.442595	-4.588986	2.001388	-2.587598	38813.777543
HLA A*3201	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.530639	1.942822	-2.587817	33934.292727
HLA A*3301	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.616346	2.028058	-2.588288	41337.638715
HLA A*2403	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.408245	1.819741	-2.588504	25600.280872
HLA A*2902	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.447972	1.859413	-2.588559	28052.538822
HLA B*5301	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.604518	2.015621	-2.588897	40227.065975
HLA B*2705	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.933038	1.343697	-2.589341	8571.126279
HLA A*2501	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.440421	1.851066	-2.589355	27568.994533
HLA B*4601	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.389186	1.799748	-2.589438	24501.107050
HLA A*6901	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-2.862316	0.272858	-2.589458	728.310366
HLA A*0301	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-3.976438	1.386802	-2.589635	9471.910387
HLA A*0206	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.312851	1.723131	-2.589720	20551.850880
HLA B*1501	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.284528	1.694587	-2.589941	19254.307278
HLA B*4002	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.618446	2.028437	-2.590009	41538.050009
HLA A*0203	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.418857	1.828833	-2.590025	26233.567479
HLA B*3901	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.313380	1.723131	-2.590249	20576.882339
HLA B*5101	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.353365	1.762988	-2.590378	22561.369563
HLA A*6801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.091962	1.501143	-2.590818	12358.386067
HLA B*0803	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.276258	1.685171	-2.591086	18891.120194
HLA B*3501	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.180951	1.589799	-2.591152	15168.786968
HLA B*1509	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.342452	1.751118	-2.591334	22001.490418
HLA B*5801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.342346	1.751011	-2.591336	21996.134917
HLA B*5301	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.464926	1.873374	-2.591552	29169.303273
HLA B*3501	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.413975	1.822112	-2.591863	25940.307746
HLA A*0201	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.342913	1.751011	-2.591902	22024.831813
HLA B*1502	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.583418	1.991397	-2.592021	38319.305822
HLA B*3501	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-3.924754	1.332686	-2.592068	8409.179241
HLA B*0802	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.392022	1.799748	-2.592273	24661.616287
HLA A*3201	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.443409	1.851066	-2.592344	27759.361475
HLA A*8001	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.401758	1.809179	-2.592579	25220.738667
HLA B*0702	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.414769	1.822112	-2.592657	25987.784095
HLA A*0211	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.470034	1.877371	-2.592663	29514.391668
HLA A*0219	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.433659	1.840969	-2.592690	27143.078920
HLA B*0702	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.458004	1.865170	-2.592834	28708.101499

HLA B*0803	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.452401	1.859413	-2.592988	28340.072132
HLA A*1101	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.228923	1.635751	-2.593171	16940.360061
HLA A*0250	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-3.522428	0.929186	-2.593242	3329.873979
HLA B*5401	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.515431	1.922093	-2.593337	32766.540091
HLA B*4002	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.621460	2.028058	-2.593403	41827.363838
HLA B*2705	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.422295	1.828833	-2.593462	26442.021285
HLA A*3301	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.631340	2.037813	-2.593527	42789.782458
HLA A*6802	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.311570	1.718039	-2.593531	20491.345257
HLA B*1502	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.471112	1.877371	-2.593741	29587.771076
HLA B*4001	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.356845	1.762988	-2.593857	22742.858368
HLA A*1101	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.471246	1.877371	-2.593875	29596.896277
HLA B*4801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.192675	1.598716	-2.593959	15583.850823
HLA A*2402	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.585391	1.991397	-2.593994	38493.836767
HLA B*4403	1:118-126	9	VIADACQAL	1.609592	0.433733	-4.637453	2.043325	-2.594128	43396.373513
HLA B*3801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.423072	1.828833	-2.594240	26489.412725
HLA A*0201	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.397230	1.802719	-2.594511	24959.181804
HLA A*3201	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.516861	1.922093	-2.594768	32874.671499
HLA B*4002	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.554996	1.960098	-2.594898	35891.855687
HLA A*0301	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.346552	1.751118	-2.595434	22210.173593
HLA A*3201	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.060535	1.465019	-2.595517	11495.690078
HLA B*3801	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.517731	1.922093	-2.595638	32940.541283
HLA B*3501	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.662899	1.067242	-2.595657	4601.493438
HLA B*1502	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.447018	1.851066	-2.595952	27990.991422
HLA B*2705	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.325529	1.729555	-2.595974	21160.638171
HLA B*1517	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.290587	1.694587	-2.596000	19524.828157
HLA A*3301	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.491485	1.894713	-2.596771	31008.776750
HLA B*1503	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-3.867234	1.270418	-2.596815	7366.030583
HLA A*0212	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.079458	1.482642	-2.596816	12007.643873
HLA A*0219	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.462041	1.865170	-2.596871	28976.163817
HLA A*0206	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.426192	1.828833	-2.597360	26680.406742
HLA B*0803	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.419543	1.822112	-2.597431	26275.041070
HLA B*0702	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.289222	1.691666	-2.597556	19463.555125
HLA B*4001	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.397496	1.799748	-2.597748	24974.444453
HLA A*0202	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.489869	0.892112	-2.597756	3089.360821
HLA B*5801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.350041	1.752221	-2.597820	22389.321787
HLA B*4402	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.360978	1.762988	-2.597990	22960.312298
HLA B*5301	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.541369	1.942822	-2.598547	34783.149219
HLA B*4002	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.493519	1.894713	-2.598806	31154.392589
HLA B*0702	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.408137	1.809179	-2.598958	25593.910909
HLA A*0101	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.362355	1.762988	-2.599367	23033.216466
HLA B*5101	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.402195	1.802719	-2.599475	25246.129540
HLA B*4002	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.591006	1.991397	-2.599610	38994.779553
HLA B*5801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.346853	1.746933	-2.599920	22225.558705
HLA A*6801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.903068	1.303070	-2.599997	7999.592470
HLA A*2602	1:79-87	9	EAETPAGPL	0.986891	0.274759	-3.861703	1.261650	-2.600053	7272.819848
HLA A*6802	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.409429	1.809179	-2.600250	25670.177437
HLA B*0702	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.884996	1.284672	-2.600324	7673.537579
HLA B*0803	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.292018	1.691666	-2.600352	19589.261178
HLA B*5401	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.495093	1.894713	-2.600380	31267.520501
HLA B*5701	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.351458	1.751011	-2.600447	22462.478667
HLA A*3201	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.591850	1.991397	-2.600453	39070.586863
HLA B*4403	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.451590	1.851066	-2.600525	28287.227219
HLA B*0802	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.191603	1.590840	-2.600764	15545.454254
HLA B*3801	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.420565	1.819741	-2.600824	26336.946984
HLA A*0219	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.429963	1.828833	-2.601131	26913.077966
HLA B*2705	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.220187	1.618772	-2.601415	16603.026139
HLA B*1501	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-3.638107	1.036678	-2.601429	4346.173319
HLA B*3501	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.011274	0.409720	-2.601554	1026.298846
HLA A*0301	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.364657	1.762988	-2.601669	23155.655751
HLA B*0803	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.364676	1.762988	-2.601688	23156.657929
HLA B*4402	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.404481	1.802719	-2.601761	25379.371048
HLA A*0201	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.364970	1.762988	-2.601982	23172.322594
HLA A*2402	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.469052	1.866969	-2.602083	29447.725186
HLA A*0212	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.402357	1.799748	-2.602609	25255.555234
HLA A*0101	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.395938	1.793234	-2.602704	24885.027656

HLA B*1509	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.402510	1.799748	-2.602761	25264.437729
HLA A*6901	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.137020	1.534036	-2.602984	13709.454721
HLA A*1101	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.462445	1.859413	-2.603032	29003.138712
HLA B*5801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.354294	1.751118	-2.603176	22609.632643
HLA A*2402	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.454412	1.851066	-2.603346	28471.615528
HLA A*6801	1:58-66	9	REAQNAAAL	1.509434	0.528379	-4.641323	2.037813	-2.603510	43784.766734
HLA A*0216	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.354622	1.751011	-2.603612	22626.763314
HLA B*4001	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.406544	1.802719	-2.603824	25500.206833
HLA A*0201	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.397183	1.793234	-2.603949	24956.481422
HLA A*2601	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.355076	1.751011	-2.604065	22650.400450
HLA A*2403	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.404070	1.799748	-2.604322	25355.354991
HLA A*3001	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.242691	1.638299	-2.604392	17486.005835
HLA B*4403	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.632458	2.028058	-2.604401	42900.112731
HLA B*5301	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.289664	1.685171	-2.604493	19483.360782
HLA B*0803	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.433382	1.828833	-2.604549	27125.757206
HLA A*3101	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.248799	1.644220	-2.604579	17733.696845
HLA A*3001	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-3.386317	0.781690	-2.604627	2433.982395
HLA A*3002	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-3.911883	1.306673	-2.605210	8163.626573
HLA A*2902	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.414837	1.809098	-2.605740	25991.861555
HLA B*1501	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.160661	1.554751	-2.605909	14476.404165
HLA B*1509	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.357047	1.751011	-2.606036	22753.441955
HLA B*1509	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.291471	1.685171	-2.606299	19564.584388
HLA B*1503	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.868831	1.262230	-2.606601	7393.178085
HLA B*4501	1:9-17	9	DRYELGEIL	1.564982	0.473277	-4.644958	2.038259	-2.606699	44152.743429
HLA B*2705	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.357839	1.751011	-2.606828	22794.962335
HLA B*1501	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.139800	0.532852	-2.606948	1379.748937
HLA B*4801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.407213	1.799748	-2.607465	25539.553847
HLA B*5301	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.467071	1.859413	-2.607658	29313.733528
HLA A*3201	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-3.721716	1.113773	-2.607943	5268.849756
HLA B*1509	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.354944	1.746933	-2.608012	22643.539465
HLA B*1509	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.193192	1.584939	-2.608253	15602.409384
HLA A*2902	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.293592	1.685171	-2.608421	19660.393754
HLA A*0203	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.751691	1.143250	-2.608440	5645.345734
HLA B*1517	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.473779	1.865170	-2.608609	29770.005531
HLA A*0202	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.417809	1.809179	-2.608631	26170.347151
HLA A*0101	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.258958	1.650328	-2.608631	18153.419894
HLA B*1503	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-3.167538	0.558588	-2.608950	1470.747396
HLA A*0301	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.058566	1.449604	-2.608962	11443.692469
HLA B*1503	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-3.619692	1.010656	-2.609035	4165.736330
HLA A*3101	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.372135	1.762988	-2.609148	23557.841484
HLA B*1501	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.372408	1.762988	-2.609420	23572.629779
HLA B*4801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.402655	1.793234	-2.609421	25272.913175
HLA A*6802	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.409394	1.799748	-2.609645	25668.094430
HLA B*4601	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.372681	1.762988	-2.609693	23587.427358
HLA B*4402	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.402984	1.793234	-2.609750	25292.061737
HLA B*4601	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.360797	1.751011	-2.609786	22950.749909
HLA A*3101	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.055883	1.445980	-2.609903	11373.210215
HLA A*0206	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-3.559052	0.949124	-2.609928	3622.860152
HLA B*4601	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.333087	1.723131	-2.609956	21532.133036
HLA B*3901	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.475574	1.865170	-2.610404	29893.304218
HLA A*0212	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.195424	1.584939	-2.610485	15682.802733
HLA A*3002	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.553450	1.942822	-2.610628	35764.318328
HLA B*3801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.361908	1.751011	-2.610898	23009.553271
HLA B*1801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.362044	1.751118	-2.610927	23016.774194
HLA A*6901	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.249269	1.638299	-2.610970	17752.894695
HLA A*2601	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.188563	1.577554	-2.611009	15437.009929
HLA A*8001	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.305732	1.694587	-2.611145	20217.711758
HLA B*2705	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.420302	1.809098	-2.611205	26320.994062
HLA A*3001	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.021191	1.409864	-2.611327	10500.030750
HLA A*2601	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.363579	1.752221	-2.611358	23098.228366
HLA A*3201	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.571814	1.960098	-2.611716	37308.992939
HLA B*1509	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.201584	1.589799	-2.611785	15906.844273
HLA A*2501	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.363168	1.751011	-2.612157	23076.370915
HLA A*6901	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.363304	1.751118	-2.612186	23083.612806
HLA A*2602	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.990459	1.378166	-2.612293	9782.712875

HLA B*4002	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.318464	1.706161	-2.612303	20819.191492
HLA A*3201	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.483412	1.870848	-2.612564	30437.698010
HLA A*0203	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.415305	1.802719	-2.612585	26019.858627
HLA A*0219	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.434874	1.822112	-2.612761	27219.102008
HLA B*5401	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-3.598133	0.985326	-2.612807	3963.993224
HLA B*4402	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.421909	1.809098	-2.612812	26418.571750
HLA A*2902	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.257969	1.645104	-2.612865	18112.121378
HLA B*5301	1:188-196	9	ARGDSVDAR	1.287139	0.704258	-4.604265	1.991397	-2.612868	40203.569451
HLA B*1509	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.203891	1.590840	-2.613051	15991.574426
HLA B*1501	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.630631	1.017549	-2.613082	4271.997403
HLA A*0219	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.422633	1.809179	-2.613454	26462.628280
HLA B*4001	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.336585	1.723131	-2.613454	21706.281835
HLA A*3101	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.101082	1.487180	-2.613903	12620.671389
HLA A*2402	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.199023	1.584939	-2.614084	15813.321139
HLA B*0801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.060098	1.445980	-2.614118	11484.128479
HLA B*1501	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.407458	1.793234	-2.614223	25553.927170
HLA B*3501	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.423575	1.809179	-2.614396	26520.097708
HLA B*4403	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.642867	2.028437	-2.614429	43940.667702
HLA B*1501	1:476-484	9	QTSAITNVV	1.187107	0.191059	-3.992701	1.378166	-2.614535	9833.332303
HLA B*4001	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.408014	1.793234	-2.614780	25586.711990
HLA B*4001	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.367143	1.752221	-2.614922	23288.570933
HLA B*4501	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.630562	2.015621	-2.614941	42713.228499
HLA B*1503	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.064567	1.449604	-2.614963	11602.905710
HLA B*4001	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.366126	1.751011	-2.615115	23234.081719
HLA B*5701	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.362108	1.746933	-2.615175	23020.136431
HLA B*1801	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.456151	1.840969	-2.615181	28585.824914
HLA B*4601	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.183502	1.568231	-2.615272	15258.168015
HLA B*5701	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.415025	1.799748	-2.615277	26003.113037
HLA A*6802	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.437392	1.822112	-2.615280	27377.415116
HLA A*6802	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-2.786870	0.171585	-2.615285	612.166880
HLA A*3001	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.276415	1.661000	-2.615415	18897.968759
HLA B*0802	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.378423	1.762988	-2.615435	23901.365713
HLA A*0203	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.363318	1.746933	-2.616385	23084.362097
HLA A*0201	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.103568	1.487180	-2.616389	12693.114979
HLA B*0803	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.481657	1.865170	-2.616487	30314.941783
HLA A*2902	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.438640	1.822112	-2.616528	27456.173948
HLA A*8001	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.436269	1.819741	-2.616528	27306.710577
HLA A*0216	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.438736	1.822112	-2.616624	27462.264553
HLA A*2301	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.482007	1.865170	-2.616837	30339.387705
HLA B*3901	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.105847	1.488986	-2.616861	12759.898346
HLA A*6801	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.644988	2.028058	-2.616931	44155.848737
HLA A*0250	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.559765	1.942822	-2.616943	36288.195068
HLA A*2402	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.446121	1.828833	-2.617288	27933.205595
HLA A*0201	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.866905	1.249564	-2.617341	7360.453778
HLA B*3901	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.439455	1.822112	-2.617343	27507.763952
HLA B*1801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.468814	1.851066	-2.617749	29431.639379
HLA A*0219	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.216729	1.598716	-2.618013	16471.335363
HLA B*2705	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.437820	1.819741	-2.618079	27404.384189
HLA B*1801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.612512	0.994371	-2.618141	4097.431970
HLA B*0702	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.216983	1.598716	-2.618266	16480.961850
HLA A*3301	1:145-153	9	MISATNAVK	0.938735	0.280828	-3.837865	1.219563	-2.618302	6884.381917
HLA B*5101	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.203435	1.584939	-2.618497	15974.799777
HLA A*0216	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.459680	1.840969	-2.618710	28819.049691
HLA B*3901	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.083809	1.465019	-2.618791	12128.554532
HLA B*3501	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.051239	0.432298	-2.618941	1125.222948
HLA B*4402	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.418862	1.799748	-2.619114	26233.851322
HLA A*0202	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.382149	1.762988	-2.619161	24107.323748
HLA A*3101	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-3.827551	1.208137	-2.619413	6722.808121
HLA A*0216	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.856261	1.236758	-2.619503	7182.264962
HLA B*3801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.478938	1.859413	-2.619525	30125.785838
HLA B*5701	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.382635	1.762988	-2.619647	24134.335385
HLA A*6801	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.493047	1.873374	-2.619673	31120.534097
HLA B*0803	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.419435	1.799748	-2.619687	26268.503211
HLA A*3101	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-3.413257	0.793337	-2.619920	2589.742760
HLA A*0301	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.366988	1.746933	-2.620055	23280.257170

HLA B*1517	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-3.125191	0.505009	-2.620182	1334.107945
HLA B*5301	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.383187	1.762988	-2.620200	24165.037455
HLA B*3501	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.717769	1.097502	-2.620266	5221.180169
HLA A*2403	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.423082	1.802719	-2.620362	26489.985950
HLA A*0216	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.352443	0.732039	-2.620404	2251.347621
HLA B*5401	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.423145	1.802719	-2.620426	26493.855546
HLA A*0250	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.146540	1.525910	-2.620630	14013.295972
HLA B*3501	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.423364	1.802719	-2.620644	26507.188480
HLA B*5401	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.563508	1.942822	-2.620686	36602.276468
HLA A*2601	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.211024	1.589799	-2.621226	16256.395630
HLA B*5301	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-3.595581	0.974301	-2.621280	3940.772490
HLA A*6901	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.108474	1.487180	-2.621294	12837.307337
HLA A*3101	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.306498	1.685171	-2.621327	20253.399657
HLA A*6901	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.586752	0.965301	-2.621451	3861.464069
HLA B*5101	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.443616	1.822112	-2.621504	27772.580028
HLA A*3002	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.240407	1.618772	-2.621635	17394.298537
HLA B*1503	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-3.527108	0.905205	-2.621903	3365.952414
HLA B*3501	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.267132	1.645104	-2.622028	18498.321000
HLA A*2602	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.479319	1.857104	-2.622215	30152.199711
HLA B*1501	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.255098	1.632662	-2.622437	17992.779149
HLA A*1101	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.231512	1.609050	-2.622462	17041.655014
HLA A*2402	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.442319	1.819741	-2.622578	27689.767627
HLA A*0203	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.415993	1.793234	-2.622759	26061.135346
HLA B*0803	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.431857	1.809098	-2.622760	27030.685180
HLA B*3501	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.208003	1.585042	-2.622961	16143.690483
HLA B*4402	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.373994	1.751011	-2.622983	23658.866725
HLA A*2402	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.268589	1.645104	-2.623485	18560.470968
HLA A*2601	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.374924	1.751118	-2.623806	23709.605826
HLA A*0219	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.818787	1.194908	-2.623879	6588.508900
HLA B*0801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-3.945476	1.321448	-2.624028	8820.151954
HLA A*2402	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.054483	1.430389	-2.624093	11336.598698
HLA A*2603	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.584231	1.960098	-2.624133	38391.099899
HLA A*2902	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.353706	1.729555	-2.624152	22579.074410
HLA A*8001	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.269416	1.645104	-2.624312	18595.848994
HLA B*1502	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.465309	1.840969	-2.624340	29195.036456
HLA B*1509	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.465382	1.840969	-2.624413	29199.933066
HLA B*4001	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.353976	1.729555	-2.624422	22593.126064
HLA B*0802	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.375582	1.751118	-2.624464	23745.547616
HLA A*0201	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.376729	1.752221	-2.624508	23808.319300
HLA B*5801	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.354249	1.729555	-2.624694	22607.308766
HLA B*0802	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.243518	1.618772	-2.624745	17519.335828
HLA A*2501	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.434124	1.809098	-2.625027	27172.169025
HLA B*4501	1:280-288	9	EPPEAPKVL	1.851918	0.176140	-4.653085	2.028058	-2.625027	44986.744085
HLA B*4002	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.640665	2.015621	-2.625044	43718.493136
HLA A*3301	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.622487	1.997366	-2.625121	41926.365791
HLA B*4601	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.310384	1.685171	-2.625213	20435.439427
HLA A*0203	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-3.424060	0.798791	-2.625268	2654.969643
HLA B*4501	1:504-512	9	TVDVAQKNL	1.658841	0.369596	-4.653818	2.028437	-2.625380	45062.740673
HLA B*1501	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-3.928513	1.303070	-2.625442	8482.283537
HLA A*3101	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.372662	1.746933	-2.625729	23586.406538
HLA A*2402	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.485197	1.859413	-2.625784	30563.100706
HLA B*3901	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.419116	1.793234	-2.625882	26249.183401
HLA A*2902	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.258646	1.632662	-2.625984	18140.362929
HLA B*1801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.428739	1.802719	-2.626020	26837.328851
HLA B*5101	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.255347	1.629324	-2.626023	18003.100036
HLA A*0206	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-3.466050	0.839877	-2.626173	2924.486060
HLA A*1101	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.115475	1.488986	-2.626489	13045.940818
HLA A*6901	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.389667	1.762988	-2.626679	24528.294519
HLA A*2603	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.500326	1.873374	-2.626952	31646.504439
HLA A*2403	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.277463	1.650328	-2.627135	18943.621030
HLA B*5701	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.420399	1.793234	-2.627164	26326.832849
HLA B*2705	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.312367	1.685171	-2.627196	20528.959891
HLA A*0202	1:456-464	9	NSPSTPELV	0.868149	0.229670	-3.725052	1.097819	-2.627233	5309.481150
HLA B*0803	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.246034	1.618772	-2.627262	17621.137341
HLA B*4402	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.333435	1.706161	-2.627274	21549.379934

HLA B*0702	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.321899	1.694587	-2.627312	20984.508754
HLA A*0206	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.468359	1.840969	-2.627389	29400.766533
HLA B*3501	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.420864	1.793234	-2.627630	26355.048157
HLA B*1517	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.449772	1.822112	-2.627659	28169.029044
HLA B*0803	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.468645	1.840969	-2.627676	29420.177635
HLA A*0201	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.864799	1.236758	-2.628041	7324.862071
HLA A*0216	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.437392	1.809179	-2.628214	27377.415116
HLA A*8001	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.431002	1.802719	-2.628282	26977.508739
HLA A*0216	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.154472	1.525910	-2.628562	14271.583279
HLA A*3301	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.588727	1.960098	-2.628630	38790.686808
HLA B*0801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.278988	1.650328	-2.628660	19010.249324
HLA A*0202	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.320564	1.691666	-2.628898	20920.126166
HLA A*6802	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.431772	1.802719	-2.629053	27025.421305
HLA A*6801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.314430	1.685171	-2.629259	20626.701990
HLA A*2601	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.267800	1.638299	-2.629501	18526.763822
HLA B*0702	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.238692	1.609050	-2.629642	17325.740106
HLA B*0801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.228998	1.598716	-2.630282	16943.292970
HLA B*5401	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.811541	1.181170	-2.630371	6479.497479
HLA A*0206	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.322117	1.691666	-2.630451	20995.069130
HLA A*3002	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-3.943338	1.312789	-2.630549	8776.837061
HLA A*0301	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-3.855355	1.224706	-2.630649	7167.282482
HLA A*8001	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.381721	1.751011	-2.630711	24083.599362
HLA A*0250	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.893148	1.262230	-2.630918	7818.948223
HLA A*3001	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-3.994181	1.363134	-2.631047	9866.903740
HLA A*2902	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.382288	1.751011	-2.631277	24115.019635
HLA A*0203	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.394397	1.762988	-2.631409	24796.870021
HLA A*0219	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.821574	1.190001	-2.631572	6630.917524
HLA B*0803	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.424816	1.793234	-2.631581	26595.958578
HLA A*0219	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.394637	1.762988	-2.631649	24810.556925
HLA B*4801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.868573	1.236758	-2.631815	7388.779804
HLA B*4001	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.378780	1.746933	-2.631847	23921.027964
HLA A*6801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.049253	1.417212	-2.632041	11200.897417
HLA A*6801	1:427-435	9	REIPDVSTL	1.524929	0.472437	-4.629512	1.997366	-2.632146	42610.063285
HLA B*0801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.425612	1.793234	-2.632378	26644.779054
HLA B*4001	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.282794	1.650328	-2.632466	19177.587744
HLA A*2603	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.499633	1.866969	-2.632664	31596.039515
HLA A*6802	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-3.893712	1.261014	-2.632698	7829.106731
HLA B*4801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.355839	1.723131	-2.632708	22690.259731
HLA B*4402	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.222621	1.589799	-2.632823	16696.341464
HLA A*0219	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.115612	1.482642	-2.632970	13050.034932
HLA A*3001	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.218505	1.585464	-2.633041	16538.839032
HLA B*3901	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.384184	1.751118	-2.633066	24220.530669
HLA A*3001	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.577645	0.944464	-2.633181	3781.337087
HLA B*5101	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.474533	1.840969	-2.633564	29821.748275
HLA B*5801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.351634	1.718039	-2.633594	22471.594480
HLA A*3301	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-3.867407	1.233662	-2.633746	7368.980030
HLA A*0202	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-3.883826	1.249564	-2.634262	7652.891935
HLA B*0702	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.434150	1.799748	-2.634402	27173.786056
HLA B*0802	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.427663	1.793234	-2.634429	26770.915528
HLA A*2402	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.511911	1.877371	-2.634540	32502.072664
HLA A*2603	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-3.888656	1.254080	-2.634576	7738.488151
HLA B*3801	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.475607	1.840969	-2.634638	29895.568376
HLA A*2603	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.577509	1.942822	-2.634687	37801.469081
HLA A*0219	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.385718	1.751011	-2.634707	24306.244822
HLA A*0101	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.386066	1.751118	-2.634948	24325.713740
HLA A*2601	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.398055	1.762988	-2.635067	25006.621099
HLA A*0250	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.220065	1.584939	-2.635126	16598.356128
HLA B*1509	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.268042	1.632662	-2.635380	18537.090156
HLA A*3201	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.502363	1.866969	-2.635394	31795.287027
HLA A*0206	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.052636	1.417212	-2.635425	11288.495864
HLA A*2902	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.252542	1.616917	-2.635625	17887.185447
HLA A*0219	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.220601	1.584939	-2.635662	16618.842080
HLA A*3101	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-3.871120	1.235214	-2.635906	7432.237271
HLA B*4403	1:181-189	9	QYLSPEQAR	1.176259	0.839362	-4.651611	2.015621	-2.635990	44834.407536
HLA B*5801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.359126	1.723131	-2.635995	22862.640990

HLA A*2601	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.383328	1.746933	-2.636396	24172.882539
HLA B*5701	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.119239	1.482642	-2.636597	13159.496685
HLA A*0101	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.235360	1.598716	-2.636644	17193.338982
HLA A*1101	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.445820	1.809098	-2.636723	27913.869501
HLA B*5101	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.501942	1.865170	-2.636772	31764.512323
HLA A*2301	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.514261	1.877371	-2.636890	32678.381751
HLA A*0211	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.446196	1.809179	-2.637017	27938.041711
HLA A*6901	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.189426	0.552387	-2.637039	1546.770535
HLA A*3201	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-3.903566	1.266360	-2.637206	8008.772438
HLA A*0212	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.440153	1.802719	-2.637434	27551.997222
HLA B*4601	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.384562	1.746933	-2.637629	24241.635751
HLA A*6901	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.367486	1.729555	-2.637931	23306.972533
HLA B*1501	1:475-483	9	NQTSAITNV	1.108161	0.235536	-3.981733	1.343697	-2.638037	9588.116887
HLA B*1502	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.495162	1.857104	-2.638058	31272.426347
HLA B*5801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.344346	1.706161	-2.638185	22097.634530
HLA A*3001	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.286713	1.648439	-2.638274	19351.423590
HLA A*3101	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.247354	1.609050	-2.638305	17674.793427
HLA A*3002	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.460873	1.822112	-2.638761	28898.359817
HLA B*7301	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.283005	1.644220	-2.638785	19186.927394
HLA B*3501	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-2.529761	-0.109105	-2.638866	338.657725
HLA B*5801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.284030	1.645104	-2.638926	19232.237239
HLA A*0212	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.402423	1.762988	-2.639435	25259.381157
HLA B*0801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.173573	1.534036	-2.639537	14913.290208
HLA A*6801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.654572	1.014988	-2.639584	4514.110981
HLA B*1509	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.432856	1.793234	-2.639621	27092.905711
HLA A*0301	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.345800	1.706161	-2.639639	22171.757391
HLA A*2501	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.386613	1.746933	-2.639680	24356.395737
HLA A*0219	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.386723	1.746933	-2.639791	24362.589498
HLA A*0202	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-3.666559	1.026649	-2.639911	4640.441528
HLA A*2501	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.462158	1.822112	-2.640046	28984.002769
HLA A*0101	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.391204	1.751011	-2.640193	24615.230984
HLA B*5701	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.239305	1.598716	-2.640589	17350.221002
HLA A*0101	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.285698	1.645104	-2.640594	19306.250724
HLA A*2301	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.460589	1.819741	-2.640848	28879.449239
HLA B*0803	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.450056	1.809179	-2.640877	28187.474431
HLA A*0201	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.393055	1.751118	-2.641937	24720.389518
HLA B*1501	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.371586	1.729555	-2.642031	23528.038149
HLA B*2705	1:521-529	9	SQASVDSPR	0.518283	0.661153	-3.821498	1.179436	-2.642062	6629.769703
HLA A*2301	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.442009	1.799748	-2.642261	27670.001274
HLA A*2403	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.336926	1.694587	-2.642339	21723.315659
HLA B*1502	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.442162	1.799748	-2.642414	27679.732941
HLA A*2601	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.251633	1.609050	-2.642583	17849.775525
HLA B*1509	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.360675	1.718039	-2.642635	22944.294444
HLA A*0301	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.365895	1.723131	-2.642764	23221.766991
HLA A*0211	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-3.571969	0.929186	-2.642783	3732.235492
HLA A*2301	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.471742	1.828833	-2.642909	29630.700027
HLA B*5301	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.227955	1.584939	-2.643016	16902.644175
HLA A*2602	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.603240	1.960098	-2.643142	40108.852571
HLA B*4601	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.395619	1.752221	-2.643398	24866.725357
HLA A*0211	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.484401	1.840969	-2.643432	30507.100800
HLA B*5801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.053482	1.409864	-2.643618	11310.502310
HLA B*4001	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.242395	1.598716	-2.643678	17474.090630
HLA B*0702	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.130907	1.487180	-2.643727	13517.825053
HLA B*4601	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.108756	1.465019	-2.643737	12845.643852
HLA A*0206	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.452988	1.809179	-2.643810	28378.427226
HLA A*1101	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.463660	1.819741	-2.643919	29084.371507
HLA A*0212	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.182924	1.538857	-2.644068	15237.875451
HLA A*0250	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.242787	1.598716	-2.644071	17489.884757
HLA A*2301	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.466265	1.822112	-2.644153	29259.389635
HLA A*2603	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.395193	1.751011	-2.644183	24842.388027
HLA A*0219	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.437423	1.793234	-2.644189	27379.340598
HLA B*1517	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.453376	1.809179	-2.644197	28403.770019
HLA A*0201	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.367368	1.723131	-2.644237	23300.668978
HLA B*1502	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.453341	1.809098	-2.644243	28401.465194
HLA B*4402	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.282585	1.638299	-2.644286	19168.356339

HLA A*0250	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.566419	1.922093	-2.644326	36848.440211
HLA B*7301	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.466474	1.822112	-2.644362	29273.480842
HLA B*3501	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.396681	1.752221	-2.644460	24927.605615
HLA A*2902	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.453656	1.809179	-2.644477	28422.061595
HLA A*0212	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.437811	1.793234	-2.644576	27403.791177
HLA B*4601	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.274181	1.629324	-2.644857	18800.992079
HLA A*2301	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.454304	1.809179	-2.645125	28464.531109
HLA B*0702	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.438459	1.793234	-2.645225	27444.739146
HLA B*5701	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.397446	1.752221	-2.645226	24971.607325
HLA A*6802	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.110316	1.465019	-2.645297	12891.870519
HLA B*4501	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-3.518448	0.873123	-2.645325	3299.497246
HLA A*0212	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.100378	1.454961	-2.645417	12600.205071
HLA B*1503	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-3.343270	0.697848	-2.645422	2204.297298
HLA B*5301	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.496555	1.851066	-2.645489	31372.911395
HLA A*1101	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.264407	1.618772	-2.645635	18382.598801
HLA A*0216	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.398189	1.752221	-2.645968	25014.333422
HLA A*3101	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.296341	1.650328	-2.646013	19785.230263
HLA B*1502	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.568541	1.922093	-2.646448	37028.890030
HLA B*0801	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.931140	1.284672	-2.646468	8533.742020
HLA B*1801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.295394	1.648439	-2.646956	19742.141782
HLA A*3101	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.201720	1.554751	-2.646969	15911.836203
HLA B*3901	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.399190	1.752221	-2.646969	25072.048254
HLA B*3501	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.276659	1.629324	-2.647335	18908.604286
HLA B*1501	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.399702	1.752221	-2.647481	25101.634563
HLA A*2602	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.932775	1.284672	-2.648103	8565.934541
HLA A*0216	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.441450	1.793234	-2.648216	27634.397589
HLA B*1501	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.277583	1.629324	-2.648259	18948.848379
HLA B*3901	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.174264	1.525910	-2.648354	14937.028780
HLA A*6901	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.297041	1.648439	-2.648603	19817.152687
HLA A*3101	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.371804	1.723131	-2.648673	23539.878547
HLA B*4801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.399871	1.751118	-2.648753	25111.413856
HLA A*6801	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.490157	1.840969	-2.649188	30914.140421
HLA A*0301	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.367347	1.718039	-2.649308	23299.534520
HLA A*0101	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.396246	1.746933	-2.649313	24902.669813
HLA B*4601	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.379118	1.729555	-2.649564	23939.670280
HLA A*2501	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.449325	1.799748	-2.649577	28140.089568
HLA B*5301	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.571889	1.922093	-2.649796	37315.452299
HLA A*0202	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.645842	0.995952	-2.649890	4424.269217
HLA A*3002	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-3.650992	1.001026	-2.649965	4477.046623
HLA B*3901	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.356251	1.706161	-2.650089	22711.751466
HLA B*1502	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.509576	1.859413	-2.650162	32327.764136
HLA B*4001	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.401337	1.751118	-2.650219	25196.327478
HLA A*2301	1:144-152	9	IMISATNAV	0.995514	0.289158	-3.934960	1.284672	-2.650288	8609.140041
HLA B*1801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.184325	1.534036	-2.650289	15287.086133
HLA A*3001	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.267264	1.616917	-2.650346	18503.925985
HLA B*5701	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.344964	1.694587	-2.650377	22129.097441
HLA A*2403	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.235417	1.584939	-2.650478	17195.571464
HLA A*2602	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.228096	1.577554	-2.650541	16908.131552
HLA B*4601	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.283266	1.632662	-2.650605	19198.452560
HLA A*0201	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.397665	1.746933	-2.650732	24984.174194
HLA B*0801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.061122	1.409864	-2.651258	11511.248198
HLA B*4402	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.402423	1.751118	-2.651305	25259.381157
HLA B*5101	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.301689	1.650328	-2.651361	20030.349948
HLA A*2602	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.528759	1.877371	-2.651388	33787.745468
HLA B*4001	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.236356	1.584939	-2.651418	17232.822209
HLA B*0702	1:79-87	9	EAETPAGPL	0.986891	0.274759	-3.913133	1.261650	-2.651483	8187.155832
HLA B*3901	1:145-153	9	MISATNAVK	0.938735	0.280828	-3.871402	1.219563	-2.651838	7437.063747
HLA B*0801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.370035	1.718039	-2.651996	23444.180455
HLA A*1101	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.403092	1.751011	-2.652082	25298.356574
HLA A*2902	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.343791	1.691666	-2.652125	22069.439735
HLA A*0101	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.381726	1.729555	-2.652172	24083.859943
HLA A*2402	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.461371	1.809179	-2.652192	28931.522258
HLA A*2603	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.370674	1.718039	-2.652635	23478.703722
HLA A*3001	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.297053	1.644220	-2.652833	19817.688737
HLA B*4001	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.371012	1.718039	-2.652973	23497.001323

HLA B*5801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.344752	1.691666	-2.653086	22118.325627
HLA B*3901	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.207946	1.554751	-2.653195	16141.594565
HLA B*5101	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.338453	1.685171	-2.653282	21799.838598
HLA B*1517	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.272151	1.618772	-2.653379	18713.318590
HLA B*1502	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.416637	1.762988	-2.653649	26099.794663
HLA A*0203	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.231312	1.577554	-2.653758	17033.820371
HLA A*6802	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-3.680863	1.026649	-2.654214	4795.821048
HLA B*4601	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.263448	1.609050	-2.654399	18342.068836
HLA B*2705	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.360618	1.706161	-2.654457	22941.315612
HLA B*7301	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.614621	1.960098	-2.654523	41173.818264
HLA A*3002	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.239582	1.585042	-2.654540	17361.300345
HLA A*2603	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.339802	1.685171	-2.654631	21867.638336
HLA A*2601	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.384238	1.729555	-2.654683	24223.544556
HLA B*7301	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.597547	1.942822	-2.654725	39586.530081
HLA B*1517	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.448073	1.793234	-2.654839	28059.065310
HLA A*2603	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.464285	1.809179	-2.655106	29126.254933
HLA A*3101	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-3.775618	1.120342	-2.655276	5965.099600
HLA A*3001	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.242319	1.586804	-2.655515	17471.065839
HLA B*0801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.350109	1.694587	-2.655522	22392.834651
HLA B*7301	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.533371	1.877371	-2.656000	34148.470217
HLA B*4601	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.190100	1.534036	-2.656064	15491.723846
HLA A*2501	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.521272	0.865145	-2.656126	3321.022754
HLA B*3501	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.385802	1.729555	-2.656248	24310.979070
HLA A*0212	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.182318	1.525910	-2.656408	15216.622001
HLA A*0301	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.275210	1.618772	-2.656438	18845.594444
HLA B*1501	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.379616	1.723131	-2.656485	23967.142355
HLA B*5701	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.066865	1.409864	-2.657001	11664.457883
HLA A*6801	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.617142	1.960098	-2.657044	41413.519537
HLA A*0301	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.342259	1.685171	-2.657088	21991.732481
HLA B*1503	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.247230	1.589799	-2.657431	17669.726364
HLA A*6802	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.408679	1.751118	-2.657562	25625.915213
HLA A*2402	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.479834	1.822112	-2.657721	30187.944174
HLA A*0212	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.408959	1.751118	-2.657841	25642.417895
HLA B*0801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.409037	1.751118	-2.657919	25646.996150
HLA A*3201	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.680990	1.022974	-2.658016	4797.222275
HLA B*3501	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-3.928475	1.270418	-2.658057	8481.549357
HLA B*4601	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.409448	1.751118	-2.658330	25671.288444
HLA B*4402	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.405501	1.746933	-2.658568	25439.029075
HLA A*6901	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.654741	0.995952	-2.658789	4515.869624
HLA B*5801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.277578	1.618772	-2.658806	18948.643357
HLA B*5101	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.468018	1.809179	-2.658839	29377.712618
HLA B*3901	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.249760	1.590840	-2.658920	17772.978657
HLA A*0206	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-3.763339	1.104337	-2.659002	5798.815497
HLA A*0212	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.388561	1.729555	-2.659006	24465.874566
HLA B*3801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.344212	1.685171	-2.659041	22090.821473
HLA A*3002	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.114456	1.454961	-2.659495	13015.346290
HLA A*0219	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.462320	1.802719	-2.659601	28994.824005
HLA B*1509	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.268744	1.609050	-2.659694	18567.099217
HLA B*3501	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.193737	1.534036	-2.659701	15622.004173
HLA A*8001	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.411922	1.752221	-2.659701	25817.945173
HLA B*5101	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-3.645104	0.985326	-2.659778	4416.760068
HLA B*3901	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.410803	1.751011	-2.659793	25751.546724
HLA A*0216	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.462527	1.802719	-2.659808	29008.630864
HLA A*0101	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.382981	1.723131	-2.659850	24153.535938
HLA A*0211	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.054713	1.394783	-2.659930	11342.610606
HLA A*2602	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.383274	1.723131	-2.660143	24169.874956
HLA B*0801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.412695	1.752221	-2.660474	25863.938252
HLA A*2501	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.310866	1.650328	-2.660538	20458.115458
HLA B*1509	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.390121	1.729555	-2.660566	24553.918097
HLA B*5701	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.345854	1.685171	-2.660683	22174.516338
HLA B*5801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.322120	1.661000	-2.661120	20995.182711
HLA B*4501	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.621296	1.960098	-2.661198	41811.527139
HLA A*0201	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.246229	1.584939	-2.661290	17629.051375
HLA B*3901	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.780091	1.118640	-2.661451	6026.860219
HLA A*0211	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.534781	0.873256	-2.661525	3425.952915

HLA A*2602	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.216602	1.554751	-2.661851	16466.524229
HLA A*6901	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.380030	1.718039	-2.661990	23989.973309
HLA A*2602	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.247044	1.584939	-2.662106	17662.176267
HLA A*2403	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.026853	1.364704	-2.662149	10637.824711
HLA B*7301	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.295366	1.632662	-2.662704	19740.860190
HLA A*6901	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.738519	1.075727	-2.662792	5476.704783
HLA A*2601	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.685863	1.022974	-2.662889	4851.350733
HLA B*1501	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-2.930522	0.267585	-2.662937	852.161759
HLA A*2602	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.514077	1.851066	-2.663011	32664.595319
HLA A*3002	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.150191	1.487180	-2.663012	14131.601899
HLA B*5701	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.392668	1.729555	-2.663113	24698.333160
HLA B*1503	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.386373	1.723131	-2.663242	24342.959374
HLA A*0212	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.248964	1.585464	-2.663499	17740.413730
HLA A*0212	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.853574	1.190001	-2.663572	7137.951815
HLA B*1503	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-3.777859	1.113773	-2.664086	5995.965264
HLA A*3002	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.202975	1.538857	-2.664118	15957.870063
HLA A*0203	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.416395	1.752221	-2.664174	26085.255424
HLA A*0201	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.393765	1.729555	-2.664210	24760.810368
HLA B*4601	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.314557	1.650328	-2.664229	20632.728631
HLA B*0801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.356161	1.691666	-2.664495	22707.082960
HLA B*3801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.300281	1.635751	-2.664530	19965.546182
HLA A*3002	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.541992	1.877371	-2.664621	34833.050820
HLA A*6901	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.370848	1.706161	-2.664687	23488.104876
HLA B*5701	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.415836	1.751118	-2.664718	26051.690872
HLA A*2501	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.473967	1.809179	-2.664788	29782.892514
HLA B*4402	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.356587	1.691666	-2.664921	22729.328396
HLA A*0101	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.383054	1.718039	-2.665014	24157.586984
HLA B*4002	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.487197	1.822112	-2.665084	30704.131980
HLA A*0203	1:412-420	9	AGDEITVNV	1.300588	0.029163	-3.994867	1.329751	-2.665116	9882.502684
HLA B*4501	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.587299	1.922093	-2.665206	38663.305599
HLA B*4601	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.741729	1.075727	-2.666001	5517.327044
HLA B*5401	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.327178	1.661000	-2.666178	21241.153610
HLA A*8001	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.413136	1.746933	-2.666204	25890.256789
HLA A*6802	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.429329	1.762988	-2.666341	26873.795535
HLA A*2501	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.469477	1.802719	-2.666758	29476.574224
HLA B*1502	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.486518	1.819741	-2.666777	30656.164867
HLA A*0301	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.358537	1.691666	-2.666871	22831.617285
HLA A*1101	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.476276	1.809179	-2.667098	29941.697466
HLA B*4801	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.397007	1.729555	-2.667453	24946.357591
HLA A*3101	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.132481	1.465019	-2.667462	13566.911015
HLA A*0201	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.318076	1.650328	-2.667748	20800.615913
HLA B*3801	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.489948	1.822112	-2.667836	30899.259459
HLA B*5101	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.313170	1.645104	-2.668067	20566.977363
HLA A*0206	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.533247	1.865170	-2.668077	34138.680430
HLA B*4801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.386376	1.718039	-2.668336	24343.091067
HLA B*1517	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.468096	1.799748	-2.668347	29382.957782
HLA A*0250	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.545730	1.877371	-2.668359	35134.157517
HLA B*1501	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.419623	1.751118	-2.668505	26279.874447
HLA A*0301	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.267247	1.598716	-2.668531	18503.225269
HLA A*0250	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.528137	1.859413	-2.668723	33739.341364
HLA B*1509	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.203003	1.534036	-2.668967	15958.906060
HLA A*2402	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.223815	1.554751	-2.669063	16742.289854
HLA A*2601	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.529218	0.860149	-2.669069	3382.344266
HLA A*3101	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.387214	1.718039	-2.669175	24390.151049
HLA A*0101	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.375357	1.706161	-2.669195	23733.218583
HLA B*5301	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.546608	1.877371	-2.669237	35205.316370
HLA A*0203	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.254422	1.585042	-2.669380	17964.767362
HLA A*0211	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.534572	1.865170	-2.669402	34243.002675
HLA B*1517	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.399126	1.729555	-2.669572	25068.386322
HLA B*3501	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.469341	1.799748	-2.669593	29467.326705
HLA B*3501	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.420702	1.751011	-2.669691	26345.212119
HLA A*3201	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.081591	1.411765	-2.669826	12066.772680
HLA B*0803	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.260718	1.590840	-2.669878	18227.126908
HLA A*6901	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.331233	1.661000	-2.670234	21440.421096
HLA A*1101	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.433629	1.762988	-2.670641	27141.170054

HLA B*5701	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.331936	1.661000	-2.670936	21475.130260
HLA A*2402	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.536120	1.865170	-2.670950	34365.300858
HLA B*1509	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.423267	1.752221	-2.671047	26501.309693
HLA A*3301	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.422180	1.751011	-2.671169	26435.012842
HLA B*0702	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.422400	1.751118	-2.671283	26448.459246
HLA A*0212	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.362965	1.691666	-2.671300	23065.637120
HLA B*4403	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.332349	1.661000	-2.671350	21495.587339
HLA A*2402	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.471310	1.799748	-2.671561	29601.219723
HLA A*6802	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-2.944506	0.272858	-2.671648	880.047626
HLA B*3901	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.471514	1.799748	-2.671766	29615.155122
HLA A*3002	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.270807	1.598716	-2.672091	18655.500542
HLA A*3002	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.363771	1.691666	-2.672105	23108.477266
HLA A*2602	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.419250	1.746933	-2.672317	26257.278944
HLA B*4402	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.395485	1.723131	-2.672354	24859.058544
HLA A*0216	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.564681	0.892112	-2.672569	3670.125676
HLA B*5301	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.258237	1.585464	-2.672773	18123.295064
HLA A*0211	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.581907	0.909118	-2.672789	3818.628065
HLA A*0212	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.395950	1.723131	-2.672819	24885.700791
HLA A*3201	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.482033	1.809179	-2.672854	30341.193218
HLA A*2603	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.667250	0.994371	-2.672879	4647.828057
HLA B*0702	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.425187	1.752221	-2.672966	26618.701524
HLA A*6901	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.570649	0.897363	-2.673286	3720.905393
HLA A*6801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.203417	1.529572	-2.673845	15974.108417
HLA B*5801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.052063	1.378166	-2.673897	11273.604733
HLA B*2705	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.420920	1.746933	-2.673988	26358.470249
HLA B*1501	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.365698	1.691666	-2.674032	23211.216705
HLA B*4001	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.359277	1.685171	-2.674105	22870.558159
HLA B*0802	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.365858	1.691666	-2.674192	23219.757043
HLA A*6901	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.368816	1.694587	-2.674229	23378.447791
HLA B*4403	1:202-210	9	LGCVLYEVL	1.630459	0.329639	-4.634716	1.960098	-2.674619	43123.727047
HLA B*3501	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.260100	1.585464	-2.674636	18201.211777
HLA B*1503	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-3.475072	0.799991	-2.675080	2985.874694
HLA A*8001	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.468655	1.793234	-2.675420	29420.814281
HLA B*4403	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-3.473056	0.797462	-2.675594	2972.047320
HLA A*2602	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.535030	1.859413	-2.675617	34279.145651
HLA B*1503	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.393826	1.718039	-2.675787	24764.293397
HLA B*1501	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.116025	1.440103	-2.675922	13062.466316
HLA A*2601	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.394047	1.718039	-2.676007	24776.889975
HLA B*1503	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.320372	1.644220	-2.676151	20910.847828
HLA A*2603	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.261820	1.585464	-2.676356	18273.432186
HLA A*0101	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.361570	1.685171	-2.676399	22991.635256
HLA B*3901	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.020401	1.343697	-2.676705	10480.961941
HLA A*8001	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.368508	1.691666	-2.676842	23361.885461
HLA B*0702	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.406584	1.729555	-2.677029	25502.552147
HLA B*2705	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.262074	1.585042	-2.677032	18284.111888
HLA A*8001	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.362646	1.685171	-2.677475	23048.672936
HLA B*7301	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.599568	1.922093	-2.677475	39771.135703
HLA B*5401	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.550863	1.873374	-2.677489	35551.928904
HLA B*4801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.383660	1.706161	-2.677498	24191.328512
HLA A*3001	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.081060	1.403484	-2.677576	12052.028437
HLA A*2301	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.262704	1.585042	-2.677662	18310.640339
HLA A*0212	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.424618	1.746933	-2.677686	26583.875304
HLA B*0801	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.407610	1.729555	-2.678056	25562.914604
HLA A*0202	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.519310	1.840969	-2.678340	33060.512768
HLA A*2501	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.339673	1.661000	-2.678673	21861.132721
HLA A*3201	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.256454	1.577554	-2.678900	18049.031468
HLA B*1501	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.385180	1.706161	-2.679019	24276.151320
HLA B*4601	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.385253	1.706161	-2.679091	24280.222931
HLA A*1101	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.329457	1.650328	-2.679129	21352.911502
HLA A*0250	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.442148	1.762988	-2.679160	27678.834490
HLA A*0201	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.312202	1.632662	-2.679541	20521.187205
HLA A*3101	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.371482	1.691666	-2.679816	23522.438316
HLA B*0801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.264914	1.585042	-2.679872	18404.092086
HLA A*3002	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.266787	1.586804	-2.679982	18483.615989
HLA A*6802	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.432296	1.752221	-2.680076	27058.044590

HLA A*6802	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.412904	0.732827	-2.680077	2587.642079
HLA B*3901	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.482975	1.802719	-2.680255	30407.085804
HLA B*4001	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.309827	1.629324	-2.680503	20409.255046
HLA B*4403	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.502638	1.822112	-2.680525	31815.418448
HLA A*0250	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-3.937704	1.257069	-2.680635	8663.711279
HLA B*4801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.428154	1.746933	-2.681222	26801.201633
HLA B*3501	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.373002	1.691666	-2.681337	23604.915774
HLA A*0206	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-3.586028	0.904590	-2.681439	3855.035278
HLA A*3002	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.548514	1.866969	-2.681545	35360.116220
HLA B*0702	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.089241	1.407681	-2.681561	12281.207086
HLA B*1517	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.326899	1.645104	-2.681795	21227.483449
HLA B*1801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.280701	1.598716	-2.681984	19085.370153
HLA B*2705	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.327136	1.645104	-2.682032	21239.085290
HLA A*2501	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.445045	1.762988	-2.682057	27864.080347
HLA B*5101	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.475374	1.793234	-2.682140	29879.561224
HLA B*5701	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.405284	1.723131	-2.682153	25426.370971
HLA A*6901	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.273081	1.590840	-2.682241	18753.451407
HLA A*3101	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.114188	1.431809	-2.682378	13007.321844
HLA A*0201	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.400513	1.718039	-2.682473	25148.528297
HLA A*2301	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.374222	1.691666	-2.682556	23671.285192
HLA B*5101	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.273441	1.590840	-2.682601	18768.980309
HLA A*0219	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-3.814925	1.132158	-2.682766	6530.171446
HLA B*5401	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.560165	1.877371	-2.682794	36321.583988
HLA A*2902	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.312137	1.629324	-2.682812	20518.078955
HLA A*2603	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.548056	1.865170	-2.682886	35322.833499
HLA A*0101	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.377535	1.694587	-2.682948	23852.538840
HLA A*3001	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.113436	1.430389	-2.683047	12984.823510
HLA A*3002	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.548399	1.865170	-2.683229	35350.744042
HLA A*0212	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.435480	1.752221	-2.683259	27257.119633
HLA B*4501	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.542713	1.859413	-2.683299	34890.950872
HLA A*0203	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.375002	1.691666	-2.683336	23713.838993
HLA B*7301	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.548511	1.865170	-2.683341	35359.924927
HLA A*0301	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.215935	1.532461	-2.683474	16441.244346
HLA B*2705	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.334182	1.650328	-2.683854	21586.484204
HLA B*1509	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.390060	1.706161	-2.683898	24550.464657
HLA A*2603	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.541226	1.857104	-2.684122	34771.672561
HLA B*4002	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.551119	1.866969	-2.684150	35572.899274
HLA A*3101	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.252528	1.568231	-2.684297	17886.604850
HLA B*4002	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.606475	1.922093	-2.684382	40408.755819
HLA A*0211	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.435581	1.751011	-2.684570	27263.461064
HLA B*4403	1:222-230	9	VSVAYQHVR	1.263150	0.658943	-4.606720	1.922093	-2.684627	40431.497332
HLA B*4402	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.414210	1.729555	-2.684656	25954.344962
HLA B*5401	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.874738	1.190001	-2.684736	7494.415595
HLA A*0219	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.407892	1.723131	-2.684761	25579.515096
HLA B*4801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.379503	1.694587	-2.684917	23960.919503
HLA A*0301	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.320724	1.635751	-2.684973	20927.823520
HLA A*0301	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.314481	1.629324	-2.685157	20629.157075
HLA A*0219	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.436319	1.751118	-2.685201	27309.813005
HLA B*1801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.379924	1.694587	-2.685337	23984.133781
HLA A*2301	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.026077	1.340547	-2.685531	10618.850333
HLA B*4001	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.380443	1.694587	-2.685856	24012.826012
HLA A*2403	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.438219	1.752221	-2.685999	27429.599078
HLA A*0219	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-3.525933	0.839877	-2.686056	3356.860002
HLA B*7301	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.302985	1.616917	-2.686068	20090.255158
HLA B*3801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.495420	1.809098	-2.686322	31291.041725
HLA A*0203	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.437580	1.751118	-2.686463	27389.266383
HLA A*0216	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.948718	1.262230	-2.686488	8886.246507
HLA A*0201	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.381273	1.694587	-2.686686	24058.726901
HLA B*3901	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-3.836065	1.149326	-2.686739	6855.912239
HLA A*3002	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.486508	1.799748	-2.686760	30655.501488
HLA A*3001	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-2.675786	-0.010996	-2.686782	474.008553
HLA A*2603	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.537887	1.851066	-2.686821	34505.391802
HLA B*4601	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.404972	1.718039	-2.686933	25408.082889
HLA A*0201	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.393295	1.706161	-2.687134	24734.034208
HLA B*5301	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.319798	1.632662	-2.687137	20883.263448

HLA B*1509	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.331687	1.644220	-2.687467	21462.818915
HLA A*0211	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.509592	1.822112	-2.687480	32328.988387
HLA A*2402	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.316885	1.629324	-2.687561	20743.641867
HLA B*4403	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.544731	1.857104	-2.687627	35053.469755
HLA A*1101	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.242857	1.554751	-2.688106	17492.723537
HLA B*4402	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-3.791293	1.103143	-2.688151	6184.341501
HLA B*3501	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.439425	1.751118	-2.688307	27505.829438
HLA B*4403	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.583039	1.894713	-2.688326	38285.944538
HLA A*2601	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.382985	1.694587	-2.688399	24153.797275
HLA A*3002	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.547849	1.859413	-2.688435	35306.021351
HLA B*4402	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.440729	1.752221	-2.688508	27588.539480
HLA B*5401	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.545614	1.857104	-2.688511	35124.845228
HLA A*0219	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.440778	1.752221	-2.688557	27591.673928
HLA A*0203	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.143524	1.454961	-2.688563	13916.292744
HLA A*3201	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.548001	1.859413	-2.688588	35318.438642
HLA B*1517	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.435565	1.746933	-2.688632	27262.428637
HLA B*1517	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.321307	1.632662	-2.688645	20955.920231
HLA B*0801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.175867	1.487180	-2.688687	14992.241403
HLA A*3101	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.318057	1.629324	-2.688733	20799.715700
HLA A*0216	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.383404	1.694587	-2.688817	24177.067625
HLA A*0301	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.327122	1.638299	-2.688823	21238.395895
HLA B*5701	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.380526	1.691666	-2.688860	24017.373178
HLA A*3001	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.278668	1.589799	-2.688870	18996.267773
HLA A*2403	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.407051	1.718039	-2.689012	25530.022161
HLA A*2403	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.243818	1.554751	-2.689067	17531.471570
HLA B*4403	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.556098	1.866969	-2.689129	35983.037494
HLA B*1503	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.441391	1.752221	-2.689170	27630.660366
HLA B*0802	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.383963	1.694587	-2.689376	24208.216944
HLA A*0216	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.176656	1.487180	-2.689476	15019.517924
HLA A*0211	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.577547	0.887960	-2.689587	3780.478007
HLA B*5801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.144656	1.454961	-2.689695	13952.627756
HLA A*0212	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.223979	1.534036	-2.689943	16748.631230
HLA A*0211	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.275123	1.585042	-2.690081	18841.822576
HLA B*3501	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.030729	1.340547	-2.690183	10733.206377
HLA A*0203	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.420065	1.729555	-2.690510	26306.616231
HLA A*0201	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.382384	1.691666	-2.690718	24120.369071
HLA A*6801	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.585436	1.894713	-2.690722	38497.793671
HLA A*2402	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.268511	1.577554	-2.690957	18557.157731
HLA A*2602	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.284387	0.593391	-2.690996	1924.807824
HLA B*5301	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.192440	1.501143	-2.691296	15575.422412
HLA A*2902	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.442679	1.751118	-2.691561	27712.696297
HLA A*0216	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.442815	1.751118	-2.691697	27721.393173
HLA B*1501	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.409965	1.718039	-2.691925	25701.859974
HLA A*0201	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.767658	1.075727	-2.691930	5856.762921
HLA B*7301	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.586679	1.894713	-2.691965	38608.125665
HLA A*3002	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.386890	1.694587	-2.692303	24371.949018
HLA A*0211	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.343007	1.650328	-2.692679	22029.598404
HLA A*6801	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.559688	1.866969	-2.692719	36281.717248
HLA B*0802	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.422306	1.729555	-2.692752	26442.736536
HLA B*0801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.322308	1.629324	-2.692983	21004.271206
HLA A*0301	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.343371	1.650328	-2.693043	22048.078693
HLA B*5701	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.133233	1.440103	-2.693129	13590.417912
HLA B*4801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.378359	1.685171	-2.693188	23897.874767
HLA A*0216	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.422788	1.729555	-2.693234	26472.078520
HLA A*6802	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.422823	1.729555	-2.693269	26474.226772
HLA B*1502	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.037590	1.343697	-2.693893	10904.103779
HLA A*2501	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.312682	1.618772	-2.693910	20543.847246
HLA B*5701	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.400148	1.706161	-2.693987	25127.449269
HLA A*0206	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-3.728811	1.034768	-2.694043	5355.638554
HLA A*0201	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.228114	1.534036	-2.694078	16908.863336
HLA B*0803	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.446445	1.752221	-2.694224	27954.067327
HLA A*8001	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.445479	1.751118	-2.694362	27891.981500
HLA B*5401	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.279834	1.584939	-2.694895	19047.309003
HLA B*4601	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.386601	1.691666	-2.694935	24355.736919
HLA A*3001	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.285787	1.590840	-2.694947	19310.220030

HLA A*0206	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.838217	1.143250	-2.694967	6889.970745
HLA A*2402	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.504184	1.809098	-2.695086	31928.873832
HLA A*1101	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.380359	1.685171	-2.695187	24008.149825
HLA A*2402	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.284995	1.589799	-2.695197	19275.047010
HLA A*2601	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.356338	1.661000	-2.695338	22716.298039
HLA A*0216	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.418705	1.723131	-2.695574	26224.344256
HLA B*4601	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.280593	1.584939	-2.695654	19080.621256
HLA B*3901	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.126137	1.430389	-2.695748	13370.183475
HLA B*4601	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.390372	1.694587	-2.695785	24568.135447
HLA A*1101	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.325158	1.629324	-2.695833	21142.558579
HLA A*0206	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.442874	1.746933	-2.695941	27725.142668
HLA B*1517	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.184983	1.488986	-2.695996	15310.260084
HLA B*5401	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.090839	1.394783	-2.696056	12326.469468
HLA B*5401	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.561325	1.865170	-2.696155	36418.782709
HLA B*5701	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.414497	1.718039	-2.696457	25971.480652
HLA A*2403	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.281979	1.585464	-2.696514	19141.620742
HLA B*1801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.447925	1.751011	-2.696915	28049.503764
HLA A*2601	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.347257	1.650328	-2.696929	22246.249233
HLA B*3501	1:578-586	9	LRALGWTGM	0.993924	0.288236	-3.979111	1.282160	-2.696951	9530.403637
HLA A*0212	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.092145	1.394783	-2.697362	12363.602053
HLA B*1801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.460394	1.762988	-2.697406	28866.484677
HLA A*0211	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.526621	1.828833	-2.697789	33621.817194
HLA B*1801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.506970	1.809098	-2.697873	32134.392201
HLA A*3301	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.571449	1.873374	-2.698075	37277.721238
HLA A*2501	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.450324	1.752221	-2.698103	28204.863779
HLA B*0801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.187121	1.488986	-2.698134	15385.818314
HLA A*1101	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.336983	1.638299	-2.698683	21726.136340
HLA B*1801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.276255	1.577554	-2.698701	18891.017995
HLA B*4801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.288614	1.589799	-2.698815	19436.302642
HLA B*4001	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-3.821555	1.122659	-2.698896	6630.630550
HLA A*0301	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.343195	1.644220	-2.698974	22039.134683
HLA A*2403	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-3.700138	1.001026	-2.699112	5013.466812
HLA A*2601	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.405414	1.706161	-2.699252	25433.937559
HLA A*0211	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.451496	1.752221	-2.699276	28281.106651
HLA B*3801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.499337	1.799748	-2.699588	31574.509539
HLA A*6901	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.391394	1.691666	-2.699728	24626.019767
HLA A*0101	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.391476	1.691666	-2.699811	24630.683049
HLA B*4001	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.286628	1.586804	-2.699824	19347.655151
HLA B*3901	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.111603	1.411765	-2.699839	12930.146716
HLA A*0211	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.187111	1.487180	-2.699932	15385.485376
HLA B*7301	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.570961	1.870848	-2.700113	37235.797815
HLA B*3901	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.329532	1.629324	-2.700208	21356.608362
HLA A*0219	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.392127	1.691666	-2.700461	24667.620765
HLA B*5101	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.423798	1.723131	-2.700667	26533.730936
HLA B*5401	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.100030	1.398961	-2.701069	12590.120584
HLA B*3801	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.494311	1.793234	-2.701077	31211.242986
HLA A*2902	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.286022	1.584939	-2.701083	19320.669471
HLA A*2601	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.255859	1.554751	-2.701108	18024.344622
HLA B*4001	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.407566	1.706161	-2.701404	25560.287181
HLA A*2301	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.269653	1.568231	-2.701423	18606.012520
HLA A*2403	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.131997	1.430389	-2.701608	13551.799967
HLA A*6901	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.111669	1.409864	-2.701805	12932.105483
HLA A*0201	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.667184	0.965301	-2.701883	4647.124072
HLA B*1517	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.080228	1.378166	-2.702063	12028.969675
HLA A*8001	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.300995	1.598716	-2.702279	19998.408660
HLA B*4801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.236403	1.534036	-2.702367	17234.686863
HLA A*2403	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.347680	1.645104	-2.702576	22267.922738
HLA B*0803	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.425760	1.723131	-2.702629	26653.861756
HLA B*0802	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.454887	1.752221	-2.702666	28502.746248
HLA A*2501	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.081140	1.378166	-2.702974	12054.245446
HLA A*0250	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.595097	0.892112	-2.702985	3936.383193
HLA B*0803	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.454107	1.751118	-2.702989	28451.598891
HLA B*3501	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.607963	0.904921	-2.703042	4054.741282
HLA A*0202	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.612216	0.909118	-2.703097	4094.639924
HLA B*3501	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.421150	1.718039	-2.703111	26372.448401

HLA A*0250	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-3.825911	1.122659	-2.703252	6697.469977
HLA A*0216	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.394923	1.691666	-2.703257	24826.937458
HLA B*3901	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.421470	1.718039	-2.703431	26391.858936
HLA B*7301	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.554625	1.851066	-2.703559	35861.189784
HLA B*3501	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.265692	1.561867	-2.703826	18437.077326
HLA B*4402	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.389226	1.685171	-2.704054	24503.360474
HLA A*8001	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.433762	1.729555	-2.704208	27149.540696
HLA B*2705	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.336999	1.632662	-2.704337	21726.959107
HLA A*2601	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.396133	1.691666	-2.704467	24896.204060
HLA B*4501	1:579-587	9	RALGWTGML	1.320466	0.574247	-4.599458	1.894713	-2.704744	39761.024590
HLA A*0301	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.365778	1.661000	-2.704778	23215.486481
HLA B*5801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.353276	1.648439	-2.704838	22556.731969
HLA B*4601	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.135239	1.430389	-2.704850	13653.351525
HLA B*1503	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.802369	1.097502	-2.704867	6344.084161
HLA A*2403	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.434458	1.729555	-2.704903	27193.050821
HLA A*0250	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.159867	1.454961	-2.704906	14449.957631
HLA B*0702	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.334560	1.629324	-2.705236	21605.294053
HLA A*2403	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.456355	1.751118	-2.705237	28599.282295
HLA B*5401	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.546268	1.840969	-2.705298	35177.710954
HLA B*4002	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.468293	1.762988	-2.705305	29396.313334
HLA A*2403	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.428441	1.723131	-2.705310	26818.896438
HLA A*8001	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.423509	1.718039	-2.705470	26516.080830
HLA B*1501	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.699922	0.994371	-2.705551	5010.972181
HLA A*0216	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.452793	1.746933	-2.705861	28365.687582
HLA A*2301	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.887115	1.181170	-2.705945	7711.073803
HLA A*0301	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.069125	1.363134	-2.705991	11725.321617
HLA A*0219	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.274498	1.568231	-2.706267	18814.728118
HLA B*1517	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.458723	1.752221	-2.706503	28755.664997
HLA A*2402	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.457520	1.751011	-2.706510	28676.125944
HLA B*5101	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.506303	1.799748	-2.706555	32085.058555
HLA B*4801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.232616	1.525910	-2.706706	17085.041077
HLA A*0203	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.245588	1.538857	-2.706731	17603.034250
HLA B*7301	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.566262	1.859413	-2.706848	36835.086451
HLA B*1503	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.284422	1.577554	-2.706868	19249.620484
HLA B*4001	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.316425	1.609050	-2.707375	20721.658247
HLA B*1509	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.510130	1.802719	-2.707411	32369.064446
HLA A*2902	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.430595	1.723131	-2.707464	26952.272008
HLA B*5101	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.316789	1.609050	-2.707739	20739.041324
HLA B*3801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.454774	1.746933	-2.707841	28495.345768
HLA A*3101	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.237538	1.529572	-2.707966	17279.779581
HLA A*3002	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.536884	1.828833	-2.708051	34425.775558
HLA B*3801	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.459245	1.751118	-2.708127	28790.221164
HLA B*5801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.341113	1.632662	-2.708451	21933.750309
HLA B*4002	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.579374	1.870848	-2.708526	37964.192712
HLA B*0702	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.209713	1.501143	-2.708570	16207.396149
HLA A*0203	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.426634	1.718039	-2.708595	26707.556098
HLA A*0250	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.573834	1.865170	-2.708664	37482.977621
HLA B*4002	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.651616	1.942822	-2.708794	44834.892637
HLA B*5801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.353032	1.644220	-2.708812	22544.044479
HLA B*5401	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.518057	1.809098	-2.708960	32965.321048
HLA A*0202	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.432184	1.723131	-2.709053	27051.019213
HLA A*2501	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.460333	1.751118	-2.709215	28862.424686
HLA A*0206	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.512498	1.802719	-2.709779	32546.060556
HLA A*2603	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.538836	1.828833	-2.710003	34580.889095
HLA B*5301	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.513058	1.802719	-2.710338	32587.992343
HLA B*1501	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.288167	1.577554	-2.710613	19416.334740
HLA A*6801	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.278901	1.568231	-2.710670	19006.444501
HLA A*0250	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.433925	1.723131	-2.710794	27159.677032
HLA A*6901	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.355196	1.644220	-2.710976	22656.650656
HLA A*0219	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.320071	1.609050	-2.711021	20896.372793
HLA B*1801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.463408	1.752221	-2.711187	29067.540653
HLA A*2402	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.143368	1.431809	-2.711559	13911.324781
HLA B*5701	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.279871	1.568231	-2.711640	19048.957776
HLA A*6901	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.273899	1.561867	-2.712032	18788.790686
HLA A*2602	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.511916	1.799748	-2.712168	32502.424332

HLA B*5401	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.563452	1.851066	-2.712386	36597.524434
HLA A*0212	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.407321	1.694587	-2.712735	25545.910281
HLA A*1101	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.459762	1.746933	-2.712829	28824.506983
HLA B*1801	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.512646	1.799748	-2.712898	32557.154893
HLA B*1517	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-3.708859	0.995952	-2.712908	5115.162472
HLA B*4501	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.655758	1.942822	-2.712936	45264.557193
HLA B*3801	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.442496	1.729555	-2.712941	27701.004800
HLA A*2301	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.515778	1.802719	-2.713059	32792.785572
HLA B*0702	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.363438	1.650328	-2.713110	23090.732052
HLA A*2602	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.573341	0.860149	-2.713192	3744.045671
HLA B*4001	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.298672	1.585464	-2.713207	19891.695301
HLA B*3501	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.178301	1.465019	-2.713282	15076.503505
HLA B*1517	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-3.172134	0.458556	-2.713578	1486.393101
HLA B*0801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.909416	1.195398	-2.714018	8117.385501
HLA A*0212	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.446060	0.732039	-2.714021	2792.930555
HLA B*5401	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.534083	1.819741	-2.714342	34204.492169
HLA A*2301	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.465666	1.751011	-2.714656	29219.053500
HLA B*1517	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.465793	1.751118	-2.714675	29227.590626
HLA A*0206	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.292239	1.577554	-2.714685	19599.225430
HLA B*0702	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.656955	0.942253	-2.714702	4538.941757
HLA A*2301	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.359822	1.645104	-2.714718	22899.280887
HLA A*3101	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.300215	1.585464	-2.714751	19962.522092
HLA B*5301	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.124657	1.409864	-2.714793	13324.692378
HLA A*0216	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-3.847098	1.132158	-2.714940	7032.316867
HLA A*3301	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.582140	1.866969	-2.715171	38206.698664
HLA A*2603	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.524312	1.809098	-2.715214	33443.493601
HLA A*0211	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.508476	1.793234	-2.715242	32246.019319
HLA A*2902	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.462351	1.746933	-2.715418	28996.863241
HLA A*2603	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.224661	1.509182	-2.715478	16774.928242
HLA A*2602	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.028455	1.312789	-2.715666	10677.145931
HLA B*2705	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.439046	1.723131	-2.715915	27481.882507
HLA B*5401	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.361311	1.645104	-2.716208	22977.957285
HLA B*0802	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.306063	1.589799	-2.716265	20233.139598
HLA A*0206	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.516213	1.799748	-2.716465	32825.621988
HLA A*2403	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.352217	1.635751	-2.716465	22501.763785
HLA B*2705	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.271336	1.554751	-2.716584	18678.222310
HLA A*3002	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.509895	1.793234	-2.716661	32351.557876
HLA B*5801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.352604	1.635751	-2.716853	22521.858540
HLA B*2705	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-3.508439	0.791452	-2.716987	3224.326139
HLA B*4801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.301989	1.584939	-2.717051	20044.225084
HLA B*5801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.355464	1.638299	-2.717165	22670.627942
HLA A*0219	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.204535	1.487180	-2.717355	16015.296468
HLA A*6901	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.814863	1.097502	-2.717361	6529.252996
HLA A*0203	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.423690	1.706161	-2.717529	26527.128709
HLA A*0219	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.447093	1.729555	-2.717539	27995.837543
HLA A*0216	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.367982	1.650328	-2.717654	23333.592320
HLA B*5101	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.468756	1.751011	-2.717745	29427.659101
HLA B*0803	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.436406	1.718039	-2.718366	27315.280045
HLA B*3801	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.521152	1.802719	-2.718432	33201.031861
HLA A*0202	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.899717	1.181170	-2.718547	7938.117030
HLA B*0702	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.436673	1.718039	-2.718634	27332.131322
HLA B*1501	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.305622	1.586804	-2.718817	20212.571759
HLA B*1502	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.448595	1.729555	-2.719040	28092.784362
HLA A*8001	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.442221	1.723131	-2.719090	27683.476802
HLA A*0212	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.425333	1.706161	-2.719171	26627.631284
HLA B*4402	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.369499	1.650328	-2.719172	23415.280946
HLA B*4501	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.576341	1.857104	-2.719237	37699.968222
HLA B*1501	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.184677	1.465019	-2.719659	15299.496384
HLA A*0212	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.370040	1.650328	-2.719712	23444.434117
HLA A*0301	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.368210	1.648439	-2.719771	23345.840051
HLA A*0203	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.052472	1.332686	-2.719786	11284.221807
HLA B*0801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.329015	1.609050	-2.719966	21331.205368
HLA A*3001	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.282014	1.561867	-2.720147	19143.174115
HLA A*0216	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.150675	1.430389	-2.720286	14147.359460
HLA A*0202	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.542515	1.822112	-2.720403	34875.098955

HLA A*0301	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.337323	1.616917	-2.720406	21743.185744
HLA A*2501	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.415021	1.694587	-2.720434	26002.831690
HLA A*2602	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.252925	1.532461	-2.720464	17902.965537
HLA A*3002	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.529567	1.809098	-2.720470	33850.683071
HLA A*6801	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.549531	1.828833	-2.720698	35443.043746
HLA A*0301	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.209990	1.488986	-2.721004	16217.745718
HLA A*2403	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.427301	1.706161	-2.721140	26748.621353
HLA A*0219	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.353943	1.632662	-2.721282	22591.414961
HLA B*4001	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.369807	1.648439	-2.721369	23431.881132
HLA A*0101	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.365761	1.644220	-2.721541	23214.607346
HLA B*0803	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.451297	1.729555	-2.721742	28268.104840
HLA B*3501	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.427917	1.706161	-2.721756	26786.561489
HLA B*5701	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.367105	1.645104	-2.722001	23286.555203
HLA B*3501	1:140-148	9	KPANIMISA	1.205138	-0.289626	-3.637609	0.915512	-2.722097	4341.191565
HLA A*2601	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.132208	1.409864	-2.722344	13558.399810
HLA A*2601	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.291179	1.568231	-2.722949	19551.464353
HLA A*3201	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.486008	1.762988	-2.723020	30620.197303
HLA B*1801	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.408508	1.685171	-2.723337	25615.796976
HLA A*0216	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.441389	1.718039	-2.723350	27630.510888
HLA A*0201	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-3.985591	1.262230	-2.723361	9673.667907
HLA B*1502	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.588671	1.865170	-2.723501	38785.650655
HLA B*0802	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.373837	1.650328	-2.723509	23650.292825
HLA A*0212	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.441589	1.718039	-2.723549	27643.219440
HLA A*2601	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.368710	1.645104	-2.723606	23372.757117
HLA A*0203	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.163781	1.440103	-2.723677	14580.781963
HLA A*2403	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.372234	1.648439	-2.723796	23563.194795
HLA B*7301	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.564897	1.840969	-2.723927	36719.490175
HLA A*0250	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.526849	1.802719	-2.724130	33639.465184
HLA B*0801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.430304	1.706161	-2.724143	26934.197780
HLA A*3301	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.581296	1.857104	-2.724192	38132.567527
HLA A*0211	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.527065	1.802719	-2.724346	33656.212043
HLA B*3901	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.454017	1.729555	-2.724463	28445.750532
HLA A*0206	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.517775	1.793234	-2.724541	32943.927346
HLA A*0202	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.553412	1.828833	-2.724580	35761.222766
HLA A*3002	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.213670	1.488986	-2.724684	16355.724261
HLA A*0201	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.739689	1.014988	-2.724701	5491.479603
HLA A*2601	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.357564	1.632662	-2.724902	22780.538668
HLA B*3901	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.311751	1.586804	-2.724947	20499.882940
HLA A*3001	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.915384	1.190001	-2.725382	8229.697334
HLA B*4403	1:419-427	9	NVSTGPEQR	1.203923	0.738899	-4.668293	1.942822	-2.725471	46590.007318
HLA B*0802	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.431671	1.706161	-2.725510	27019.135241
HLA A*1101	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.370634	1.645104	-2.725530	23476.544529
HLA A*0301	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.358243	1.632662	-2.725581	22816.182940
HLA B*4402	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.420173	1.694587	-2.725586	26313.163576
HLA B*1801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.363966	1.638299	-2.725667	23118.855782
HLA A*0206	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.443785	1.718039	-2.725746	27783.399888
HLA A*2601	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.370124	1.644220	-2.725904	23449.000506
HLA B*4601	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.215155	1.488986	-2.726168	16411.741006
HLA B*5801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.215155	1.488986	-2.726168	16411.741006
HLA A*0101	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.335249	1.609050	-2.726199	21639.567707
HLA A*6802	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.432442	1.706161	-2.726281	27067.121736
HLA A*0211	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-3.996610	1.270153	-2.726457	9922.252137
HLA A*0101	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.387525	1.661000	-2.726525	24407.574407
HLA B*4002	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.567521	1.840969	-2.726552	36942.052182
HLA B*5701	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.359437	1.632662	-2.726775	22878.973155
HLA B*4801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.377138	1.650328	-2.726810	23830.741115
HLA B*1502	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.067405	1.340547	-2.726858	11678.980704
HLA A*3201	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.592228	1.865170	-2.727058	39104.631862
HLA A*3002	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.490350	1.762988	-2.727362	30927.857313
HLA A*3201	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.266639	1.538857	-2.727782	18477.317421
HLA A*0301	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.282644	1.554751	-2.727892	19170.948982
HLA B*2705	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.314726	1.586804	-2.727921	20640.766892
HLA B*0803	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.131565	1.403484	-2.728081	13538.316952
HLA B*1502	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.475128	1.746933	-2.728195	29862.593306
HLA B*7301	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.595219	1.866969	-2.728250	39374.866663

HLA B*0802	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.446379	1.718039	-2.728340	27949.833252
HLA B*0702	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.434507	1.706161	-2.728346	27196.140336
HLA A*3201	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.031495	1.303070	-2.728425	10752.152418
HLA A*3002	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.531149	1.802719	-2.728429	33974.153145
HLA B*0702	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.361255	1.632662	-2.728593	22974.974082
HLA B*1502	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.010782	1.282160	-2.728623	10251.380473
HLA A*0203	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.423244	1.694587	-2.728657	26499.876040
HLA B*4501	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.550910	1.822112	-2.728798	35555.775752
HLA B*4001	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.373985	1.645104	-2.728881	23658.354763
HLA B*0802	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.374090	1.645104	-2.728986	23664.114973
HLA A*1101	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.297269	1.568231	-2.729038	19827.554650
HLA A*1101	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.447568	1.718039	-2.729529	28026.448050
HLA A*0202	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.594740	1.865170	-2.729570	39331.435845
HLA A*0201	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.184536	1.454961	-2.729575	15294.531075
HLA B*5301	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.595048	1.865170	-2.729878	39359.319735
HLA B*4801	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.298254	1.568231	-2.730023	19872.549608
HLA B*4001	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.298284	1.568231	-2.730053	19873.947265
HLA A*0206	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-3.874648	1.144551	-2.730098	7492.875083
HLA A*0216	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.366184	1.635751	-2.730433	23237.224277
HLA B*1501	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.366236	1.635751	-2.730485	23239.990079
HLA A*0203	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.033605	1.303070	-2.730535	10804.514326
HLA A*2902	1:585-593	9	GMLDKGADV	0.832496	0.121837	-3.684899	0.954333	-2.730566	4840.602097
HLA A*2301	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.416076	1.685171	-2.730904	26066.070388
HLA B*1502	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.481950	1.751011	-2.730940	30335.448775
HLA B*0702	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.140840	1.409864	-2.730976	13830.581625
HLA A*1101	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.482246	1.751118	-2.731129	30356.133862
HLA A*2601	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.360482	1.629324	-2.731158	22934.118362
HLA A*3201	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.130225	1.398961	-2.731265	13496.634000
HLA B*1501	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.392672	1.661000	-2.731673	24698.600392
HLA A*8001	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.392947	1.661000	-2.731948	24714.238493
HLA B*3901	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.426681	1.694587	-2.732094	26710.445953
HLA B*1509	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-3.429571	0.697387	-2.732184	2688.880190
HLA A*6901	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.368553	1.635751	-2.732801	23364.286903
HLA B*0702	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.266961	1.534036	-2.732925	18491.017050
HLA B*4403	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.604006	1.870848	-2.733158	40179.651914
HLA B*5101	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.462722	1.729555	-2.733168	29021.659268
HLA A*2601	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.144952	1.411765	-2.733187	13962.141751
HLA A*0202	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.319998	1.586804	-2.733194	20892.868628
HLA B*7301	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.606710	1.873374	-2.733336	40430.622422
HLA A*3101	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.394392	1.661000	-2.733392	24796.601726
HLA A*0202	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.526725	1.793234	-2.733490	33629.821320
HLA A*8001	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.384026	1.650328	-2.733699	24211.753224
HLA B*7301	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.205118	1.471168	-2.733949	16036.797851
HLA A*0219	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.428540	1.694587	-2.733953	26824.990795
HLA B*4001	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.323901	1.589799	-2.734102	21081.454338
HLA A*0219	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.877360	1.143250	-2.734110	7539.799515
HLA A*6901	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.319183	1.585042	-2.734141	20853.684667
HLA B*5801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.351211	1.616917	-2.734294	22449.722741
HLA A*2501	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.463942	1.729555	-2.734387	29103.258824
HLA A*2603	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.266963	1.532461	-2.734503	18491.117085
HLA B*4402	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.370470	1.635751	-2.734718	23467.655827
HLA B*2705	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.364070	1.629324	-2.734745	23124.359537
HLA A*6802	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.426869	1.691666	-2.735203	26722.008499
HLA A*2402	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.181275	1.445980	-2.735295	15180.115677
HLA B*4801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.380476	1.645104	-2.735372	24014.644775
HLA A*2603	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.594815	1.859413	-2.735402	39338.245353
HLA B*0803	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.430086	1.694587	-2.735499	26920.650063
HLA A*2501	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.147292	1.411765	-2.735527	14037.576303
HLA A*2601	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.113803	1.378166	-2.735637	12995.786583
HLA A*0219	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.600919	0.865145	-2.735774	3989.508481
HLA A*0201	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.396876	1.661000	-2.735876	24938.801142
HLA A*0212	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.320952	1.585042	-2.735910	20938.808471
HLA A*3001	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.176130	1.440103	-2.736026	15001.328068
HLA B*1517	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.147809	1.411765	-2.736044	14054.293430
HLA B*1509	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.354843	1.618772	-2.736071	22638.272619

HLA A*3101	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.321121	1.584939	-2.736182	20946.965977
HLA B*0802	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.421585	1.685171	-2.736414	26398.855938
HLA A*0250	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.545600	1.809179	-2.736422	35123.705118
HLA B*0801	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.291259	1.554751	-2.736508	19555.060906
HLA A*3002	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.545878	1.809179	-2.736699	35146.134087
HLA A*2402	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-3.737744	1.001026	-2.736718	5466.936145
HLA B*1517	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.786623	1.049687	-2.736935	6118.186160
HLA A*0212	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.754632	1.017549	-2.737083	5683.712469
HLA B*1503	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.102022	1.364704	-2.737318	12648.011533
HLA A*0201	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.597950	0.860149	-2.737801	3962.320886
HLA A*0216	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.370721	1.632662	-2.738059	23481.244203
HLA A*2602	1:106-114	9	TEGPMTPKR	1.370212	0.494958	-4.603261	1.865170	-2.738091	40110.805479
HLA A*2601	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.373952	1.635751	-2.738200	23656.562984
HLA A*6801	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.589677	1.851066	-2.738611	38875.560263
HLA A*0212	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.371421	1.632662	-2.738760	23519.129951
HLA B*0803	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.444937	1.706161	-2.738775	27857.147097
HLA A*2501	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.371593	1.632662	-2.738931	23528.420004
HLA A*2601	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.387508	1.648439	-2.739070	24406.650128
HLA B*1517	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.457180	1.718039	-2.739140	28653.640239
HLA B*4601	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.294053	1.554751	-2.739301	19681.251479
HLA B*5101	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.457365	1.718039	-2.739326	28665.888884
HLA B*0803	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.384618	1.645104	-2.739514	24244.783425
HLA A*0250	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.532812	1.793234	-2.739578	34104.530524
HLA B*1517	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.377948	1.638299	-2.739649	23875.260624
HLA A*3101	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.372385	1.632662	-2.739723	23571.354561
HLA A*2902	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.390142	1.650328	-2.739814	24555.113632
HLA A*0201	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.384139	1.644220	-2.739919	24218.041220
HLA B*4801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.384151	1.644220	-2.739931	24218.696314
HLA A*0101	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.378310	1.638299	-2.740011	23895.159939
HLA A*3101	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.388471	1.648439	-2.740033	24460.845491
HLA A*3002	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.921262	1.181170	-2.740092	8341.848051
HLA A*0101	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.358955	1.618772	-2.740183	22853.613815
HLA B*0801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.317895	1.577554	-2.740341	20791.952982
HLA A*0211	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.487606	1.746933	-2.740673	30733.048022
HLA A*3002	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.326450	1.585464	-2.740985	21205.560656
HLA B*1509	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.402030	1.661000	-2.741031	25236.570837
HLA A*8001	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.447218	1.706161	-2.741057	28003.865776
HLA B*4601	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.402270	1.661000	-2.741270	25250.500439
HLA B*4801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.326767	1.585464	-2.741303	21221.053477
HLA A*0203	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.328130	1.586804	-2.741325	21287.744108
HLA A*2403	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.230361	1.488986	-2.741374	16996.540039
HLA A*0250	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.756399	1.014988	-2.741411	5706.882255
HLA B*4002	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.275466	1.534036	-2.741430	18856.710552
HLA B*5701	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.389909	1.648439	-2.741471	24541.965949
HLA A*0211	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.464661	1.723131	-2.741529	29151.477017
HLA A*2601	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.360308	1.618772	-2.741536	22924.938943
HLA A*3201	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.191383	1.449604	-2.741778	15537.550940
HLA A*0250	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.319364	1.577554	-2.741809	20862.373318
HLA A*0101	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.358936	1.616917	-2.742019	22852.624752
HLA A*0206	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.267929	1.525910	-2.742019	18532.277168
HLA A*0101	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.390703	1.648439	-2.742265	24586.883032
HLA B*4402	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.341115	1.598716	-2.742399	21933.868968
HLA A*0250	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.583540	1.840969	-2.742571	38330.087104
HLA A*2902	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.460624	1.718039	-2.742585	28881.792853
HLA A*6802	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.381172	1.638299	-2.742873	24053.130884
HLA B*3901	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.938273	1.195398	-2.742875	8675.061178
HLA A*0219	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.460998	1.718039	-2.742958	28906.646862
HLA B*0702	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.208247	1.465019	-2.743229	16152.775938
HLA A*0202	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.328635	1.585042	-2.743593	21312.518845
HLA A*2402	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.495855	1.752221	-2.743634	31322.374399
HLA A*3101	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.245064	1.501143	-2.743920	17581.810662
HLA B*1503	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.189959	1.445980	-2.743979	15486.696151
HLA B*3901	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.362789	1.618772	-2.744017	23056.280328
HLA A*6801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-3.982814	1.238694	-2.744120	9612.007099
HLA A*2603	1:549-557	9	SVIELQVSK	0.982858	0.255246	-3.982330	1.238104	-2.744226	9601.301088

HLA B*1501	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.334034	1.589799	-2.744235	21579.128287
HLA A*3002	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.299090	1.554751	-2.744339	19910.859438
HLA B*3801	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.496571	1.752221	-2.744350	31374.099486
HLA A*0216	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.321969	1.577554	-2.744415	20987.914746
HLA A*6802	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.439028	1.694587	-2.744441	27480.693141
HLA B*1509	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.389649	1.645104	-2.744545	24527.232979
HLA B*5701	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.161779	1.417212	-2.744567	14513.730497
HLA A*0206	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.199653	1.454961	-2.744692	15836.264715
HLA A*2301	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.497001	1.752221	-2.744780	31405.175529
HLA A*2501	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.462985	1.718039	-2.744946	29039.249039
HLA B*4402	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.332220	1.586804	-2.745416	21489.192409
HLA A*1101	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.451774	1.706161	-2.745612	28299.166138
HLA A*0101	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.382311	1.635751	-2.746560	24116.324266
HLA B*4002	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-3.289256	0.542619	-2.746636	1946.504931
HLA B*1503	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.395313	1.648439	-2.746875	24849.243095
HLA A*3301	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.606367	1.859413	-2.746954	40398.701153
HLA B*0803	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.332594	1.585464	-2.747129	21507.684771
HLA A*3001	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.229865	1.482642	-2.747223	16977.149785
HLA A*6901	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.364227	1.616917	-2.747310	23132.742771
HLA B*5701	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.202716	1.454961	-2.747756	15948.376554
HLA A*8001	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.356951	1.609050	-2.747901	22748.395677
HLA B*4402	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.333017	1.584939	-2.748078	21528.638726
HLA A*0250	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.570441	1.822112	-2.748329	37191.305837
HLA A*3301	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.692794	0.944464	-2.748330	4929.395386
HLA B*1502	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.824092	1.075727	-2.748365	6669.484600
HLA A*0250	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.621684	0.873256	-2.748428	4184.890907
HLA A*0250	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.365196	0.616515	-2.748680	2318.438406
HLA A*0219	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.399119	1.650328	-2.748792	25067.979474
HLA A*0203	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-3.642848	0.894030	-2.748818	4393.881115
HLA B*5101	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.501207	1.752221	-2.748986	31710.771137
HLA A*0201	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.397493	1.648439	-2.749055	24974.309344
HLA B*1509	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.070506	1.321448	-2.749058	11762.679425
HLA B*4601	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.397590	1.648439	-2.749151	24979.849396
HLA B*3901	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-3.772197	1.022881	-2.749316	5918.298276
HLA B*0702	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-3.711143	0.961636	-2.749507	5142.130948
HLA A*0301	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.358558	1.609050	-2.749508	22832.728961
HLA B*5101	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.500631	1.751118	-2.749513	31668.768798
HLA B*4501	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.590485	1.840969	-2.749516	38947.975115
HLA A*0206	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-3.496269	0.746693	-2.749576	3135.224410
HLA A*6801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.121424	1.371517	-2.749907	13225.871537
HLA A*3201	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.181754	1.431809	-2.749945	15196.877964
HLA B*1501	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.071761	1.321448	-2.750313	11796.709535
HLA B*1501	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.388749	1.638299	-2.750450	24476.465471
HLA A*0201	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.289647	1.538857	-2.750791	19482.622976
HLA B*3801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.367831	1.616917	-2.750914	23325.514861
HLA A*0219	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.336604	1.585464	-2.751140	21707.221284
HLA A*2403	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.383862	1.632662	-2.751200	24202.586157
HLA A*3201	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.573359	1.822112	-2.751247	37442.038686
HLA A*0202	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.503469	1.752221	-2.751249	31876.406561
HLA A*0203	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.768992	1.017549	-2.751443	5874.787360
HLA A*0219	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.001187	1.249564	-2.751623	10027.370354
HLA A*2602	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.573846	1.822112	-2.751733	37483.991529
HLA B*1502	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.561081	1.809179	-2.751902	36398.298228
HLA A*2403	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.329617	1.577554	-2.752062	21360.768095
HLA A*0212	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.182534	1.430389	-2.752145	15224.197348
HLA B*4601	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.371447	1.618772	-2.752675	23520.529587
HLA A*2603	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.447375	1.694587	-2.752789	28014.017969
HLA B*0802	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.397038	1.644220	-2.752817	24948.112094
HLA A*0206	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-3.789583	1.036678	-2.752905	6160.032995
HLA A*0219	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.459229	1.706161	-2.753067	28789.130922
HLA B*1501	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.829073	1.075727	-2.753346	6746.417009
HLA B*5301	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.575481	1.822112	-2.753369	37625.395405
HLA B*4801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.414443	1.661000	-2.753443	25968.249288
HLA A*0101	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.386242	1.632662	-2.753580	24335.585699
HLA B*1502	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.386343	1.632662	-2.753681	24341.247428

HLA A*2603	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.556448	1.802719	-2.753728	36012.054159
HLA B*0802	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.383110	1.629324	-2.753786	24160.723744
HLA A*2501	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.392158	1.638299	-2.753859	24669.355664
HLA B*7301	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.573726	1.819741	-2.753985	37473.650959
HLA A*3301	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.582847	1.828833	-2.754014	38268.964242
HLA B*1502	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.293047	1.538857	-2.754190	19635.733585
HLA B*0802	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.371442	1.616917	-2.754525	23520.275101
HLA B*0803	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.371471	1.616917	-2.754553	23521.802056
HLA A*1101	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.353490	1.598716	-2.754774	22567.839380
HLA B*1509	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-3.991545	1.236758	-2.754787	9807.194064
HLA A*2902	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.461042	1.706161	-2.754881	28909.618268
HLA B*0801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.399159	1.644220	-2.754939	25070.285035
HLA B*5401	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.564133	1.809179	-2.754954	36654.986177
HLA B*1501	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.403412	1.648439	-2.754973	25316.976561
HLA A*6801	1:5-13	9	SHLSDRYEL	1.470025	0.387079	-4.612220	1.857104	-2.755116	40946.800224
HLA A*1101	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.478318	1.723131	-2.755187	30082.790578
HLA B*3501	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.393542	1.638299	-2.755243	24748.088080
HLA B*4801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.393779	1.638299	-2.755480	24761.614100
HLA A*6802	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.403959	1.648439	-2.755521	25348.908836
HLA A*3301	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.633055	1.877371	-2.755684	42959.102805
HLA B*4001	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.374530	1.618772	-2.755757	23688.066871
HLA B*5801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.345969	1.589799	-2.756171	22180.395239
HLA B*4001	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.417229	1.661000	-2.756229	26135.400571
HLA A*2601	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.288802	1.532461	-2.756341	19444.716322
HLA A*2602	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.565524	1.809179	-2.756345	36772.567614
HLA A*1101	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-3.488755	0.732333	-2.756422	3081.448960
HLA B*1517	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.462591	1.706161	-2.756429	29012.868378
HLA B*4402	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.365496	1.609050	-2.756446	23200.420187
HLA B*4801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.365665	1.609050	-2.756615	23209.458790
HLA B*4001	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.394930	1.638299	-2.756631	24827.340395
HLA A*2603	1:377-385	9	LQNRGFKIR	1.180205	0.641907	-4.578768	1.822112	-2.756656	37911.241099
HLA B*4002	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.630172	1.873374	-2.756798	42674.887461
HLA A*6801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.644986	0.887960	-2.757026	4415.565520
HLA B*0803	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.392816	1.635751	-2.757064	24706.752355
HLA B*5101	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.291609	1.534036	-2.757573	19570.830077
HLA A*8001	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.387109	1.629324	-2.757785	24384.214111
HLA A*0201	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.393774	1.635751	-2.758023	24761.346187
HLA A*3201	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.586857	1.828833	-2.758025	38624.002720
HLA B*7301	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.521088	1.762988	-2.758100	33196.182640
HLA B*0802	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.390762	1.632662	-2.758101	24590.208564
HLA B*4001	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.343148	1.585042	-2.758106	22036.750226
HLA A*2602	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.452739	1.694587	-2.758152	28362.158332
HLA A*1101	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.449927	1.691666	-2.758261	28179.088667
HLA B*3501	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.259485	1.501143	-2.758341	18175.431818
HLA B*1509	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.345178	1.586804	-2.758373	22139.994276
HLA A*2902	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.402639	1.644220	-2.758419	25271.956127
HLA B*5701	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.396953	1.638299	-2.758654	24943.253772
HLA A*6901	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.080510	1.321448	-2.759062	12036.781258
HLA B*5701	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.403499	1.644220	-2.759279	25322.044663
HLA A*0211	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.453963	1.694587	-2.759377	28442.211320
HLA A*3101	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.285049	1.525646	-2.759403	19277.445504
HLA B*4801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.376386	1.616917	-2.759468	23789.521871
HLA B*3801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.410103	1.650328	-2.759775	25710.064892
HLA B*1501	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.298716	1.538857	-2.759860	19893.740031
HLA B*4601	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.345004	1.585042	-2.759962	22131.132706
HLA A*0211	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.777535	1.017549	-2.759986	5991.490558
HLA A*0219	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.345062	1.585042	-2.760020	22134.126083
HLA B*5801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.337739	1.577554	-2.760185	21764.015911
HLA A*0212	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.395971	1.635751	-2.760220	24886.912480
HLA A*2402	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.563012	1.802719	-2.760293	36560.519296
HLA B*5301	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.511345	1.751011	-2.760334	32459.724618
HLA B*4402	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.408879	1.648439	-2.760440	25637.701759
HLA B*5801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.347381	1.586804	-2.760577	22252.628684
HLA A*2603	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.338369	1.577554	-2.760814	21795.593362
HLA B*4601	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.399122	1.638299	-2.760823	25068.115089

HLA B*0802	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.409476	1.648439	-2.761037	25672.955044
HLA A*8001	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.393706	1.632662	-2.761044	24757.461763
HLA B*5401	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.554310	1.793234	-2.761076	35835.202526
HLA A*0301	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.346585	1.585464	-2.761120	22211.855821
HLA B*4501	1:545-553	9	VPVDSVIEL	1.517874	0.349095	-4.628128	1.866969	-2.761159	42474.505613
HLA A*0201	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.351004	1.589799	-2.761206	22439.037640
HLA B*0801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.378195	1.616917	-2.761277	23888.826540
HLA B*5401	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.329565	1.568231	-2.761334	21358.225940
HLA B*5801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.352287	1.590840	-2.761447	22505.416043
HLA B*0803	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.405672	1.644220	-2.761452	25449.077489
HLA B*4501	1:46-54	9	LARDPSFYL	1.468873	0.401975	-4.632414	1.870848	-2.761566	42895.703346
HLA A*0101	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.351432	1.589799	-2.761633	22461.141992
HLA A*2301	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.348676	1.586804	-2.761871	22319.059369
HLA B*1503	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-3.837818	1.075727	-2.762091	6883.637082
HLA B*0801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.324018	1.561867	-2.762151	21087.157526
HLA A*0201	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.288080	1.525910	-2.762170	19412.448641
HLA A*0301	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-3.494563	0.732333	-2.762230	3122.934717
HLA A*0219	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.339832	1.577554	-2.762278	21869.176309
HLA B*0802	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.398064	1.635751	-2.762313	25007.162237
HLA B*4601	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.398203	1.635751	-2.762452	25015.145384
HLA A*2603	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.895559	1.133041	-2.762518	7862.468326
HLA A*0216	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.349454	1.586804	-2.762649	22359.061317
HLA A*0212	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.424261	1.661000	-2.763261	26562.024285
HLA A*2601	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.348265	1.584939	-2.763326	22297.939232
HLA B*1801	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.413837	1.650328	-2.763509	25932.029350
HLA A*2902	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.399274	1.635751	-2.763523	25076.931661
HLA B*4601	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.407805	1.644220	-2.763585	25574.395462
HLA B*0702	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.350410	1.586804	-2.763605	22408.346293
HLA A*2603	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.338167	0.574537	-2.763630	2178.547768
HLA A*2403	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.250862	1.487180	-2.763683	17818.130189
HLA B*5701	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.070412	1.306673	-2.763739	11760.134309
HLA B*1801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.353577	1.589799	-2.763778	22572.357144
HLA B*1801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.408003	1.644220	-2.763783	25586.019893
HLA B*1801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.481918	1.718039	-2.763878	30333.151302
HLA B*1503	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.425107	1.661000	-2.764107	26613.805831
HLA A*0211	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.455805	1.691666	-2.764139	28563.100968
HLA B*1517	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.341736	1.577554	-2.764181	21965.217536
HLA A*0206	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-3.970479	1.206278	-2.764201	9342.848071
HLA B*5301	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.573463	1.809179	-2.764284	37450.952267
HLA A*2403	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.204511	1.440103	-2.764408	16014.430082
HLA A*2601	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.351343	1.586804	-2.764538	22456.525000
HLA B*1509	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.196472	1.431809	-2.764662	15720.688052
HLA B*1503	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.077503	1.312789	-2.764714	11953.718585
HLA B*0802	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.363640	1.598716	-2.764923	23101.477525
HLA A*3301	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.003706	1.238694	-2.765012	10085.692049
HLA B*2705	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.483062	1.718039	-2.765022	30413.172875
HLA B*1801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.410317	1.645104	-2.765213	25722.725071
HLA A*2403	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.394672	1.629324	-2.765348	24812.570342
HLA A*0250	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.594206	1.828833	-2.765374	39283.164724
HLA B*5701	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.384318	1.618772	-2.765545	24228.000553
HLA B*5101	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.064379	1.298743	-2.765636	11597.885162
HLA A*0201	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.403995	1.638299	-2.765695	25350.965942
HLA A*3001	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.295324	1.529572	-2.765752	19738.937958
HLA B*4403	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-3.870222	1.104337	-2.765885	7416.893835
HLA A*8001	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.384750	1.618772	-2.765978	24252.129587
HLA A*3001	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-3.865664	1.099547	-2.766117	7339.459219
HLA B*4403	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.639970	1.873374	-2.766596	43648.541547
HLA A*0203	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-3.674754	0.908065	-2.766689	4728.836607
HLA A*2501	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.352177	1.585464	-2.766712	22499.694436
HLA B*1502	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.560146	1.793234	-2.766912	36320.012056
HLA A*3301	1:324-332	9	RSIGSVGRW	1.364284	0.476685	-4.607897	1.840969	-2.766928	40541.229661
HLA B*1503	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.353741	1.586804	-2.766937	22580.906739
HLA B*1509	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.396267	1.629324	-2.766943	24903.882329
HLA B*1503	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.174772	1.407681	-2.767091	14954.493439
HLA A*2902	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.354157	1.586804	-2.767353	22602.539450

HLA B*5401	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.567105	1.799748	-2.767357	36906.695237
HLA A*0212	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.354214	1.586804	-2.767409	22605.474295
HLA B*2705	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.415862	1.648439	-2.767423	26053.241222
HLA B*4002	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.596295	1.828833	-2.767462	39472.547885
HLA A*0202	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.611798	0.844164	-2.767633	4090.698846
HLA B*4801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.358614	1.590840	-2.767774	22835.693694
HLA A*0202	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.570561	1.802719	-2.767842	37201.568496
HLA A*6801	1:247-255	9	LDAVVLKAL	1.627601	0.231812	-4.627334	1.859413	-2.767921	42396.910138
HLA B*1517	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.416390	1.648439	-2.767952	26084.973189
HLA A*0250	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-2.909898	0.141914	-2.767984	812.640124
HLA B*4601	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.358046	1.589799	-2.768247	22805.816922
HLA A*0301	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.358133	1.589799	-2.768334	22810.382325
HLA A*2501	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.413498	1.645104	-2.768394	25911.835543
HLA B*0801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.406715	1.638299	-2.768416	25510.279412
HLA B*1502	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.081384	1.312789	-2.768595	12061.029416
HLA A*3001	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.090139	1.321448	-2.768690	12306.613397
HLA A*8001	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.417177	1.648439	-2.768739	26132.290185
HLA A*0301	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.353732	1.584939	-2.768793	22580.418104
HLA B*1517	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.836178	1.067242	-2.768936	6857.692777
HLA B*0802	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.378162	1.609050	-2.769112	23887.017306
HLA A*2301	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.464094	1.694587	-2.769507	29113.494575
HLA B*4001	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.324269	1.554751	-2.769518	21099.367532
HLA B*4001	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.413970	1.644220	-2.769750	25940.027079
HLA B*0801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.405872	1.635751	-2.770121	25460.782698
HLA A*6801	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.579266	1.809098	-2.770169	37954.746312
HLA B*3901	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.180044	1.409864	-2.770180	15137.144295
HLA B*4601	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.182003	1.411765	-2.770238	15205.595086
HLA A*2602	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.599145	1.828833	-2.770312	39732.426215
HLA A*0250	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.462074	1.691666	-2.770408	28978.358510
HLA A*8001	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.360231	1.589799	-2.770432	22920.846603
HLA A*6802	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.431453	1.661000	-2.770453	27005.544801
HLA B*1502	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.903646	1.133041	-2.770605	8010.245677
HLA B*1501	1:145-153	9	MISATNAVK	0.938735	0.280828	-3.990234	1.219563	-2.770671	9777.633549
HLA B*5801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-3.960837	1.190001	-2.770836	9137.702200
HLA B*1503	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.586165	0.815296	-2.770868	3856.245076
HLA B*3801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.380084	1.609050	-2.771034	23992.958506
HLA B*3801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.356535	1.585464	-2.771070	22726.623368
HLA B*4001	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.305112	1.534036	-2.771076	20188.857215
HLA B*4001	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.407021	1.635751	-2.771269	25528.226734
HLA A*0203	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.415582	1.644220	-2.771362	26036.474147
HLA A*0203	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.420070	1.648439	-2.771631	26306.900864
HLA A*6901	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.281093	1.509182	-2.771911	19102.620651
HLA A*6801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.349623	1.577554	-2.772068	22367.772137
HLA A*3101	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.358948	1.586804	-2.772143	22853.242911
HLA A*2902	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.410714	1.638299	-2.772415	25746.253373
HLA A*0201	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.389599	1.616917	-2.772682	24524.446656
HLA A*3001	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-3.741607	0.968816	-2.772791	5515.775159
HLA B*3901	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.219013	1.445980	-2.773032	16558.176558
HLA A*6901	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.359850	1.586804	-2.773046	22900.767526
HLA B*1501	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.035320	1.262230	-2.773090	10847.268086
HLA B*0802	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.358654	1.585464	-2.773190	22837.793947
HLA A*0212	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.411774	1.638299	-2.773475	25809.147322
HLA B*4801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.402829	1.629324	-2.773505	25283.032751
HLA A*2603	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.525794	1.752221	-2.773573	33557.852730
HLA A*0203	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-3.906207	1.132158	-2.774049	8057.619867
HLA B*1517	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.312940	1.538857	-2.774084	20556.076277
HLA B*0702	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.418383	1.644220	-2.774163	26204.915158
HLA A*6802	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.418416	1.644220	-2.774195	26206.899953
HLA B*3801	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.418655	1.644220	-2.774435	26221.365139
HLA A*0301	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.359491	1.585042	-2.774449	22881.820105
HLA A*2902	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.329297	1.554751	-2.774546	21345.057798
HLA A*3002	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.504383	1.729555	-2.774829	31943.559400
HLA A*0203	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.435889	1.661000	-2.774889	27282.789404
HLA A*0101	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.081563	1.306673	-2.774889	12065.989347
HLA B*4601	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.360517	1.585464	-2.775053	22935.979503

HLA A*3001	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-3.970507	1.195398	-2.775109	9343.454616
HLA A*3001	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.284333	1.509182	-2.775150	19245.663634
HLA A*0201	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.360212	1.585042	-2.775170	22919.854630
HLA A*0201	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.362023	1.586804	-2.775219	23015.653557
HLA B*4001	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.392165	1.616917	-2.775247	24669.756043
HLA A*0301	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.366222	1.590840	-2.775382	23239.235737
HLA A*3002	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.215521	1.440103	-2.775418	16425.597422
HLA A*2601	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.392466	1.616917	-2.775548	24686.844922
HLA A*2501	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.365350	1.589799	-2.775552	23192.639767
HLA B*1801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.467261	1.691666	-2.775596	29326.581651
HLA B*4402	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.420775	1.645104	-2.775671	26349.630754
HLA A*0216	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.481849	1.706161	-2.775688	30328.392805
HLA B*0803	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.424266	1.648439	-2.775827	26562.311682
HLA B*5701	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.411600	1.635751	-2.775849	25798.817168
HLA A*2902	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.436890	1.661000	-2.775890	27345.738177
HLA A*2501	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.482432	1.706161	-2.776271	30369.110277
HLA A*0301	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.353845	1.577554	-2.776290	22586.282428
HLA A*0212	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.424790	1.648439	-2.776351	26594.375932
HLA A*0206	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.505939	1.729555	-2.776384	32058.165458
HLA B*1501	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.420650	1.644220	-2.776430	26342.076762
HLA A*3001	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-3.185648	0.409024	-2.776624	1533.373377
HLA A*2301	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.506221	1.729555	-2.776666	32078.983949
HLA B*5301	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.569964	1.793234	-2.776730	37150.484485
HLA A*0216	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.366595	1.589799	-2.776797	23259.234085
HLA A*2902	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.208722	1.431809	-2.776912	16170.437302
HLA A*2501	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.468596	1.691666	-2.776930	29416.835467
HLA B*1509	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.362646	1.585464	-2.777181	23048.672936
HLA B*4801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.425965	1.648439	-2.777526	26666.409625
HLA A*3101	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.362665	1.585042	-2.777623	23049.670483
HLA B*0801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.364474	1.586804	-2.777669	23145.886789
HLA A*0301	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.346239	1.568231	-2.778009	22194.198782
HLA A*3201	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.034428	1.256417	-2.778011	10824.991635
HLA B*4002	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.364861	1.586804	-2.778057	23166.556766
HLA A*3001	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.249232	1.471168	-2.778063	17751.358103
HLA A*3201	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.571320	1.793234	-2.778086	37266.631129
HLA B*4801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.413867	1.635751	-2.778116	25933.853177
HLA B*0802	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.355724	1.577554	-2.778170	22684.245690
HLA B*4402	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.407512	1.629324	-2.778187	25557.106977
HLA A*0301	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.149900	1.371517	-2.778383	14122.125229
HLA A*3301	1:455-463	9	ANSPSTPEL	1.461049	0.390017	-4.629517	1.851066	-2.778451	42610.524319
HLA B*1503	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.369380	1.590840	-2.778540	23408.821460
HLA B*2705	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.312799	1.534036	-2.778763	20549.404994
HLA A*0206	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-3.672579	0.893801	-2.778778	4705.206467
HLA B*4403	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.587962	1.809179	-2.778783	38722.334918
HLA A*0219	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.439805	1.661000	-2.778806	27529.946170
HLA B*5301	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.501947	1.723131	-2.778816	31764.856010
HLA A*0301	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.365644	1.586804	-2.778839	23208.328772
HLA B*0801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.250061	1.471168	-2.778893	17785.290099
HLA A*2403	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.365700	1.586804	-2.778896	23211.342275
HLA A*2603	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.111740	1.332686	-2.779054	12934.204491
HLA A*2603	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.542111	1.762988	-2.779123	34842.662736
HLA B*5801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.266319	1.487180	-2.779140	18463.727828
HLA A*0101	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.364345	1.584939	-2.779406	23139.000896
HLA B*4501	1:296-304	9	LLSSAAGNL	1.424780	0.448594	-4.652819	1.873374	-2.779445	44959.251306
HLA A*3001	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-3.864908	1.085412	-2.779496	7326.685126
HLA B*3901	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.440508	1.661000	-2.779508	27574.513458
HLA B*4402	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.423780	1.644220	-2.779559	26532.582604
HLA B*0803	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.369434	1.589799	-2.779635	23411.734341
HLA A*3001	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.305344	1.525646	-2.779698	20199.672839
HLA A*0201	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.357266	1.577554	-2.779711	22764.892540
HLA B*0702	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.357367	1.577554	-2.779812	22770.188844
HLA A*0101	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.348382	1.568231	-2.780151	22303.971516
HLA A*0301	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.342137	1.561867	-2.780271	21985.546764
HLA A*0201	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.689410	0.909118	-2.780292	4891.143400
HLA B*7301	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.589512	1.809098	-2.780415	38860.841177

HLA A*3301	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.589719	1.809179	-2.780540	38879.346072
HLA A*3001	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.113586	1.332686	-2.780901	12989.320062
HLA A*0203	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.419370	1.638299	-2.781071	26264.524441
HLA A*1101	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.366142	1.585042	-2.781100	23234.961593
HLA B*3501	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.399913	1.618772	-2.781141	25113.859274
HLA A*2301	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.413883	1.632662	-2.781222	25934.835290
HLA A*0202	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.513321	0.732039	-2.781282	3260.777712
HLA A*3001	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.198722	1.417212	-2.781511	15802.374745
HLA A*0301	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.976480	1.194908	-2.781572	9472.832788
HLA B*3801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.500027	1.718039	-2.781988	31624.768989
HLA B*4402	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.399065	1.616917	-2.782148	25064.860523
HLA B*1503	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.038628	1.256417	-2.782212	10930.208554
HLA B*1801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.308180	1.525910	-2.782270	20332.002944
HLA A*3201	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.488482	1.706161	-2.782321	30795.126504
HLA B*1501	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.265004	1.482642	-2.782362	18407.875910
HLA A*3101	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.372232	1.589799	-2.782433	23563.067321
HLA A*0202	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.597907	0.815296	-2.782611	3961.935062
HLA A*2403	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.443861	1.661000	-2.782861	27788.210068
HLA B*1502	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.192783	1.409864	-2.782919	15587.729423
HLA B*1502	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.372772	1.589799	-2.782974	23592.404493
HLA B*0702	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.400066	1.616917	-2.783149	25122.691935
HLA B*4002	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.602951	1.819741	-2.783210	40082.172362
HLA B*3801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.489438	1.706161	-2.783277	30863.006682
HLA B*1502	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.186801	1.403484	-2.783317	15374.502440
HLA A*2601	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.200531	1.417212	-2.783320	15868.338643
HLA A*2403	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.317576	1.534036	-2.783540	20776.661035
HLA B*0801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.902189	1.118640	-2.783549	7983.423270
HLA A*6801	1:23-31	9	SEVHLARDL	1.447686	0.429685	-4.661261	1.877371	-2.783890	45841.705843
HLA B*5801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.322855	1.538857	-2.783998	21030.763871
HLA B*3501	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.191791	1.407681	-2.784111	15552.183645
HLA A*2902	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.323466	1.538857	-2.784609	21060.365951
HLA A*2603	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.584364	1.799748	-2.784616	38402.940146
HLA A*2402	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.502661	1.718039	-2.784622	31817.139674
HLA B*2705	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.383352	1.598716	-2.784636	24174.190300
HLA A*2301	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.490930	1.706161	-2.784769	30969.212058
HLA A*0101	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.369915	1.585042	-2.784873	23437.712996
HLA B*4601	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.310816	1.525910	-2.784906	20455.791391
HLA A*0212	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.834815	1.049687	-2.785128	6836.208873
HLA A*0212	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.429489	1.644220	-2.785269	26883.683483
HLA A*3101	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.163438	1.378166	-2.785272	14569.269970
HLA A*2501	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.240336	1.454961	-2.785376	17391.475729
HLA A*0206	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.537767	1.752221	-2.785546	34495.872928
HLA B*3901	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.268277	1.482642	-2.785635	18547.121229
HLA B*5801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.814398	1.028753	-2.785645	6522.262878
HLA B*4801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.404453	1.618772	-2.785680	25377.723506
HLA A*3101	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.319845	1.534036	-2.785809	20885.523093
HLA B*7301	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.588669	1.802719	-2.785949	38785.440830
HLA B*1503	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.241015	1.454961	-2.786055	17418.687837
HLA A*2402	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.515748	1.729555	-2.786193	32790.479384
HLA A*2601	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.371811	1.585464	-2.786347	23540.260594
HLA A*6802	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.601807	0.815296	-2.786511	3997.675127
HLA B*3901	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.815333	1.028753	-2.786580	6536.321326
HLA A*0212	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.403565	1.616917	-2.786647	25325.880658
HLA A*2403	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.403698	1.616917	-2.786781	25333.691444
HLA B*5101	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.478722	1.691666	-2.787056	30110.795670
HLA A*0211	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.376889	1.589799	-2.787090	23817.079336
HLA A*0250	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.181999	1.394783	-2.787216	15205.430566
HLA B*3501	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.045794	1.258359	-2.787436	11112.054886
HLA B*3501	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-3.614091	0.826538	-2.787552	4112.355070
HLA A*8001	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.378418	1.590840	-2.787578	23901.107106
HLA B*3801	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.482312	1.694587	-2.787725	30360.732464
HLA B*0802	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.274963	1.487180	-2.787784	18834.892463
HLA A*1101	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.373252	1.585464	-2.787787	23618.455853
HLA A*2301	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.538989	1.751118	-2.787871	34593.051353
HLA B*4601	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.374795	1.586804	-2.787991	23702.552227

HLA B*1517	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.708206	0.920120	-2.788086	5107.475309
HLA B*4403	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.551103	1.762988	-2.788115	35571.552181
HLA A*0250	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-3.901132	1.112976	-2.788156	7964.011662
HLA A*2602	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.597268	1.809098	-2.788170	39561.053393
HLA B*4402	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.356476	1.568231	-2.788245	22723.549863
HLA B*1801	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.494429	1.706161	-2.788267	31219.686596
HLA B*5701	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.121044	1.332686	-2.788358	13214.285434
HLA B*4001	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.271032	1.482642	-2.788391	18665.191780
HLA B*0702	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.356622	1.568231	-2.788391	22731.172918
HLA B*5101	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.365999	1.577554	-2.788444	23227.295245
HLA A*2902	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.366158	1.577554	-2.788604	23235.841499
HLA A*2603	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.202430	1.413806	-2.788624	15937.853995
HLA B*3501	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.275894	1.487180	-2.788714	18875.286009
HLA A*2603	1:137-145	9	RDVKPANIM	0.886768	0.128226	-3.803840	1.014994	-2.788846	6365.605398
HLA B*4001	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.366422	1.577554	-2.788867	23249.924538
HLA B*5401	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.518527	1.729555	-2.788973	33001.008098
HLA B*0801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.220789	1.431809	-2.788979	16626.036124
HLA B*5101	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.495173	1.706161	-2.789012	31273.272260
HLA B*7301	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.617936	1.828833	-2.789104	41489.315195
HLA A*0203	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.110579	1.321448	-2.789131	12899.684168
HLA A*2902	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.357362	1.568231	-2.789131	22769.942477
HLA B*0803	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.439702	1.650328	-2.789374	27523.393855
HLA B*5701	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.406391	1.616917	-2.789474	25491.241445
HLA B*2705	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.427783	1.638299	-2.789484	26778.302759
HLA A*3201	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.598598	1.809098	-2.789500	39682.374878
HLA A*0206	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.540638	1.751118	-2.789520	34724.676625
HLA A*6901	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.027661	1.238104	-2.789557	10657.640155
HLA B*1501	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.206856	1.417212	-2.789645	16101.126931
HLA B*3801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.379553	1.589799	-2.789754	23963.641802
HLA B*1501	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.406732	1.616917	-2.789814	25511.245485
HLA B*5701	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.375068	1.585042	-2.790026	23717.431364
HLA A*3301	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.388770	1.598716	-2.790054	24477.657235
HLA A*2902	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.379879	1.589799	-2.790081	23981.668629
HLA A*2602	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.592806	1.802719	-2.790087	39156.708231
HLA B*0803	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.655371	0.865145	-2.790226	4522.421708
HLA B*5701	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.375209	1.584939	-2.790270	23725.131134
HLA A*0203	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.426035	1.635751	-2.790284	26670.737845
HLA A*2601	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.279373	1.488986	-2.790387	19027.123116
HLA A*0101	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.273236	1.482642	-2.790594	18760.148573
HLA A*0101	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.316540	1.525910	-2.790630	20727.151967
HLA A*1101	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.434886	1.644220	-2.790665	27219.838279
HLA A*3002	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.359075	1.568231	-2.790844	22859.920096
HLA A*0212	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.368517	1.577554	-2.790963	23362.391007
HLA B*4001	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.381907	1.590840	-2.791067	24093.894441
HLA B*5701	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.368642	1.577554	-2.791087	23369.090528
HLA B*5301	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.482799	1.691666	-2.791133	30394.750885
HLA A*3301	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.600357	1.809098	-2.791260	39843.494346
HLA B*1503	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.735761	0.944464	-2.791297	5442.031308
HLA A*0211	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.368945	1.577554	-2.791391	23385.404941
HLA B*4601	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.888952	1.097502	-2.791450	7743.764859
HLA A*0101	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.382382	1.590840	-2.791542	24120.238583
HLA B*5101	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.429975	1.638299	-2.791676	26913.805960
HLA A*2501	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.376740	1.584939	-2.791802	23808.963311
HLA B*4002	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.601163	1.809179	-2.791984	39917.496252
HLA A*0219	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.430638	1.638299	-2.792339	26954.896695
HLA B*0702	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.382140	1.589799	-2.792341	24106.802081
HLA B*2705	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.453390	1.661000	-2.792390	28404.692001
HLA A*8001	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.378183	1.585464	-2.792719	23888.180369
HLA A*0216	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-3.906132	1.112976	-2.793156	8056.225081
HLA B*5801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.355128	1.561867	-2.793261	22653.096406
HLA A*0206	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.441908	1.648439	-2.793470	27663.565282
HLA A*2403	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.437834	1.644220	-2.793614	27405.273732
HLA A*3002	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.410627	1.616917	-2.793710	25741.100367
HLA A*2403	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.319669	1.525910	-2.793759	20877.050685
HLA A*2601	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.355684	1.561867	-2.793818	22682.159559

HLA A*6802	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.188667	1.394783	-2.793884	15440.684917
HLA B*1502	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.517143	1.723131	-2.794012	32896.020227
HLA B*4601	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.411057	1.616917	-2.794140	25766.596925
HLA A*3201	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.051264	1.257069	-2.794195	11252.887549
HLA B*4501	1:563-571	9	MPDLSGMFW	1.613233	0.215600	-4.623211	1.828833	-2.794378	41996.283658
HLA A*3001	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.295523	1.501143	-2.794380	19748.016809
HLA B*1502	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.597101	1.802719	-2.794382	39545.860826
HLA A*8001	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.411407	1.616917	-2.794490	25787.375069
HLA B*1517	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.384461	1.589799	-2.794662	24235.997191
HLA B*0702	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.413545	1.618772	-2.794773	25914.639298
HLA B*5401	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.557895	1.762988	-2.794907	36132.264220
HLA A*0211	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.327834	0.532852	-2.794982	2127.326019
HLA B*1501	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.249951	1.454961	-2.794990	17780.768501
HLA A*3001	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.065290	1.270153	-2.795137	11622.255120
HLA A*0211	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.116650	1.321448	-2.795202	13081.277135
HLA A*2902	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.093992	1.298743	-2.795249	12416.286157
HLA A*0219	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.431070	1.635751	-2.795319	26981.741486
HLA B*1503	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.020063	1.224706	-2.795357	10472.800199
HLA B*5301	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.595372	1.799748	-2.795624	39388.714986
HLA A*2501	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.424987	1.629324	-2.795663	26606.463979
HLA B*4402	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.414461	1.618772	-2.795689	25969.373195
HLA A*3301	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.414490	1.618772	-2.795717	25971.059147
HLA A*0101	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.383058	1.586804	-2.796254	24157.848365
HLA A*2402	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.519458	1.723131	-2.796327	33071.782472
HLA A*8001	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.381461	1.584939	-2.796522	24069.141558
HLA B*1517	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.351279	1.554751	-2.796528	22453.245082
HLA B*4002	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.605639	1.809098	-2.796542	40331.006660
HLA A*1101	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.381822	1.584939	-2.796884	24089.202467
HLA A*0206	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.387764	1.590840	-2.796924	24421.046435
HLA B*1503	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-3.751615	0.954621	-2.796994	5644.368516
HLA A*0101	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.351848	1.554751	-2.797096	22482.659968
HLA B*7301	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.590405	1.793234	-2.797171	38940.811830
HLA B*5401	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.549406	1.752221	-2.797186	35432.882827
HLA B*1502	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.458481	1.661000	-2.797482	28739.646269
HLA A*2603	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.059201	1.261650	-2.797551	11460.420142
HLA B*3801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.426951	1.629324	-2.797627	26727.068686
HLA B*5401	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.426980	1.629324	-2.797655	26728.803828
HLA A*6802	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.433448	1.635751	-2.797696	27129.866443
HLA B*0801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.176040	1.378166	-2.797875	14998.244475
HLA A*0203	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.388758	1.590840	-2.797918	24476.995137
HLA A*2301	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.515992	1.718039	-2.797953	32808.933432
HLA B*5401	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.695336	0.897363	-2.797973	4958.334216
HLA A*6802	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-3.992907	1.194908	-2.798000	9838.014775
HLA A*3301	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.006210	1.208137	-2.798073	10144.023684
HLA B*7301	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-3.808849	1.010656	-2.798192	6439.450593
HLA A*0216	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.442418	1.644220	-2.798198	27696.059882
HLA B*4403	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.591441	1.793234	-2.798207	39033.826215
HLA A*0211	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.690524	0.892112	-2.798412	4903.701793
HLA A*2603	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.549547	1.751118	-2.798430	35444.385972
HLA A*6802	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-3.552943	0.754459	-2.798484	3572.258752
HLA B*3501	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.324526	1.525910	-2.798616	21111.813032
HLA A*0219	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.442911	1.644220	-2.798691	27727.542611
HLA A*2902	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.248353	1.449604	-2.798749	17715.478116
HLA A*3101	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.389592	1.590840	-2.798752	24524.048635
HLA A*0211	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.550003	1.751118	-2.798885	35481.605038
HLA B*1503	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.715278	0.916314	-2.798964	5191.325086
HLA A*6901	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.325064	1.525910	-2.799154	21137.983918
HLA B*4601	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.131856	1.332686	-2.799170	13547.401857
HLA B*1502	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.551392	1.752221	-2.799171	35595.229951
HLA B*3901	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.061428	1.262230	-2.799197	11519.346741
HLA A*2301	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.522495	1.723131	-2.799364	33303.930138
HLA B*5101	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.288520	1.488986	-2.799533	19432.097167
HLA B*5401	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.449929	1.650328	-2.799602	28179.241113
HLA A*0212	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.009448	1.209597	-2.799850	10219.928205
HLA A*3002	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.552130	1.752221	-2.799909	35655.747139

HLA B*5401	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.361807	1.561867	-2.799941	23004.201291
HLA A*6802	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.417288	1.616917	-2.800370	26138.935551
HLA A*2301	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.050070	1.249564	-2.800507	11222.004553
HLA B*1503	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.287808	1.487180	-2.800628	19400.270236
HLA B*5101	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.495258	1.694587	-2.800671	31279.363511
HLA A*0219	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.334727	1.534036	-2.800691	21613.594286
HLA A*6802	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.385802	1.585042	-2.800760	24310.979070
HLA B*1801	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.409962	1.609050	-2.800913	25701.720930
HLA A*0219	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.449570	1.648439	-2.801131	28155.926438
HLA B*2705	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.386190	1.584939	-2.801251	24332.689509
HLA A*2601	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.392141	1.590840	-2.801301	24668.421473
HLA A*8001	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.439923	1.638299	-2.801624	27537.393875
HLA B*5401	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.211567	0.409720	-2.801848	1627.674041
HLA B*5801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.219233	1.417212	-2.802022	16566.599022
HLA A*0211	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.817011	1.014988	-2.802023	6561.617743
HLA B*2705	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.370310	1.568231	-2.802079	23459.024311
HLA A*0202	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.021858	1.219563	-2.802295	10516.175485
HLA A*0216	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.197129	1.394783	-2.802346	15744.519307
HLA A*2402	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.387459	1.585042	-2.802417	24403.877503
HLA A*2301	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.379980	1.577554	-2.802426	23987.248019
HLA B*1502	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.328435	1.525910	-2.802525	21302.720737
HLA B*2705	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.039352	1.236758	-2.802594	10948.436150
HLA B*1501	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.393478	1.590840	-2.802638	24744.473464
HLA B*0702	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.438419	1.635751	-2.802668	27442.215221
HLA B*5401	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.210615	1.407681	-2.802935	16241.100348
HLA A*6901	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.135878	1.332686	-2.803193	13673.457082
HLA A*0216	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.388267	1.585042	-2.803225	24449.335450
HLA A*8001	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.358020	1.554751	-2.803268	22804.459816
HLA B*0803	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.435931	1.632662	-2.803269	27285.446277
HLA A*0211	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.532897	1.729555	-2.803342	34111.173233
HLA A*2902	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.290721	1.487180	-2.803542	19530.849833
HLA A*0201	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.394383	1.590840	-2.803543	24796.065144
HLA A*0250	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.555825	1.752221	-2.803604	35960.463525
HLA B*0801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-3.853310	1.049687	-2.803623	7133.628185
HLA A*0219	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.064689	1.261014	-2.803674	11606.170232
HLA B*4402	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.388751	1.585042	-2.803709	24476.597886
HLA A*3301	1:487-495	9	IVGSGPATK	0.962871	0.205808	-3.972396	1.168679	-2.803717	9384.182958
HLA B*3801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.464724	1.661000	-2.803724	29155.735397
HLA A*3001	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.211405	1.407681	-2.803724	16270.649014
HLA B*1517	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.337943	1.534036	-2.803907	21774.261782
HLA A*0250	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.551277	1.746933	-2.804344	35585.795455
HLA B*4001	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.244558	1.440103	-2.804455	17561.372686
HLA A*3002	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.551620	1.746933	-2.804687	35613.913779
HLA B*4801	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.359474	1.554751	-2.804723	22880.953604
HLA A*2902	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.390412	1.585464	-2.804948	24570.395036
HLA A*0219	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.421630	0.616515	-2.805115	2640.159667
HLA A*0202	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.145718	1.340547	-2.805171	13986.787444
HLA A*2402	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.499849	1.694587	-2.805262	31611.769088
HLA B*4403	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.511505	1.706161	-2.805343	32471.667853
HLA B*5301	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.414506	1.609050	-2.805456	25972.042669
HLA B*1509	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.390666	1.585042	-2.805624	24584.754927
HLA B*3501	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-3.950213	1.144551	-2.805662	8916.873982
HLA A*0206	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.392480	1.586804	-2.805675	24687.646253
HLA B*0802	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.373963	1.568231	-2.805733	23657.202890
HLA B*2705	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.391300	1.585464	-2.805836	24620.691382
HLA A*3002	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-3.926191	1.120342	-2.805850	8437.066930
HLA B*1501	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-3.939034	1.133041	-2.805993	8690.280195
HLA B*0803	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.415068	1.609050	-2.806018	26005.645291
HLA B*5301	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.435372	1.629324	-2.806048	27250.337409
HLA B*4001	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.344926	1.538857	-2.806069	22127.182068
HLA B*4601	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.205094	1.398961	-2.806134	16035.930302
HLA B*1801	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.435534	1.629324	-2.806210	27260.511378
HLA A*3201	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.553156	1.746933	-2.806224	35740.141379
HLA B*1502	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.383874	1.577554	-2.806319	24203.240833
HLA A*2902	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.454833	1.648439	-2.806394	28499.199945

HLA A*0206	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.512607	1.706161	-2.806445	32554.160811
HLA B*1503	1:450-458	9	GRFKQANSP	0.757924	0.058749	-3.623319	0.816673	-2.806646	4200.677907
HLA B*5701	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.393511	1.586804	-2.806707	24746.347643
HLA B*1509	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.423733	1.616917	-2.806815	26529.711993
HLA B*2705	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.416125	1.609050	-2.807075	26069.031862
HLA B*5801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.341174	1.534036	-2.807138	21936.835664
HLA A*0211	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-3.951904	1.144551	-2.807354	8951.674009
HLA A*3001	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-3.314146	0.506563	-2.807583	2061.322541
HLA A*8001	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.394500	1.586804	-2.807696	24802.773249
HLA B*1501	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-3.921497	1.113773	-2.807724	8346.362119
HLA A*2501	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.296715	1.488986	-2.807728	19802.256293
HLA B*5401	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.558741	1.751011	-2.807730	36202.702545
HLA A*3002	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.558945	1.751118	-2.807828	36219.745732
HLA A*2402	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.295086	1.487180	-2.807907	19728.155572
HLA A*0202	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.951307	1.143250	-2.808057	8939.381855
HLA B*1801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.393610	1.585464	-2.808145	24751.971032
HLA A*8001	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.452838	1.644220	-2.808618	28368.603381
HLA B*2705	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.297741	1.488986	-2.808755	19849.126616
HLA A*0202	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.555727	1.746933	-2.808794	35952.293685
HLA B*0702	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.826399	1.017549	-2.808851	6705.010594
HLA B*5801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.273889	1.465019	-2.808871	18788.384110
HLA B*0801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.334819	1.525910	-2.808909	21618.154926
HLA B*1502	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.394108	1.585042	-2.809066	24780.375266
HLA B*5101	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.427924	1.618772	-2.809152	26786.996229
HLA B*0702	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.447728	1.638299	-2.809429	28036.760105
HLA A*6801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.617714	0.807959	-2.809755	4146.804026
HLA A*0203	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.426721	1.616917	-2.809804	26712.902575
HLA A*3001	1:458-466	9	PSTPELVGK	1.142224	0.018975	-3.971118	1.161199	-2.809919	9356.606097
HLA A*0219	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.399874	1.589799	-2.810075	25111.549706
HLA A*6802	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.400950	1.590840	-2.810110	25173.846472
HLA A*1101	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.458632	1.648439	-2.810193	28749.598603
HLA A*0216	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.016708	1.206278	-2.810429	10392.206157
HLA A*0101	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.388081	1.577554	-2.810527	24438.888495
HLA B*4403	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.630325	1.819741	-2.810584	42689.896417
HLA B*3801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.459062	1.648439	-2.810623	28778.075079
HLA B*7301	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.610423	1.799748	-2.810674	40777.689401
HLA A*0211	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.529044	1.718039	-2.811004	33809.870051
HLA B*5301	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.563297	1.752221	-2.811076	36584.459522
HLA B*4002	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.182741	1.371517	-2.811224	15231.446861
HLA A*3201	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.614269	1.802719	-2.811549	41140.419948
HLA A*8001	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.447352	1.635751	-2.811601	28012.502482
HLA B*5701	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.402498	1.590840	-2.811658	25263.754350
HLA A*8001	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.396775	1.585042	-2.811733	24933.000422
HLA A*0202	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-3.924862	1.112976	-2.811886	8411.272166
HLA B*5401	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.563158	1.751118	-2.812040	36572.784231
HLA A*2501	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.460521	1.648439	-2.812082	28874.918790
HLA A*6901	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.344553	1.532461	-2.812092	22108.157061
HLA B*3801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.444852	1.632662	-2.812190	27851.722278
HLA A*3201	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.535592	1.723131	-2.812460	34323.496001
HLA A*0212	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.402305	1.589799	-2.812507	25252.549558
HLA B*5701	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.367300	1.554751	-2.812549	23297.013698
HLA A*0203	1:456-464	9	NSPSTPELV	0.868149	0.229670	-3.910553	1.097819	-2.812734	8138.667802
HLA B*0802	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.451198	1.638299	-2.812899	28261.682623
HLA B*4402	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.184513	1.371517	-2.812995	15293.703680
HLA B*2705	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.390593	1.577554	-2.813039	24580.632248
HLA A*3002	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.448926	1.635751	-2.813175	28114.221555
HLA B*0802	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.398222	1.584939	-2.813283	25016.228040
HLA B*5401	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.498477	1.685171	-2.813305	31512.053249
HLA B*1517	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.400144	1.586804	-2.813339	25127.177397
HLA A*1101	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.403344	1.589799	-2.813545	25313.004973
HLA B*3801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.400407	1.586804	-2.813602	25142.406758
HLA A*2301	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.452143	1.638299	-2.813843	28323.212318
HLA B*1502	1:585-593	9	GMLDKGADV	0.832496	0.121837	-3.768456	0.954333	-2.814123	5867.545543
HLA B*4801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.391864	1.577554	-2.814310	24652.678994
HLA A*2402	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.462807	1.648439	-2.814368	29027.311961

HLA B*1509	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.508977	1.694587	-2.814390	32283.198030
HLA A*0219	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.401253	1.586804	-2.814448	25191.420820
HLA B*0702	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.246262	1.431809	-2.814452	17630.386622
HLA B*3501	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.458822	1.644220	-2.814602	28762.199467
HLA A*0101	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.376510	1.561867	-2.814644	23796.343879
HLA B*1501	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.127636	1.312789	-2.814847	13416.410518
HLA B*5801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.340840	1.525910	-2.814930	21919.990164
HLA B*1503	1:585-593	9	GMLDKGADV	0.832496	0.121837	-3.769528	0.954333	-2.815194	5882.038115
HLA A*0201	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.232529	1.417212	-2.815318	17081.621576
HLA A*2403	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.453797	1.638299	-2.815498	28431.288704
HLA B*0803	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.400562	1.585042	-2.815520	25151.385525
HLA B*4501	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.624738	1.809179	-2.815559	42144.220516
HLA A*3101	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.393227	1.577554	-2.815672	24730.154069
HLA A*0216	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.453982	1.638299	-2.815683	28443.442301
HLA B*5101	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.405538	1.589799	-2.815740	25441.231128
HLA A*3001	1:348-356	9	IAINTFGGI	0.883060	0.298110	-3.997127	1.181170	-2.815957	9934.068390
HLA B*4002	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.567277	1.751011	-2.816266	36921.273378
HLA B*4402	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.407216	1.590840	-2.816376	25539.692013
HLA B*1509	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.415171	1.598716	-2.816455	26011.836285
HLA B*4402	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.350530	1.534036	-2.816494	22414.529707
HLA B*1509	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.454962	1.638299	-2.816663	28507.680970
HLA A*2601	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.401781	1.585042	-2.816739	25222.103118
HLA A*0216	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.465321	1.648439	-2.816882	29195.826177
HLA A*0219	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.407791	1.590840	-2.816951	25573.565347
HLA B*3501	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.371743	1.554751	-2.816992	23536.567728
HLA A*1101	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.403858	1.586804	-2.817054	25343.012726
HLA A*0216	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.434042	1.616917	-2.817125	27167.024567
HLA B*4601	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.394714	1.577554	-2.817160	24814.986659
HLA B*4501	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.610399	1.793234	-2.817165	40775.483433
HLA A*6802	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.227052	1.409864	-2.817188	16867.567113
HLA B*7301	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.546766	1.729555	-2.817211	35218.079293
HLA A*1101	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.449993	1.632662	-2.817331	28183.357471
HLA B*1502	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.467903	1.650328	-2.817575	29369.926072
HLA A*2603	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.509280	1.691666	-2.817614	32305.735553
HLA B*1502	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.512569	1.694587	-2.817982	32551.343103
HLA A*0301	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.327373	1.509182	-2.818191	21250.693472
HLA B*0803	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.250317	1.431809	-2.818508	17795.780784
HLA B*4601	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.409593	1.590840	-2.818753	25679.900375
HLA B*4001	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.380812	1.561867	-2.818946	24033.230032
HLA A*6802	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.405818	1.586804	-2.819013	25457.614875
HLA A*2603	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.886325	1.067242	-2.819084	7697.069940
HLA B*5401	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.542224	1.723131	-2.819093	34851.711668
HLA B*1509	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-3.574394	0.755176	-2.819217	3753.130859
HLA A*8001	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.358215	1.538857	-2.819358	22814.701792
HLA A*2603	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.000647	1.181170	-2.819477	10014.901312
HLA A*2603	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.236775	1.417212	-2.819563	17249.424724
HLA B*5801	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.352151	1.532461	-2.819690	22498.355546
HLA B*4402	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.405576	1.585464	-2.820111	25443.433371
HLA A*2403	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.411332	1.590840	-2.820492	25782.911237
HLA B*5701	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.410362	1.589799	-2.820563	25725.369192
HLA A*6801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-3.776257	0.955683	-2.820573	5973.883644
HLA A*0216	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.481826	1.661000	-2.820826	30326.752117
HLA A*3201	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.261176	1.440103	-2.821073	18246.365367
HLA B*5101	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.375928	1.554751	-2.821176	23764.438862
HLA A*2501	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.375930	1.554751	-2.821179	23764.567425
HLA A*6901	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.360101	1.538857	-2.821245	22914.027659
HLA A*0201	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.153955	1.332686	-2.821269	14254.607693
HLA A*0202	1:266-274	9	AAEMRADLV	0.998847	0.162308	-3.982631	1.161155	-2.821476	9607.951963
HLA A*2402	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.527888	1.706161	-2.821726	33719.999144
HLA B*1502	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.355797	1.534036	-2.821761	22688.050306
HLA B*5401	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.254187	0.432298	-2.821889	1795.506969
HLA B*2705	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.286957	1.465019	-2.821939	19362.314315
HLA A*2402	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.221141	1.398961	-2.822181	16639.533352
HLA A*2402	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.573493	1.751118	-2.822376	37453.586232
HLA A*0211	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.529020	1.706161	-2.822859	33808.041024

HLA A*0250	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.253343	1.430389	-2.822954	17920.213684
HLA B*4601	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.305786	1.482642	-2.823144	20220.227553
HLA A*2403	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.362087	1.538857	-2.823230	23019.015630
HLA B*1502	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.471676	1.648439	-2.823238	29626.212001
HLA A*2601	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-3.890493	1.067242	-2.823252	7771.295430
HLA A*2403	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.155981	1.332686	-2.823295	14321.236789
HLA B*3901	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.122082	1.298743	-2.823340	13245.920858
HLA A*2301	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.378228	1.554751	-2.823476	23890.635911
HLA B*0802	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.362343	1.538857	-2.823486	23032.593438
HLA A*0202	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.574624	1.751118	-2.823506	37551.173244
HLA B*4501	1:194-202	9	DARSDVYSL	1.476461	0.343280	-4.643703	1.819741	-2.823962	44025.375480
HLA A*2602	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.586996	1.762988	-2.824008	38636.332831
HLA B*4002	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.627022	1.802719	-2.824302	42366.415886
HLA A*2603	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.109183	1.284672	-2.824512	12858.297899
HLA A*2601	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.358555	1.534036	-2.824519	22832.605439
HLA A*2501	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.392799	1.568231	-2.824568	24705.816747
HLA B*1502	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.575690	1.751118	-2.824572	37643.515647
HLA A*3201	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.577666	1.752221	-2.825445	37815.173182
HLA A*0301	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.351110	1.525646	-2.825463	22444.500976
HLA B*1502	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.543732	1.718039	-2.825693	34972.967298
HLA A*3001	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-3.619734	0.793337	-2.826397	4166.142001
HLA B*5701	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.365282	1.538857	-2.826425	23189.001433
HLA A*0219	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.352118	1.525646	-2.826471	22496.651620
HLA B*5801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.356067	1.529572	-2.826495	22702.169779
HLA A*2301	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.475165	1.648439	-2.826726	29865.178271
HLA B*3501	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.443677	1.616917	-2.826760	27776.486713
HLA A*0216	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.352590	1.525646	-2.826944	22521.127508
HLA A*2402	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.076643	1.249564	-2.827080	11930.073407
HLA A*2403	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.416987	1.589799	-2.827189	26120.841497
HLA A*0201	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.257600	1.430389	-2.827211	18096.744332
HLA A*0219	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.444591	1.616917	-2.827674	27835.002404
HLA A*2501	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.471998	1.644220	-2.827778	29648.177749
HLA A*0250	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.034226	1.206278	-2.827947	10819.956474
HLA B*5101	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.413510	1.585464	-2.828045	25912.536453
HLA A*0211	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.414884	1.586804	-2.828080	25994.673969
HLA A*0101	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.362333	1.534036	-2.828297	23032.095029
HLA A*0301	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.362390	1.534036	-2.828354	23035.085649
HLA A*0202	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.557940	1.729555	-2.828385	36135.978370
HLA A*6801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.135098	1.306673	-2.828425	13648.920457
HLA B*4002	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.413508	1.584939	-2.828569	25912.396270
HLA B*2705	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.418434	1.589799	-2.828636	26208.034189
HLA B*5801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.354406	1.525646	-2.828760	22615.504554
HLA A*0250	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.418564	1.589799	-2.828765	26215.833390
HLA B*1801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.413834	1.584939	-2.828895	25931.889061
HLA B*3901	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.467388	1.638299	-2.829089	29335.150195
HLA B*1509	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.406868	1.577554	-2.829314	25519.251496
HLA B*0803	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.416130	1.586804	-2.829325	26069.313925
HLA B*3501	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.465107	1.635751	-2.829356	29181.456611
HLA B*0803	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.458848	1.629324	-2.829524	28763.911122
HLA B*0802	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.246901	1.417212	-2.829689	17656.348654
HLA A*0211	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-3.972974	1.143250	-2.829724	9396.680050
HLA A*0202	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.474023	1.644220	-2.829803	29786.759696
HLA A*2902	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.318988	1.488986	-2.830002	20844.323031
HLA B*1503	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-3.798878	0.968816	-2.830062	6293.287916
HLA B*1801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.420906	1.590840	-2.830066	26357.614684
HLA B*1517	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.466326	1.635751	-2.830575	29263.505466
HLA B*4801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.225591	1.394783	-2.830808	16810.903963
HLA B*1509	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.248024	1.417212	-2.830812	17702.065768
HLA B*0702	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.261202	1.430389	-2.830813	18247.451218
HLA A*6802	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.069003	1.238104	-2.830899	11722.023581
HLA A*0201	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.392799	1.561867	-2.830933	24705.816747
HLA A*3301	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.537229	1.706161	-2.831068	34453.163673
HLA B*1509	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.313795	1.482642	-2.831154	20596.595177
HLA A*2902	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.277317	1.445980	-2.831337	18937.268156
HLA A*3101	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.093710	1.262230	-2.831479	12408.228285

HLA A*3101	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.116152	1.284672	-2.831481	13066.282864
HLA A*2601	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.277503	1.445980	-2.831523	18945.363319
HLA A*2501	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.467501	1.635751	-2.831750	29342.768780
HLA B*7301	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.582952	1.751011	-2.831942	38278.281764
HLA A*2603	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.262382	1.430389	-2.831992	18297.074348
HLA A*2602	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.482362	1.650328	-2.832034	30364.181872
HLA A*3001	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.226911	1.394783	-2.832129	16862.092901
HLA B*0803	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.470541	1.638299	-2.832242	29548.900457
HLA B*4002	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.579426	1.746933	-2.832493	37968.711386
HLA A*0101	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.371351	1.538857	-2.832494	23515.313184
HLA A*0206	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.070610	1.238104	-2.832506	11765.479689
HLA B*1801	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.468486	1.635751	-2.832734	29409.356752
HLA A*2402	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.287885	1.454961	-2.832925	19403.734004
HLA B*5101	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.139731	1.306673	-2.833058	13795.310733
HLA B*4001	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.359549	1.525910	-2.833639	22884.915017
HLA B*1509	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.359686	1.525910	-2.833776	22892.096825
HLA B*4402	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.411386	1.577554	-2.833832	25786.119538
HLA B*0801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.060408	1.226371	-2.834037	11492.332286
HLA A*8001	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.402359	1.568231	-2.834129	25255.691864
HLA A*6901	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.360440	1.525646	-2.834793	22931.885192
HLA B*1517	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.451741	1.616917	-2.834823	28297.022884
HLA A*3301	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.364439	1.529572	-2.834866	23144.008615
HLA A*0101	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.367328	1.532461	-2.834868	23298.526158
HLA B*0803	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.433631	1.598716	-2.834915	27141.316885
HLA B*1502	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.267243	1.431809	-2.835433	18503.025070
HLA A*0206	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.245705	1.409864	-2.835841	17607.796417
HLA A*6901	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.089983	1.254080	-2.835903	12302.220072
HLA A*2602	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.290977	1.454961	-2.836017	19542.370140
HLA B*3501	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.214328	1.378166	-2.836162	16380.518178
HLA B*0803	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.404798	1.568231	-2.836567	25397.913262
HLA A*3002	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.559744	1.723131	-2.836613	36286.428275
HLA A*2501	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.453651	1.616917	-2.836733	28421.754076
HLA A*0216	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.428034	1.590840	-2.837195	26793.808085
HLA A*0212	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.428051	1.590840	-2.837211	26794.822765
HLA B*1503	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.681380	0.844164	-2.837216	4801.532315
HLA A*6801	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.427069	1.589799	-2.837270	26734.299188
HLA B*0801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.202035	1.364704	-2.837331	15923.375276
HLA A*3201	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.566995	1.729555	-2.837440	36897.312357
HLA A*0212	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.018634	1.181170	-2.837464	10438.409523
HLA A*6801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-3.998781	1.161199	-2.837582	9971.975044
HLA A*0301	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.367220	1.529572	-2.837648	23292.728927
HLA B*4402	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.392468	1.554751	-2.837717	24686.978475
HLA B*1801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.236751	1.398961	-2.837791	17248.491575
HLA B*4501	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.646967	1.809098	-2.837869	44357.443016
HLA A*2301	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.467381	1.629324	-2.838057	29334.674099
HLA A*2402	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.470889	1.632662	-2.838227	29572.568660
HLA A*0219	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.377114	1.538857	-2.838257	23829.451934
HLA A*6801	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.589378	1.751011	-2.838368	38848.859753
HLA A*6901	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.088019	1.249564	-2.838456	12246.706852
HLA A*1101	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.499466	1.661000	-2.838466	31583.905739
HLA A*0250	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.556591	1.718039	-2.838552	36023.940215
HLA B*4002	1:93-101	9	EYVDGVTLR	1.073712	0.719522	-4.631862	1.793234	-2.838627	42841.203662
HLA A*2601	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.364598	1.525910	-2.838688	23152.524225
HLA B*1517	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.482947	1.644220	-2.838726	30405.111881
HLA A*0202	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.095937	1.257069	-2.838868	12472.028275
HLA A*2301	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.424278	1.584939	-2.839339	26563.030187
HLA A*0301	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.340556	1.501143	-2.839413	21905.646109
HLA A*1101	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.348763	1.509182	-2.839580	22323.527331
HLA A*2403	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.218049	1.378166	-2.839883	16521.490321
HLA B*3801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.458796	1.618772	-2.840024	28760.487915
HLA B*1509	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.295411	1.454961	-2.840450	19742.889415
HLA A*2601	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.858113	1.017549	-2.840564	7212.948260
HLA B*0802	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.272637	1.431809	-2.840828	18734.286383
HLA B*3501	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.153636	1.312789	-2.840846	14244.123795
HLA A*2902	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.431827	1.590840	-2.840987	27028.784218

HLA B*0702	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.123149	1.282160	-2.840989	13278.494012
HLA A*2902	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.366774	1.525646	-2.841127	23268.799122
HLA B*4501	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.640910	1.799748	-2.841161	43743.097326
HLA A*2301	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.111735	1.270418	-2.841317	12934.064546
HLA B*0702	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.367448	1.525910	-2.841538	23304.955210
HLA B*2705	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.750859	0.909118	-2.841740	5634.544674
HLA A*0202	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.112111	1.270153	-2.841958	12945.264890
HLA B*0801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.240921	1.398961	-2.841961	17414.918918
HLA B*5101	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.427069	1.585042	-2.842027	26734.299188
HLA A*1101	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.329558	1.487180	-2.842379	21357.879305
HLA A*2602	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.471930	1.629324	-2.842606	29643.526707
HLA B*1503	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.343916	1.501143	-2.842772	22075.768483
HLA A*2601	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.381674	1.538857	-2.842818	24080.993711
HLA B*1517	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.433979	1.590840	-2.843139	27163.056651
HLA B*1509	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.273650	1.430389	-2.843260	18778.019376
HLA B*1502	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.535049	1.691666	-2.843383	34280.629254
HLA A*3301	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.606494	1.762988	-2.843506	40410.504712
HLA B*4002	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.643290	1.799748	-2.843541	43983.477087
HLA B*3501	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.063265	1.219563	-2.843702	11568.182950
HLA B*1509	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.125907	1.282160	-2.843747	13363.096895
HLA B*0803	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.428822	1.584939	-2.843883	26842.410876
HLA B*0803	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.376440	1.532461	-2.843979	23792.482124
HLA B*1503	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-3.793182	0.949124	-2.844058	6211.299194
HLA B*1502	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.442801	1.598716	-2.844085	27720.493369
HLA A*2902	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.274512	1.430389	-2.844123	18815.338841
HLA B*4801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.406255	1.561867	-2.844388	25483.244222
HLA A*2602	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.595560	1.751118	-2.844442	39405.765762
HLA A*3002	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.551166	1.706161	-2.845005	35576.748391
HLA A*2601	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.370785	1.525646	-2.845138	23484.674289
HLA B*5401	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.563207	1.718039	-2.845168	36576.939416
HLA A*0202	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.563273	1.718039	-2.845234	36582.480397
HLA B*5301	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.400019	1.554751	-2.845268	25119.973862
HLA A*0250	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.596443	1.751118	-2.845325	39486.003330
HLA B*0802	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.407462	1.561867	-2.845596	25554.203659
HLA A*2601	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.332904	1.487180	-2.845724	21523.049009
HLA A*2301	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.481903	1.635751	-2.846152	30332.166724
HLA A*0203	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.788455	0.942253	-2.846202	6144.057700
HLA A*0206	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-3.972533	1.126330	-2.846203	9387.127929
HLA B*3801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.431345	1.585042	-2.846303	26998.825175
HLA A*2602	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.258103	1.411765	-2.846338	18117.707360
HLA B*4002	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.538044	1.691666	-2.846378	34517.900982
HLA A*0216	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.864048	1.017549	-2.846499	7312.192499
HLA B*5801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.355684	1.509182	-2.846502	22682.159559
HLA B*3801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.437409	1.590840	-2.846569	27378.451897
HLA B*4403	1:19-27	9	FGGMSEVHL	1.633241	0.175857	-4.655737	1.809098	-2.846640	45262.353360
HLA A*3002	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.944419	1.097502	-2.846916	8798.705849
HLA B*5801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.292916	1.445980	-2.846936	19629.785766
HLA A*6901	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.348323	1.501143	-2.847180	22300.955170
HLA A*2601	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.234007	1.386802	-2.847205	17139.846272
HLA B*5401	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.553382	1.706161	-2.847221	35758.707819
HLA A*3002	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.187793	1.340547	-2.847246	15409.642113
HLA A*3002	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.373183	1.525910	-2.847273	23614.750720
HLA A*0206	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.026872	1.179436	-2.847435	10638.285116
HLA B*5701	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.381552	1.534036	-2.847516	24074.220338
HLA B*4403	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.650362	1.802719	-2.847642	44705.556884
HLA B*5301	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.278464	1.430389	-2.848074	18987.329087
HLA B*4501	1:27-35	9	LARDLRLHR	1.122977	0.679742	-4.650977	1.802719	-2.848258	44768.967064
HLA A*6801	1:379-387	9	NRGFKIRTL	1.378825	0.430354	-4.657979	1.809179	-2.848800	45496.557764
HLA B*2705	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.336148	1.487180	-2.848969	21684.451105
HLA A*0211	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.484739	1.635751	-2.848988	30530.875824
HLA B*7301	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.596056	1.746933	-2.849123	39450.772598
HLA B*5101	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.119455	1.270153	-2.849302	13166.047926
HLA B*0802	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.434345	1.585042	-2.849303	27185.990391
HLA B*5301	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.600609	1.751118	-2.849491	39866.564753
HLA B*5701	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.248701	1.398961	-2.849740	17729.667934

HLA B*5301	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.579351	1.729555	-2.849796	37962.138946
HLA B*3501	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-3.968525	1.118640	-2.849884	9300.890150
HLA A*0202	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.244784	1.394783	-2.850001	17570.495542
HLA B*4601	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.412034	1.561867	-2.850168	25824.650310
HLA B*4001	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.315266	1.465019	-2.850248	20666.465657
HLA A*3001	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.237066	1.386802	-2.850264	17260.999973
HLA B*4801	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.383044	1.532461	-2.850584	24157.064230
HLA A*0211	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-3.950466	1.099547	-2.850919	8922.085348
HLA B*1502	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.339917	1.488986	-2.850931	21873.435877
HLA B*5401	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.545711	1.694587	-2.851124	35132.636975
HLA A*6802	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.413071	1.561867	-2.851204	25886.335310
HLA B*4501	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.602392	1.751011	-2.851381	40030.597626
HLA A*2602	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.512658	1.661000	-2.851659	32558.035558
HLA B*0803	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.377614	1.525910	-2.851705	23856.926590
HLA B*4801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.390649	1.538857	-2.851793	24583.823939
HLA B*0702	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.390854	1.538857	-2.851997	24595.397293
HLA B*4402	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.381604	1.529572	-2.852032	24077.085763
HLA A*8001	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.429801	1.577554	-2.852247	26903.033664
HLA A*2602	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.604549	1.752221	-2.852328	40229.895186
HLA B*0801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.391242	1.538857	-2.852385	24617.361727
HLA A*0203	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.262476	1.409864	-2.852612	18301.034182
HLA B*4801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.318140	1.465019	-2.853121	20803.654419
HLA A*1101	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.159796	1.306673	-2.853123	14447.612641
HLA A*6801	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.485811	1.632662	-2.853149	30606.285707
HLA A*3001	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.109667	1.256417	-2.853251	12872.635652
HLA A*2403	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.156399	1.303070	-2.853328	14335.034213
HLA B*1501	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.216470	1.363134	-2.853337	16461.536389
HLA A*3002	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.431018	1.577554	-2.853464	26978.530376
HLA B*5801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.354627	1.501143	-2.853484	22627.008132
HLA A*0250	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.548103	1.694587	-2.853516	35326.655558
HLA A*0101	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.299661	1.445980	-2.853681	19937.051528
HLA B*0802	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.186402	1.332686	-2.853716	15360.369300
HLA A*2602	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.270969	1.417212	-2.853757	18662.465611
HLA A*8001	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.379694	1.525910	-2.853784	23971.421503
HLA A*0202	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.560029	1.706161	-2.853867	36310.189023
HLA B*0702	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.408691	1.554751	-2.853940	25626.608390
HLA A*0206	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.470863	1.616917	-2.853946	29570.808884
HLA A*3001	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.194493	1.340547	-2.853946	15649.241175
HLA B*0801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-3.839561	0.985326	-2.854235	6911.324483
HLA B*4001	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.198018	1.343697	-2.854321	15776.748817
HLA A*3201	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.175932	1.321448	-2.854484	14994.512553
HLA B*3801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.499612	1.645104	-2.854508	31594.501173
HLA A*0212	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.416487	1.561867	-2.854620	26090.759620
HLA B*5101	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.416557	1.561867	-2.854691	26094.994407
HLA B*1503	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.090026	1.235214	-2.854812	12303.418096
HLA B*3801	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.453538	1.598716	-2.854822	28414.374624
HLA B*1501	1:453-461	9	KQANSPSTP	0.696748	0.084681	-3.636270	0.781429	-2.854841	4327.825525
HLA B*1801	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.423493	1.568231	-2.855262	26515.076706
HLA B*0801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.267057	1.411765	-2.855292	18495.118913
HLA A*6802	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.195870	1.340547	-2.855323	15698.931043
HLA A*2501	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.387828	1.532461	-2.855367	24424.613805
HLA B*4001	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.344477	1.488986	-2.855491	22104.330107
HLA B*2705	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.305114	1.449604	-2.855510	20188.966435
HLA B*1509	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.423819	1.568231	-2.855589	26535.022868
HLA A*2602	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.573672	1.718039	-2.855633	37468.988499
HLA B*1801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.474472	1.618772	-2.855700	29817.553929
HLA B*5301	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.295836	1.440103	-2.855733	19762.230922
HLA B*2705	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.385436	1.529572	-2.855864	24290.470652
HLA B*4403	1:254-262	9	ALAKNPENR	1.033268	0.766480	-4.655965	1.799748	-2.856217	45286.111432
HLA A*0203	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.879390	1.022974	-2.856416	7575.124117
HLA A*3001	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.155243	1.298743	-2.856500	14296.929881
HLA A*0206	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-3.959343	1.102823	-2.856520	9106.316229
HLA A*1101	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.321575	1.465019	-2.856556	20968.848307
HLA A*6801	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.501695	1.645104	-2.856592	31746.473986
HLA A*2402	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.038238	1.181170	-2.857068	10920.397178

HLA A*6901	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.328318	1.471168	-2.857149	21296.959249
HLA A*8001	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.344346	1.487180	-2.857166	22097.634530
HLA B*4001	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.344409	1.487180	-2.857230	22100.862501
HLA A*3002	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.322270	1.465019	-2.857251	21002.453192
HLA B*3901	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.297443	1.440103	-2.857340	19835.493839
HLA A*2602	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.563513	1.706161	-2.857352	36602.672498
HLA A*2301	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.474378	1.616917	-2.857461	29811.102241
HLA A*0219	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.289340	1.431809	-2.857530	19468.820621
HLA A*2601	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-3.540486	0.682948	-2.857538	3471.250373
HLA B*1517	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.303603	1.445980	-2.857623	20118.859935
HLA B*4801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.387214	1.529572	-2.857642	24390.151049
HLA A*1101	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.303730	1.445980	-2.857750	20124.738197
HLA A*0301	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.345022	1.487180	-2.857843	22132.090542
HLA B*4801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.120123	1.262230	-2.857892	13186.291902
HLA A*2601	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.387501	1.529572	-2.857929	24406.254020
HLA A*2402	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.518948	1.661000	-2.857948	33032.980767
HLA B*5101	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.340887	1.482642	-2.858245	21922.361987
HLA A*2301	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.448221	1.589799	-2.858423	28068.630115
HLA A*2902	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.443520	1.585042	-2.858478	27766.420601
HLA B*1501	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.165252	1.306673	-2.858578	14630.244810
HLA A*2902	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.420486	1.561867	-2.858619	26332.103111
HLA B*1501	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.420565	1.561867	-2.858699	26336.946984
HLA A*2603	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.245541	1.386802	-2.858738	17601.129744
HLA A*3201	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.609953	1.751118	-2.858835	40733.592705
HLA A*0101	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.347842	1.488986	-2.858856	22276.236512
HLA B*1501	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-3.979280	1.120342	-2.858939	9534.116567
HLA B*0801	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.391401	1.532461	-2.858941	24626.419442
HLA A*0203	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.674331	0.815296	-2.859035	4724.234002
HLA B*4601	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.299421	1.440103	-2.859318	19926.053124
HLA A*0211	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-3.606220	0.746693	-2.859527	4038.497616
HLA B*1801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.348535	1.488986	-2.859549	22311.815926
HLA B*0801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.779687	0.920120	-2.859567	6021.254828
HLA A*0211	1:456-464	9	NSPSTPELV	0.868149	0.229670	-3.957670	1.097819	-2.859851	9071.307614
HLA A*0250	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.589435	1.729555	-2.859880	38853.904113
HLA B*5101	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.495655	1.635751	-2.859904	31307.974411
HLA A*0101	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.385690	1.525646	-2.860043	24304.666944
HLA B*5301	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.449887	1.589799	-2.860088	28176.497209
HLA A*0101	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.389710	1.529572	-2.860138	24530.683152
HLA B*4001	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.386068	1.525646	-2.860421	24325.845340
HLA B*1509	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.769697	0.909118	-2.860579	5884.329686
HLA A*2603	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.264421	1.403484	-2.860937	18383.195497
HLA A*2602	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.590539	1.729555	-2.860984	38952.821613
HLA A*0212	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.826390	0.965301	-2.861089	6704.865502
HLA B*4601	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.278419	1.417212	-2.861208	18985.377520
HLA B*5701	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.350415	1.488986	-2.861428	22408.588748
HLA B*4601	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.400296	1.538857	-2.861440	25136.014742
HLA A*2603	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.567965	1.706161	-2.861804	36979.843604
HLA B*0702	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.307863	1.445980	-2.861883	20317.159192
HLA B*4501	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.512268	1.650328	-2.861940	32528.810213
HLA B*1501	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.088329	1.226371	-2.861958	12255.455414
HLA A*0202	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.556547	1.694587	-2.861960	36020.237580
HLA A*3301	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.608898	1.746933	-2.861965	40634.769242
HLA B*5301	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.349165	1.487180	-2.861985	22344.188181
HLA B*3501	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.448799	1.586804	-2.861995	28106.009634
HLA B*1503	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.233763	1.371517	-2.862245	17130.205619
HLA B*1801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.205963	1.343697	-2.862267	16068.060912
HLA A*2402	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.302382	1.440103	-2.862278	20062.342251
HLA B*5701	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.424245	1.561867	-2.862378	26561.018421
HLA A*1101	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.274188	1.411765	-2.862423	18801.297216
HLA A*0202	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.440085	1.577554	-2.862531	27547.675017
HLA A*0301	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.308704	1.445980	-2.862724	20356.546382
HLA B*0802	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.396831	1.534036	-2.862795	24936.237867
HLA A*3201	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.072400	1.209597	-2.862803	11814.081051
HLA B*3801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.397465	1.534036	-2.863429	24972.688098
HLA B*0802	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.450411	1.586804	-2.863606	28210.509996

HLA B*7301	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.492946	1.629324	-2.863622	31113.295518
HLA B*1503	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.122420	1.258359	-2.864062	13256.243769
HLA B*0803	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.402949	1.538857	-2.864092	25290.009412
HLA A*2902	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.204728	1.340547	-2.864181	16022.402604
HLA A*1101	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.134722	1.270418	-2.864304	13637.111305
HLA B*2705	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.396824	1.532461	-2.864363	24935.833163
HLA B*5401	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.353730	1.488986	-2.864743	22580.295946
HLA A*2602	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.347480	1.482642	-2.864838	22257.685397
HLA B*5101	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.295347	1.430389	-2.864958	19740.005841
HLA A*3001	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.101806	1.236758	-2.865048	12641.718060
HLA B*5101	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.509280	1.644220	-2.865059	32305.735553
HLA B*3501	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.354138	1.488986	-2.865152	22601.561254
HLA A*0202	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-2.962376	0.096922	-2.865454	917.014829
HLA B*1501	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.397928	1.532461	-2.865468	24999.316881
HLA A*0250	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.516088	1.650328	-2.865761	32816.211439
HLA A*6901	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-3.978801	1.112976	-2.865826	9523.600354
HLA B*4402	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.427722	1.561867	-2.865855	26774.536465
HLA B*4801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.355151	1.488986	-2.866165	22654.321946
HLA B*4002	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.355217	1.488986	-2.866231	22657.753813
HLA B*3801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.120470	1.254080	-2.866390	13196.853913
HLA B*4403	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.456562	1.589799	-2.866763	28612.900804
HLA B*4501	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.613796	1.746933	-2.866864	41095.708675
HLA B*4501	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.552162	1.685171	-2.866991	35658.447752
HLA B*5401	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.558717	1.691666	-2.867052	36200.744072
HLA A*8001	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.313170	1.445980	-2.867190	20566.977363
HLA B*5301	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.349900	1.482642	-2.867258	22382.055541
HLA B*5101	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.454161	1.586804	-2.867356	28455.139271
HLA A*0212	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.284573	1.417212	-2.867361	19256.286490
HLA A*3301	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.368548	1.501143	-2.867404	23364.034108
HLA A*2902	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.332805	1.465019	-2.867787	21518.159198
HLA A*2603	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.500537	1.632662	-2.867876	31661.916558
HLA A*0201	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.397468	1.529572	-2.867896	24972.823197
HLA A*8001	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.357190	1.488986	-2.868204	22760.951903
HLA A*3201	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.023310	1.154939	-2.868370	10551.393175
HLA B*1517	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-3.982217	1.113773	-2.868445	9598.808197
HLA A*3301	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.282395	1.413806	-2.868589	19159.958586
HLA A*1101	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.351237	1.482642	-2.868595	22451.058736
HLA B*4403	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.560332	1.691666	-2.868666	36335.537866
HLA B*7301	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.554033	1.685171	-2.868861	35812.333818
HLA A*0101	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.378148	1.509182	-2.868965	23886.241962
HLA A*0201	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.394756	1.525646	-2.869110	24817.403210
HLA A*2902	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.351770	1.482642	-2.869128	22478.646579
HLA A*0301	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.334283	1.465019	-2.869264	21591.506349
HLA A*0206	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.118943	1.249564	-2.869380	13150.529623
HLA A*2902	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.247646	1.378166	-2.869480	17686.654120
HLA A*6901	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.399089	1.529572	-2.869517	25066.216541
HLA A*3002	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.587626	1.718039	-2.869586	38692.390357
HLA B*3501	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.812101	0.942253	-2.869848	6487.845552
HLA A*3101	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.241441	1.371517	-2.869923	17435.752394
HLA A*0219	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.395917	1.525910	-2.870007	24883.816058
HLA B*0702	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.402651	1.532461	-2.870190	25272.639729
HLA A*6801	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.593330	1.723131	-2.870199	39203.975596
HLA A*0201	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.603095	0.732827	-2.870268	4009.544296
HLA A*0250	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-3.969859	1.099547	-2.870312	9329.514040
HLA B*0802	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.396227	1.525910	-2.870317	24901.592071
HLA B*2705	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.105655	1.235214	-2.870441	12754.239171
HLA B*5401	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.461428	1.590840	-2.870588	28935.278893
HLA A*6801	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.617560	1.746933	-2.870628	41453.418318
HLA A*2603	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.600292	1.729555	-2.870737	39837.459434
HLA B*7301	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.576973	1.706161	-2.870812	37754.871424
HLA B*5101	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.310983	1.440103	-2.870880	20463.650014
HLA B*5701	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.358241	1.487180	-2.871061	22816.059507
HLA B*4001	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.403818	1.532461	-2.871358	25340.682084
HLA A*0211	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.520125	1.648439	-2.871686	33122.633294
HLA A*8001	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.326725	1.454961	-2.871764	21218.987113

HLA B*5301	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.589893	1.718039	-2.871853	38894.913826
HLA B*1502	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.501186	1.629324	-2.871861	31709.227208
HLA A*2902	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.191871	1.319849	-2.872022	15555.044518
HLA A*0216	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.289236	1.417212	-2.872025	19464.186909
HLA A*2402	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.507790	1.635751	-2.872039	32195.120894
HLA B*5101	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.373484	1.501143	-2.872341	23631.108791
HLA A*2601	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.275868	1.403484	-2.872384	18874.162797
HLA B*7301	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.624780	1.752221	-2.872559	42148.324636
HLA A*0301	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.355308	1.482642	-2.872667	22662.534779
HLA B*5701	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.398849	1.525910	-2.872939	25052.388600
HLA A*0212	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.109832	1.236758	-2.873074	12877.511342
HLA A*2902	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.112092	1.238694	-2.873398	12944.704642
HLA B*4402	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.360691	1.487180	-2.873512	22945.163343
HLA B*3501	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.412549	1.538857	-2.873692	25855.264602
HLA A*2902	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.285533	1.411765	-2.873769	19298.940981
HLA A*2501	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.435731	1.561867	-2.873865	27272.902206
HLA A*0301	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.180674	1.306673	-2.874000	15159.106806
HLA A*0206	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.509757	1.635751	-2.874005	32341.233442
HLA B*3501	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.383260	1.509182	-2.874078	24169.090430
HLA A*0203	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-3.572002	0.697848	-2.874154	3732.518176
HLA A*2601	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.383418	1.509182	-2.874235	24177.852409
HLA A*0203	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-3.803464	0.929186	-2.874278	6360.097827
HLA B*5301	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.459536	1.585042	-2.874494	28809.540880
HLA A*0212	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.345758	1.471168	-2.874590	22169.598454
HLA A*2902	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.408642	1.534036	-2.874606	25623.697176
HLA A*0203	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.436767	1.561867	-2.874901	27338.046514
HLA B*4001	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-3.978082	1.103143	-2.874939	9507.847780
HLA B*4403	1:38-46	9	AVKVLRADL	1.192397	0.558614	-4.626115	1.751011	-2.875104	42278.037916
HLA A*3101	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.278593	1.403484	-2.875109	18992.979492
HLA A*0211	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.519479	1.644220	-2.875259	33073.392744
HLA B*3801	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.452819	1.577554	-2.875265	28367.375640
HLA B*5301	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.494372	1.618772	-2.875600	31215.633379
HLA B*1503	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-3.671817	0.796188	-2.875630	4696.966386
HLA B*1801	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.408264	1.532461	-2.875803	25601.388853
HLA B*1509	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.408292	1.532461	-2.875831	25603.050915
HLA B*3501	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.287596	1.411765	-2.875831	19390.826737
HLA B*4403	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-3.998509	1.122659	-2.875850	9965.719123
HLA A*6802	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.307795	1.431809	-2.875985	20313.971948
HLA A*2403	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.321972	1.445980	-2.875992	20988.028289
HLA B*7301	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.526565	1.650328	-2.876237	33617.452110
HLA B*4402	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.415213	1.538857	-2.876357	26014.369389
HLA B*0802	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.408905	1.532461	-2.876444	25639.227472
HLA A*2301	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.363745	1.487180	-2.876566	23107.102149
HLA A*2603	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-3.530891	0.654207	-2.876684	3395.397642
HLA B*0802	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.431662	1.554751	-2.876911	27018.550565
HLA B*4501	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.583129	1.706161	-2.876967	38293.816010
HLA A*1101	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.468222	1.590840	-2.877382	29391.542797
HLA B*4001	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.309270	1.431809	-2.877461	20383.104216
HLA A*0203	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.218157	1.340547	-2.877610	16525.602286
HLA A*3101	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.294924	1.417212	-2.877713	19720.792774
HLA B*4801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.294948	1.417212	-2.877736	19721.859675
HLA A*0206	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.199202	1.321448	-2.877753	15819.824147
HLA A*3201	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.595884	1.718039	-2.877845	39435.195700
HLA A*0203	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.039009	1.161155	-2.877854	10939.792010
HLA B*5801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.349066	1.471168	-2.877898	22339.111815
HLA B*4402	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.403901	1.525910	-2.877991	25345.480698
HLA B*4501	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.640987	1.762988	-2.877999	43750.907318
HLA B*5301	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.068030	1.190001	-2.878028	11695.799212
HLA A*3201	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.464959	1.586804	-2.878154	29171.512594
HLA A*3301	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.523362	1.645104	-2.878259	33370.479481
HLA A*6802	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.783192	0.904921	-2.878271	6070.052386
HLA B*3901	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.057730	1.179436	-2.878294	11421.674037
HLA B*0801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-3.998814	1.120342	-2.878472	9972.730334
HLA A*2501	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.469428	1.590840	-2.878588	29473.225650
HLA B*4501	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-3.653195	0.774481	-2.878714	4499.823029

HLA A*0212	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.976348	1.097502	-2.878846	9469.963392
HLA A*6802	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.417852	1.538857	-2.878995	26172.895691
HLA A*2501	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.325007	1.445980	-2.879027	21135.239597
HLA A*2301	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.540281	1.661000	-2.879281	34696.134151
HLA A*0201	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.411750	1.532461	-2.879290	25807.751114
HLA B*0801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.128867	1.249564	-2.879304	13454.497074
HLA B*2705	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.441213	1.561867	-2.879346	27619.302312
HLA B*7301	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.597764	1.718039	-2.879724	39606.237589
HLA A*0206	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.524032	1.644220	-2.879812	33421.970385
HLA B*4001	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.142415	1.262230	-2.880184	13880.803270
HLA A*8001	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.442202	1.561867	-2.880335	27682.278711
HLA A*0202	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.518760	1.638299	-2.880461	33018.687479
HLA A*3101	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.279479	1.398961	-2.880518	19031.755738
HLA B*2705	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.471361	1.590840	-2.880521	29604.742997
HLA A*1101	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.442423	1.561867	-2.880556	27696.359549
HLA B*5101	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.497633	1.616917	-2.880716	31450.911501
HLA B*4601	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.406370	1.525646	-2.880723	25490.000333
HLA A*0211	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.290653	1.409864	-2.880789	19527.785941
HLA A*0250	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.513488	1.632662	-2.880826	32620.270748
HLA B*0801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.390036	1.509182	-2.880854	24549.136540
HLA B*0702	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.410578	1.529572	-2.881006	25738.176147
HLA A*0211	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-3.863366	0.982334	-2.881033	7300.729630
HLA B*5401	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.519333	1.638299	-2.881034	33062.301354
HLA B*1801	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.498066	1.616917	-2.881148	31482.233942
HLA A*2603	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.293249	1.411765	-2.881484	19644.871245
HLA B*0702	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.407192	1.525646	-2.881546	25538.310381
HLA A*2902	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.336898	1.454961	-2.881937	21721.905456
HLA A*6901	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.331654	1.449604	-2.882050	21461.193416
HLA A*2601	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.195104	1.312789	-2.882315	15671.268434
HLA A*2403	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-3.426531	0.543984	-2.882547	2670.122694
HLA A*2402	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.521283	1.638299	-2.882984	33211.091763
HLA A*2501	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.370174	1.487180	-2.882994	23451.664644
HLA A*1101	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.261176	1.378166	-2.883010	18246.365367
HLA B*5101	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.277837	1.394783	-2.883054	18959.922820
HLA B*1801	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.438118	1.554751	-2.883367	27423.219003
HLA B*4801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.409027	1.525646	-2.883381	25646.441167
HLA B*4601	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.338479	1.454961	-2.883518	21801.135918
HLA A*2603	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.533862	1.650328	-2.883535	34187.102595
HLA B*1509	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.216273	1.332686	-2.883587	16454.057461
HLA B*3501	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.416170	1.532461	-2.883709	26071.711580
HLA A*0101	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.385138	1.501143	-2.883994	24273.787472
HLA B*5701	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.416585	1.532461	-2.884125	26096.688514
HLA A*8001	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.418237	1.534036	-2.884201	26196.127159
HLA B*4601	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.416766	1.532461	-2.884306	26107.561653
HLA B*3801	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.522662	1.638299	-2.884363	33316.724705
HLA A*0203	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.316185	1.431809	-2.884375	20710.227010
HLA B*4002	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.529502	1.645104	-2.884398	33845.555863
HLA B*0803	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.439237	1.554751	-2.884485	27493.927735
HLA B*0801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-3.853503	0.968816	-2.884687	7136.793443
HLA A*0202	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.316509	1.431809	-2.884700	20725.694307
HLA A*0201	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.324831	1.440103	-2.884728	21126.665888
HLA B*4403	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.256484	1.371517	-2.884967	18050.300875
HLA A*2501	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.471777	1.586804	-2.884973	29633.104607
HLA A*2602	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.017314	1.132158	-2.885156	10406.721220
HLA A*3101	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.295035	1.409864	-2.885171	19725.807714
HLA A*8001	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.367834	1.482642	-2.885192	23325.641050
HLA A*6802	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.394376	1.509182	-2.885193	24795.662715
HLA B*3801	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.453811	1.568231	-2.885580	28432.211580
HLA B*0801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.340577	1.454961	-2.885616	21906.712699
HLA B*4002	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.081079	1.195398	-2.885681	12052.550050
HLA B*1501	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.415866	1.529572	-2.886294	26053.523114
HLA A*0101	1:243-251	9	LSADLDAVV	0.948699	0.148803	-3.983824	1.097502	-2.886322	9634.393081
HLA B*3901	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.285289	1.398961	-2.886329	19288.085901
HLA A*3101	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.316890	1.430389	-2.886500	20743.866310
HLA B*4002	1:8-16	9	SDRYELGEI	0.899282	0.162410	-3.948225	1.061692	-2.886533	8876.156782

HLA A*3001	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.300450	1.413806	-2.886644	19973.324517
HLA B*4601	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.264839	1.378166	-2.886673	18400.906310
HLA B*4601	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.416407	1.529572	-2.886835	26085.961025
HLA B*4001	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.396051	1.509182	-2.886868	24891.490506
HLA B*5401	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.496040	1.609050	-2.886991	31335.763855
HLA B*5701	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.416611	1.529572	-2.887039	26098.241542
HLA A*2501	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.304268	1.417212	-2.887057	20149.685473
HLA A*0206	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-3.972561	1.085412	-2.887149	9387.737348
HLA A*0212	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.030401	1.143250	-2.887150	10725.080291
HLA A*6901	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-3.775730	0.888375	-2.887355	5966.648786
HLA A*0206	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.169786	1.282160	-2.887626	14783.800705
HLA B*1501	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.413296	1.525646	-2.887650	25899.782853
HLA A*1101	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.421719	1.534036	-2.887683	26406.997641
HLA A*0211	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.504604	1.616917	-2.887687	31959.807776
HLA A*2402	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.172399	1.284672	-2.887727	14873.005094
HLA B*2705	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.319606	1.431809	-2.887796	20874.001459
HLA A*2902	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.420739	1.532461	-2.888279	26347.492612
HLA B*1502	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.318699	1.430389	-2.888309	20830.457491
HLA A*2602	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.580027	1.691666	-2.888361	38021.331885
HLA A*2301	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.532587	1.644220	-2.888366	34086.822956
HLA A*2603	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.635346	1.746933	-2.888413	43186.295342
HLA B*4501	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.422572	1.534036	-2.888536	26458.906385
HLA B*5301	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.583124	1.694587	-2.888537	38293.401682
HLA B*3901	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.320397	1.431809	-2.888588	20912.092244
HLA A*3001	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.113342	1.224706	-2.888636	12982.013956
HLA A*2501	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.473779	1.585042	-2.888737	29770.005531
HLA A*3201	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.083649	1.194908	-2.888741	12124.093591
HLA A*2403	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.421204	1.532461	-2.888744	26375.730062
HLA A*2501	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.397956	1.509182	-2.888774	25000.939856
HLA A*0101	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.300598	1.411765	-2.888833	19980.133046
HLA A*2601	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.390109	1.501143	-2.888966	24553.253936
HLA A*2402	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.505934	1.616917	-2.889016	32057.818597
HLA B*0702	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.450970	1.561867	-2.889104	28246.855934
HLA A*1101	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.321415	1.431809	-2.889605	20961.135863
HLA A*0201	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.398995	1.509182	-2.889812	25060.792910
HLA B*4402	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.304080	1.413806	-2.890274	20140.966755
HLA B*0702	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.373066	1.482642	-2.890424	23608.363925
HLA A*0212	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.416184	1.525646	-2.890537	26072.557865
HLA A*2402	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.476500	1.585464	-2.891035	29957.089641
HLA B*1509	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.392184	1.501143	-2.891040	24670.823751
HLA B*4501	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.642293	1.751118	-2.891176	43882.703716
HLA A*0203	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.362397	1.471168	-2.891229	23035.459504
HLA B*4501	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.536381	1.645104	-2.891277	34385.943339
HLA A*0219	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.362465	1.471168	-2.891297	23039.073746
HLA B*4002	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.642648	1.751118	-2.891530	43918.565847
HLA A*6901	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.153842	1.262230	-2.891612	14250.906613
HLA A*0212	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.751907	0.860149	-2.891758	5648.156177
HLA A*0212	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.421336	1.529572	-2.891764	26383.721900
HLA A*0101	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.378965	1.487180	-2.891786	23931.253548
HLA B*4501	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.583805	1.691666	-2.892139	38353.526120
HLA A*3101	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.374821	1.482642	-2.892179	23703.962779
HLA A*0206	1:456-464	9	NSPSTPELV	0.868149	0.229670	-3.990004	1.097819	-2.892185	9772.451123
HLA B*1503	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.765910	0.873256	-2.892653	5833.237076
HLA B*1517	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.102281	1.209597	-2.892683	12655.540450
HLA A*0250	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.598889	1.706161	-2.892728	39709.003788
HLA B*4601	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.379926	1.487180	-2.892747	23984.263532
HLA B*4002	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.015439	1.122659	-2.892780	10361.891289
HLA A*0101	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.324810	1.431809	-2.893000	21125.637277
HLA B*4402	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.348037	1.454961	-2.893076	22286.241251
HLA B*4801	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.177760	1.284672	-2.893089	15057.755862
HLA B*4501	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.382076	1.488986	-2.893090	24103.281130
HLA A*3002	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.526046	1.632662	-2.893384	33577.283589
HLA B*4501	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.510558	1.616917	-2.893640	32400.950716
HLA A*0101	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.358753	1.465019	-2.893734	22842.983633
HLA A*0211	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.484612	1.590840	-2.893772	30521.958019

HLA B*7301	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.588774	1.694587	-2.894188	38794.884101
HLA B*4002	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.646537	1.752221	-2.894316	44313.550447
HLA A*0211	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.532629	1.638299	-2.894330	34090.142425
HLA A*3301	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.579517	1.685171	-2.894346	37976.723086
HLA A*6801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.119094	1.224706	-2.894388	13155.083558
HLA B*1801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.326304	1.431809	-2.894495	21198.449225
HLA B*7301	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.131358	1.236758	-2.894600	13531.873296
HLA B*7301	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.586275	1.691666	-2.894609	38572.217477
HLA A*0203	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.151714	1.257069	-2.894645	14181.228693
HLA A*6901	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.326546	1.431809	-2.894737	21210.264687
HLA A*2402	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.485616	1.590840	-2.894776	30592.545933
HLA B*5301	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.601053	1.706161	-2.894892	39907.347928
HLA B*4403	1:111-119	9	TPKRAIEVI	1.642371	0.104562	-4.641969	1.746933	-2.895037	43849.954665
HLA A*0206	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.556117	1.661000	-2.895117	35984.594842
HLA B*4801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.377889	1.482642	-2.895248	23872.031779
HLA B*4002	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.624907	1.729555	-2.895353	42160.639394
HLA B*4402	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.427952	1.532461	-2.895492	26788.735262
HLA A*0201	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.152574	1.257069	-2.895505	14209.335619
HLA A*0206	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.533811	1.638299	-2.895512	34183.033972
HLA B*3501	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-3.789691	0.894030	-2.895661	6161.566140
HLA A*0206	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-3.650169	0.754459	-2.895710	4468.577529
HLA B*1502	1:358-366	9	RDVQVPDVR	1.051802	0.654359	-4.602350	1.706161	-2.896189	40026.699716
HLA B*3901	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.473840	1.577554	-2.896286	29774.193189
HLA B*2705	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.306192	1.409864	-2.896329	20239.160741
HLA B*5301	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.541522	1.645104	-2.896418	34795.382613
HLA A*0301	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.367589	1.471168	-2.896421	23312.521071
HLA B*3901	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.458479	1.561867	-2.896613	28739.490791
HLA A*0203	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.291402	1.394783	-2.896620	19561.515204
HLA B*4402	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.001187	1.104337	-2.896850	10027.370354
HLA B*4001	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.072301	1.175404	-2.896897	11811.397015
HLA B*4402	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.406172	1.509182	-2.896990	25478.419526
HLA A*2402	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.483846	1.586804	-2.897042	30468.176205
HLA B*4801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.406321	1.509182	-2.897138	25487.104637
HLA B*4402	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.422840	1.525646	-2.897193	26475.229350
HLA B*5701	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.406403	1.509182	-2.897220	25491.930979
HLA B*4601	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.159538	1.262230	-2.897307	14439.017600
HLA A*0211	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.001892	1.104337	-2.897555	10043.657656
HLA A*0212	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-3.696506	0.798791	-2.897715	4971.710598
HLA B*1503	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.863131	0.965301	-2.897830	7296.781084
HLA A*0202	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.920863	1.022974	-2.897889	8334.179737
HLA A*3002	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.147466	1.249564	-2.897902	14043.197116
HLA B*4002	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.073354	1.175404	-2.897950	11840.058193
HLA A*6802	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.107732	1.209597	-2.898134	12815.380387
HLA A*0211	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.559469	1.661000	-2.898470	36263.467792
HLA B*2705	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.424470	1.525646	-2.898824	26574.816451
HLA B*1801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.408294	1.509182	-2.899112	25603.189425
HLA B*4402	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.339231	1.440103	-2.899128	21838.909959
HLA A*2403	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.108793	1.209597	-2.899196	12846.755796
HLA B*0801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.424849	1.525646	-2.899202	26597.972991
HLA A*0201	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.400618	1.501143	-2.899475	25154.651326
HLA A*2601	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.382175	1.482642	-2.899533	24108.758388
HLA A*6802	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.370785	1.471168	-2.899616	23484.674289
HLA B*3901	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.439014	1.538857	-2.900157	27479.801151
HLA A*2403	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.462158	1.561867	-2.900292	28984.002769
HLA B*4002	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.137452	1.236758	-2.900694	13723.108175
HLA A*2902	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.410286	1.509182	-2.901104	25720.916092
HLA B*4001	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.430722	1.529572	-2.901150	26960.146834
HLA A*2602	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-3.857220	0.956046	-2.901174	7198.135416
HLA B*0803	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.435433	1.534036	-2.901397	27254.170632
HLA B*1509	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.341505	1.440103	-2.901402	21953.575342
HLA A*3301	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.562451	1.661000	-2.901451	36513.278426
HLA B*0802	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.410655	1.509182	-2.901473	25742.771499
HLA A*6801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.200226	1.298743	-2.901483	15857.182593
HLA B*1502	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.537650	1.635751	-2.901898	34486.543247
HLA B*1801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.488733	1.586804	-2.901929	30812.957674

HLA B*4402	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.245717	1.343697	-2.902020	17608.272705
HLA B*4403	1:323-331	9	DRSIGSVGR	1.099289	0.651829	-4.653247	1.751118	-2.902129	45003.539977
HLA B*0801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.138843	1.236390	-2.902454	13767.129001
HLA B*1517	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.411649	1.509182	-2.902467	25801.748278
HLA A*2902	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.224008	1.321448	-2.902559	16749.718564
HLA B*1509	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.280783	1.378166	-2.902617	19088.984236
HLA A*1101	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.480184	1.577554	-2.902629	30212.287685
HLA A*0206	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.057758	1.154939	-2.902818	11422.415541
HLA A*6802	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.432395	1.529572	-2.902823	27064.193291
HLA A*3001	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.163847	1.261014	-2.902832	14582.990782
HLA A*0203	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.432729	1.529572	-2.903157	27084.992108
HLA A*6801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.343411	1.440103	-2.903307	22050.106506
HLA B*5701	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.429002	1.525646	-2.903356	26853.594720
HLA B*4403	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.621632	1.718039	-2.903593	41843.885643
HLA B*1503	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.465586	1.561867	-2.903720	29213.679552
HLA B*4601	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.413155	1.509182	-2.903973	25891.377320
HLA B*5701	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.369159	1.465019	-2.904140	23396.920408
HLA A*0301	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.335972	1.431809	-2.904163	21675.654604
HLA A*3201	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.224139	1.319849	-2.904290	16754.793724
HLA B*1509	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.099818	1.195398	-2.904420	12583.992072
HLA B*2705	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-3.636758	0.732333	-2.904425	4332.698182
HLA B*2705	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.350457	1.445980	-2.904477	22410.770958
HLA B*1517	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.430492	1.525910	-2.904582	26945.857185
HLA B*4801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.405945	1.501143	-2.904801	25465.052997
HLA A*2301	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.490390	1.585464	-2.904925	30930.701821
HLA A*2403	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.370012	1.465019	-2.904993	23442.912185
HLA B*7301	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.628220	1.723131	-2.905089	42483.468071
HLA B*5401	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-3.859804	0.954621	-2.905183	7241.098349
HLA B*1517	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-3.567881	0.662443	-2.905438	3697.268022
HLA A*0101	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.376795	1.471168	-2.905626	23811.925983
HLA B*5801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.355525	1.449604	-2.905921	22673.816952
HLA B*4001	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.407091	1.501143	-2.905948	25532.370217
HLA A*2501	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.445038	1.538857	-2.906181	27863.628126
HLA A*3002	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.544684	1.638299	-2.906385	35049.677253
HLA A*2301	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-3.907532	1.001026	-2.906505	8082.242641
HLA B*4001	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.377856	1.471168	-2.906688	23870.223817
HLA B*4002	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.601309	1.694587	-2.906722	39930.887349
HLA A*0301	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.361701	1.454961	-2.906741	22998.601715
HLA A*3301	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.492215	1.585464	-2.906751	31060.992171
HLA A*0219	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.324006	1.417212	-2.906795	21086.587138
HLA B*3501	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.432623	1.525646	-2.906976	27078.399204
HLA B*3501	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.436596	1.529572	-2.907024	27327.252252
HLA A*2403	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.389712	1.482642	-2.907070	24530.815860
HLA B*4501	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.636626	1.729555	-2.907072	43313.813259
HLA B*1501	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.416339	1.509182	-2.907156	26081.868803
HLA B*3801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.317235	1.409864	-2.907371	20760.369508
HLA A*2601	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.169039	1.261650	-2.907389	14758.389336
HLA B*0802	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.378587	1.471168	-2.907419	23910.418688
HLA B*5701	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.408651	1.501143	-2.907508	25624.251667
HLA B*1502	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.498495	1.590840	-2.907656	31513.417093
HLA B*3501	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.362709	1.454961	-2.907749	23052.039832
HLA B*0801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.390541	1.482642	-2.907900	24577.706895
HLA B*1503	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.294774	1.386802	-2.907972	19713.965968
HLA B*3501	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.089260	1.181170	-2.908090	12281.738617
HLA A*0301	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.315800	1.407681	-2.908119	20691.860593
HLA A*2902	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.134539	1.226371	-2.908168	13631.358048
HLA A*2402	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.397273	1.488986	-2.908286	24961.612398
HLA B*4002	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.558701	1.650328	-2.908373	36199.373203
HLA A*0211	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.348500	1.440103	-2.908396	22310.005433
HLA B*5701	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.358043	1.449604	-2.908439	22805.693545
HLA B*2705	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.409619	1.501143	-2.908476	25681.428600
HLA A*0219	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.470426	1.561867	-2.908560	29541.068537
HLA B*4601	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.409718	1.501143	-2.908574	25687.264478
HLA B*4801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.339003	1.430389	-2.908614	21827.452795
HLA A*0201	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.379891	1.471168	-2.908723	23982.317328

HLA A*0212	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-3.692587	0.783751	-2.908836	4927.049206
HLA A*2601	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.363804	1.454961	-2.908843	23110.227532
HLA B*4402	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.397940	1.488986	-2.908954	24999.993108
HLA A*0206	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.104602	1.195398	-2.909204	12723.365039
HLA B*2705	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.312795	1.403484	-2.909311	20549.182655
HLA B*1501	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.145741	1.236390	-2.909352	13987.544134
HLA B*4402	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.374563	1.465019	-2.909544	23689.861036
HLA B*4501	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.661804	1.752221	-2.909583	45899.029318
HLA A*3301	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.216414	1.306673	-2.909740	16459.399205
HLA A*0211	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.242496	1.332686	-2.909810	17478.156017
HLA A*8001	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.439394	1.529572	-2.909822	27503.895061
HLA A*2602	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.555109	1.645104	-2.910005	35901.177104
HLA A*6801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-3.701111	0.790996	-2.910115	5024.708028
HLA B*1509	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.356136	1.445980	-2.910155	22705.731729
HLA A*0216	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.192398	1.282160	-2.910238	15573.905783
HLA B*1509	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.472195	1.561867	-2.910329	29661.653853
HLA A*2902	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.440130	1.529572	-2.910557	27550.506730
HLA A*2501	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.444739	1.534036	-2.910703	27844.490830
HLA B*4801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.342833	1.431809	-2.911023	22020.781021
HLA B*1503	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.149209	1.238104	-2.911106	14099.681737
HLA A*6801	1:25-33	9	VHLARDLRL	1.381366	0.381622	-4.674185	1.762988	-2.911197	47226.448483
HLA B*3901	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.443743	1.532461	-2.911283	27780.694528
HLA B*5401	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.555503	1.644220	-2.911283	35933.821129
HLA B*4501	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.547095	1.635751	-2.911343	35244.763023
HLA B*4002	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.510086	1.598716	-2.911369	32365.737469
HLA A*0212	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.173696	1.262230	-2.911465	14917.486119
HLA A*2403	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.196401	1.284672	-2.911730	15718.136844
HLA A*0219	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.366699	1.454961	-2.911738	23264.771259
HLA B*1503	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-3.703263	0.791452	-2.911811	5049.669556
HLA A*3301	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.629900	1.718039	-2.911860	42648.115359
HLA A*2501	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.394646	1.482642	-2.912004	24811.093820
HLA B*5101	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.399197	1.487180	-2.912017	25072.455168
HLA A*3001	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.255766	1.343697	-2.912069	18020.444655
HLA B*1801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.451057	1.538857	-2.912200	28252.510557
HLA B*7301	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.510920	1.598716	-2.912203	32427.955938
HLA A*6801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.941031	1.028753	-2.912278	8730.333650
HLA A*0202	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.011976	1.099547	-2.912429	10279.592308
HLA A*2301	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.503300	1.590840	-2.912460	31863.992735
HLA A*2601	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.044676	1.132158	-2.912518	11083.476964
HLA A*0216	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.474390	1.561867	-2.912523	29811.908626
HLA A*3301	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.521673	1.609050	-2.912624	33240.930101
HLA B*5301	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.551051	1.638299	-2.912752	35567.318794
HLA A*0202	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.561227	1.648439	-2.912788	36410.508742
HLA B*3801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.497795	1.584939	-2.912857	31462.653763
HLA B*4601	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.358882	1.445980	-2.912902	22849.781435
HLA B*4801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.400226	1.487180	-2.913046	25131.935581
HLA A*0202	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.503904	1.590840	-2.913064	31908.325379
HLA B*3501	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.359084	1.445980	-2.913104	22860.414780
HLA B*1517	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.316612	1.403484	-2.913129	20730.628338
HLA A*0203	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.277914	1.364704	-2.913210	18963.307968
HLA B*7301	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.558374	1.645104	-2.913271	36172.162427
HLA A*0202	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.646194	0.732827	-2.913367	4427.860895
HLA B*4403	1:350-358	9	INTFGGITR	1.090401	0.639154	-4.642949	1.729555	-2.913394	43948.988484
HLA A*3101	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.278111	1.364704	-2.913407	18971.927435
HLA A*6801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-3.188585	0.275124	-2.913461	1543.777741
HLA B*3801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.343888	1.430389	-2.913498	22074.335400
HLA B*0802	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.439624	1.525646	-2.913978	27518.480643
HLA A*2601	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.345903	1.431809	-2.914094	22177.035676
HLA A*3101	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.385321	1.471168	-2.914153	24284.032476
HLA A*8001	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.446649	1.532461	-2.914189	27967.227294
HLA A*3001	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.243941	1.329751	-2.914190	17536.404117
HLA B*3801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.385466	1.471168	-2.914298	24292.179025
HLA B*4801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.385497	1.471168	-2.914329	24293.887519
HLA A*0219	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.344731	1.430389	-2.914342	22117.248734
HLA A*6802	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.440357	1.525910	-2.914448	27564.967907

HLA A*0206	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.722472	0.807959	-2.914514	5278.036008
HLA B*0801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.415838	1.501143	-2.914695	26051.831809
HLA A*0203	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.447190	1.532461	-2.914729	28002.047861
HLA B*1501	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.806903	0.892112	-2.914791	6410.670301
HLA A*2902	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.035137	1.120342	-2.914795	10842.691815
HLA B*4403	1:571-579	9	WVDAEPRLR	1.181874	0.570347	-4.667055	1.752221	-2.914834	46457.367836
HLA A*3101	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.328708	1.413806	-2.914902	21316.093394
HLA B*3501	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-3.876646	0.961636	-2.915010	7527.409704
HLA A*2301	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.347168	1.431809	-2.915358	22241.676413
HLA A*0202	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.532392	1.616917	-2.915474	34071.520700
HLA B*1801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.500575	1.585042	-2.915533	31664.657276
HLA B*0802	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.365169	1.449604	-2.915565	23182.980619
HLA A*2902	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.048698	1.133041	-2.915658	11186.605977
HLA B*3801	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.470440	1.554751	-2.915689	29542.027436
HLA B*4001	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.346312	1.430389	-2.915923	22197.921207
HLA B*5301	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.381219	1.465019	-2.916200	24055.733521
HLA A*8001	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.348084	1.431809	-2.916274	22288.652704
HLA A*2402	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.560595	1.644220	-2.916375	36357.560515
HLA A*3002	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.333630	1.417212	-2.916418	21559.058227
HLA A*6801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-3.410574	0.494046	-2.916528	2573.792410
HLA B*0801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.170792	1.254080	-2.916711	14818.071259
HLA B*4002	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.639916	1.723131	-2.916785	43643.110808
HLA B*5301	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.945565	1.028753	-2.916812	8821.965350
HLA A*0202	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.882204	0.965301	-2.916903	7624.378291
HLA A*2902	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.315948	1.398961	-2.916987	20698.914058
HLA A*3002	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.367122	1.449604	-2.917518	23287.437063
HLA A*0219	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.492063	0.574537	-2.917526	3105.010360
HLA A*0250	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.443182	1.525646	-2.917535	27744.798315
HLA B*2705	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.400212	1.482642	-2.917570	25131.119829
HLA A*2601	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.357738	1.440103	-2.917634	22789.660268
HLA B*5401	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.553485	1.635751	-2.917734	35767.220661
HLA A*6802	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.291177	0.373369	-2.917808	1955.137866
HLA B*1517	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.237912	1.319849	-2.918062	17294.649564
HLA B*5101	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.239667	1.321448	-2.918219	17364.681892
HLA B*1501	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.419372	1.501143	-2.918229	26264.666530
HLA A*3201	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.248127	1.329751	-2.918377	17706.279983
HLA B*1509	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.448217	1.529572	-2.918644	28068.326420
HLA A*0219	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.031829	1.112976	-2.918853	10760.415441
HLA A*2602	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.383930	1.465019	-2.918911	24206.383521
HLA A*0301	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.098352	1.179436	-2.918916	12541.583020
HLA A*3201	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.181289	1.262230	-2.919059	15180.608421
HLA A*2602	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.480959	1.561867	-2.919092	30266.272751
HLA B*4402	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.041838	1.122659	-2.919179	11011.280986
HLA A*0211	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.051414	1.132158	-2.919256	11256.784343
HLA B*1509	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.474012	1.554751	-2.919260	29785.953992
HLA A*3201	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.567723	1.648439	-2.919284	36959.243488
HLA A*0206	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.189597	1.270153	-2.919444	15473.799203
HLA B*1801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.445103	1.525646	-2.919457	27867.849142
HLA B*1517	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.481365	1.561867	-2.919499	30294.612543
HLA A*0219	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.176679	1.257069	-2.919611	15020.330485
HLA A*3201	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.580636	1.661000	-2.919636	38074.643243
HLA A*0219	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.449276	1.529572	-2.919704	28136.892820
HLA A*3301	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.186120	1.266360	-2.919760	15350.400788
HLA A*6802	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.445552	1.525646	-2.919906	27896.659561
HLA B*5101	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.391169	1.471168	-2.920001	24613.233580
HLA A*2403	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.158711	1.238694	-2.920017	14411.547817
HLA B*4601	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.283489	1.363134	-2.920356	19208.321938
HLA B*0702	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.319361	1.398961	-2.920401	20862.260455
HLA B*3901	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.110819	1.190001	-2.920817	12906.804290
HLA B*7301	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-3.944019	1.022881	-2.921138	8790.617565
HLA B*0702	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.392395	1.471168	-2.921227	24682.838654
HLA A*0203	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-3.796345	0.875034	-2.921311	6256.693150
HLA A*0203	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.117078	1.195398	-2.921680	13094.163301
HLA B*1501	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.286391	1.364704	-2.921687	19337.086503
HLA B*4402	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.331595	1.409864	-2.921731	21458.291045

HLA A*2601	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.386775	1.465019	-2.921757	24365.489247
HLA A*6802	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.371365	1.449604	-2.921761	23516.076487
HLA B*5701	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.367784	1.445980	-2.921804	23322.991228
HLA A*0212	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.430988	1.509182	-2.921805	26976.633082
HLA B*1501	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.316749	1.394783	-2.921966	20737.134082
HLA A*0216	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.332002	1.409864	-2.922138	21478.383493
HLA A*0101	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.362251	1.440103	-2.922148	23027.734404
HLA B*0801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.352661	1.430389	-2.922271	22524.782908
HLA B*3501	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.317129	1.394783	-2.922346	20755.316114
HLA A*2403	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.332225	1.409864	-2.922361	21489.424919
HLA B*0801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.330080	1.407681	-2.922399	21383.545429
HLA B*5401	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.229245	1.306673	-2.922571	16952.920144
HLA B*1509	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.432141	1.509182	-2.922959	27048.385167
HLA B*1502	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.491214	1.568231	-2.922984	30989.491035
HLA A*0212	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.363414	1.440103	-2.923311	23089.482903
HLA B*4002	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.478297	1.554751	-2.923546	30081.325912
HLA A*0301	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.363668	1.440103	-2.923565	23102.977291
HLA A*0219	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.432769	1.509182	-2.923586	27087.483178
HLA B*1509	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.333533	1.409864	-2.923670	21554.276841
HLA A*0101	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.322843	1.398961	-2.923883	21030.195008
HLA A*0201	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.318741	1.394783	-2.923958	20832.486018
HLA B*7301	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.584961	1.661000	-2.923962	38455.746353
HLA B*0803	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.395210	1.471168	-2.924042	24843.328807
HLA A*0301	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.354446	1.430389	-2.924057	22617.584555
HLA A*0216	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.395426	1.471168	-2.924258	24855.696652
HLA A*8001	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.395536	1.471168	-2.924368	24862.017384
HLA A*6801	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.509865	1.585464	-2.924400	32349.282718
HLA A*2902	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.425560	1.501143	-2.924417	26641.608046
HLA B*5101	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.302734	1.378166	-2.924568	20078.629116
HLA B*3901	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.069139	1.144551	-2.924588	11725.702219
HLA A*0250	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.560409	1.635751	-2.924658	36342.025295
HLA B*1502	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.509644	1.584939	-2.924705	32332.836333
HLA B*4601	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.395940	1.471168	-2.924772	24885.162281
HLA B*0801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.374548	1.449604	-2.924944	23689.092092
HLA A*0203	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.426237	1.501143	-2.925094	26683.149306
HLA A*2402	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.407862	1.482642	-2.925220	25577.716189
HLA A*0203	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.451055	1.525646	-2.925408	28252.357715
HLA A*0212	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.426665	1.501143	-2.925521	26709.434468
HLA A*0211	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.342760	1.417212	-2.925548	22017.088301
HLA A*0101	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.375211	1.449604	-2.925607	23725.259485
HLA A*0216	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.365752	1.440103	-2.925649	23214.104997
HLA B*0801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.455234	1.529572	-2.925662	28525.576498
HLA A*2603	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.493919	1.568231	-2.925688	31183.057876
HLA A*2501	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.451391	1.525646	-2.925744	28274.222595
HLA A*3001	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-3.909825	0.984065	-2.925760	8125.030161
HLA A*6901	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.542408	0.616515	-2.925892	3486.645700
HLA A*6802	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.427104	1.501143	-2.925961	26736.468720
HLA A*3101	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.238765	1.312789	-2.925975	17328.645990
HLA A*3002	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.570282	1.644220	-2.926061	37177.626696
HLA A*0101	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.381230	1.454961	-2.926270	24056.384224
HLA B*4403	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.649412	1.723131	-2.926281	44607.955330
HLA B*0802	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.408928	1.482642	-2.926287	25640.614564
HLA A*2501	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.452255	1.525910	-2.926345	28330.568094
HLA A*0216	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.458836	1.532461	-2.926376	28763.133084
HLA A*2601	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.397599	1.471168	-2.926431	24980.389955
HLA A*3101	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.270210	1.343697	-2.926514	18629.883402
HLA A*3201	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.460782	1.534036	-2.926745	28892.263320
HLA B*5401	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.391772	1.465019	-2.926754	24647.478180
HLA B*0801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.229942	1.303070	-2.926872	16980.180924
HLA A*0301	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.338721	1.411765	-2.926956	21813.287302
HLA B*4001	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.188643	1.261650	-2.926993	15439.849616
HLA A*2602	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.516871	1.589799	-2.927072	32875.382900
HLA B*5701	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.398410	1.471168	-2.927242	25027.057185
HLA B*5801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.226052	1.298743	-2.927309	16828.738661
HLA B*1502	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.482312	1.554751	-2.927561	30360.732464

HLA A*2402	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.292575	1.364704	-2.927871	19614.393534
HLA A*3301	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.578221	1.650328	-2.927893	37863.483927
HLA B*4501	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.482935	1.554751	-2.928183	30404.289450
HLA A*3002	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.231267	1.303070	-2.928197	17032.069590
HLA A*0250	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.515163	1.586804	-2.928358	32746.338299
HLA B*2705	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.292027	1.363134	-2.928894	19589.685085
HLA B*1801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.182981	1.254080	-2.928900	15239.854025
HLA B*3801	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.454671	1.525646	-2.929024	28488.563682
HLA B*3801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.346317	1.417212	-2.929105	22198.161385
HLA A*2403	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.458683	1.529572	-2.929111	28753.020514
HLA B*4501	1:573-581	9	DAEPRLRAL	1.463541	0.259590	-4.652262	1.723131	-2.929131	44901.644023
HLA B*1501	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.187887	1.258359	-2.929528	15412.977053
HLA B*4501	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.647688	1.718039	-2.929648	44431.174664
HLA B*4801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.369805	1.440103	-2.929701	23431.754368
HLA A*2403	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.361521	1.431809	-2.929711	22989.023379
HLA B*0802	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.459377	1.529572	-2.929804	28798.944592
HLA B*1502	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.568132	1.638299	-2.929833	36994.050369
HLA B*7301	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.565597	1.635751	-2.929846	36778.735132
HLA B*3901	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.337549	1.407681	-2.929868	21754.480986
HLA A*8001	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.439155	1.509182	-2.929972	27488.722359
HLA B*4402	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.401147	1.471168	-2.929979	25185.288840
HLA B*3901	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.431204	1.501143	-2.930061	26990.062958
HLA A*2603	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-3.680543	0.750403	-2.930140	4792.293844
HLA B*0802	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.431293	1.501143	-2.930150	26995.612032
HLA A*2501	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.818157	0.887960	-2.930197	6578.963470
HLA A*0201	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.362023	1.431809	-2.930214	23015.653557
HLA A*0219	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.462715	1.532461	-2.930255	29021.188260
HLA A*3001	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.188624	1.258359	-2.930266	15439.181407
HLA A*0212	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.462837	1.532461	-2.930377	29029.353481
HLA A*0301	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.347628	1.417212	-2.930416	22265.272622
HLA A*2602	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.566356	1.635751	-2.930604	36843.058263
HLA B*1509	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.271542	1.340547	-2.930995	18687.116573
HLA A*0206	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.362867	1.431809	-2.931057	23060.396848
HLA A*3101	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.342830	1.411765	-2.931065	22020.661891
HLA B*5401	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.550067	1.618772	-2.931294	35486.788109
HLA B*4402	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.432447	1.501143	-2.931303	27067.414597
HLA A*0206	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-3.806401	0.875034	-2.931367	6403.252858
HLA A*0202	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.949075	1.017549	-2.931527	8893.556701
HLA B*1501	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.402806	1.471168	-2.931638	25281.665004
HLA A*3002	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.580241	1.648439	-2.931803	38040.054391
HLA B*5801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.343589	1.411765	-2.931824	22059.174306
HLA B*3901	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.202106	1.270153	-2.931953	15925.959796
HLA A*2603	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.403165	1.471168	-2.931997	25302.599630
HLA A*2902	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.244852	1.312789	-2.932063	17573.252337
HLA A*2603	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.550835	1.618772	-2.932063	35549.620995
HLA B*3801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.387459	1.454961	-2.932498	24403.877503
HLA A*0250	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.571142	1.638299	-2.932843	37251.312044
HLA B*1517	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.404086	1.471168	-2.932918	25356.315197
HLA A*0212	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.265647	1.332686	-2.932962	18435.182315
HLA B*4002	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.618167	1.685171	-2.932995	41511.317382
HLA A*0101	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.363426	1.430389	-2.933037	23090.107469
HLA A*0219	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.434329	1.501143	-2.933185	27184.960898
HLA B*4601	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.239897	1.306673	-2.933224	17373.890552
HLA A*2501	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.336769	1.403484	-2.933285	21715.443197
HLA A*3002	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.009344	1.075727	-2.933617	10217.495792
HLA A*2301	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.422671	1.488986	-2.933684	26464.918938
HLA B*4403	1:169-177	9	SVTQTAAVI	1.325277	0.359894	-4.618939	1.685171	-2.933768	41585.267237
HLA A*3002	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.523623	1.589799	-2.933825	33390.524394
HLA B*0803	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.495913	1.561867	-2.934047	31326.610950
HLA A*0250	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.578853	1.644220	-2.934632	37918.625260
HLA A*6801	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.553553	1.618772	-2.934781	35772.832505
HLA B*1509	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.460462	1.525646	-2.934816	28871.013802
HLA A*0202	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.570921	1.635751	-2.935169	37232.373466
HLA B*4001	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.390144	1.454961	-2.935184	24555.246473
HLA B*1801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.345354	1.409864	-2.935490	22148.979217

HLA A*8001	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.461298	1.525646	-2.935652	28926.670658
HLA B*5401	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.552630	1.616917	-2.935713	35696.857165
HLA A*3001	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-3.284237	0.348457	-2.935780	1924.141507
HLA B*0803	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.424853	1.488986	-2.935867	26598.260777
HLA A*2403	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.206330	1.270418	-2.935912	16081.627159
HLA B*4001	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.353316	1.417212	-2.936105	22558.806564
HLA A*0201	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.386258	1.449604	-2.936654	24336.507286
HLA A*3301	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.340157	1.403484	-2.936673	21885.509160
HLA A*6901	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.055324	1.118640	-2.936684	11358.576021
HLA A*0212	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.346763	1.409864	-2.936899	22220.990138
HLA A*0203	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.446224	1.509182	-2.937042	27939.855470
HLA B*1517	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.386756	1.449604	-2.937152	24364.434753
HLA B*4002	1:137-145	9	RDVKPANIM	0.886768	0.128226	-3.952416	1.014994	-2.937423	8962.237446
HLA B*4402	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.420293	1.482642	-2.937651	26320.424493
HLA A*3101	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.164044	1.226371	-2.937673	14589.619246
HLA A*0212	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.369744	1.431809	-2.937934	23428.458757
HLA B*4801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.387574	1.449604	-2.937970	24410.347452
HLA B*0702	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.447162	1.509182	-2.937979	28000.230064
HLA A*0203	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.325019	1.386802	-2.938217	21135.811301
HLA B*3501	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.237054	1.298743	-2.938312	17260.533079
HLA A*3301	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.630053	1.691666	-2.938387	42663.114898
HLA A*0211	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.370225	1.431809	-2.938416	23454.455970
HLA B*5301	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.500467	1.561867	-2.938600	31656.778351
HLA A*2601	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.803788	0.865145	-2.938643	6364.847825
HLA B*1509	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.350422	1.411765	-2.938657	22408.952435
HLA A*2603	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.555586	1.616917	-2.938668	35940.625703
HLA B*0702	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.201020	1.262230	-2.938790	15886.204651
HLA A*2402	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.404011	1.465019	-2.938992	25351.925981
HLA A*2902	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.379146	1.440103	-2.939043	23941.224462
HLA B*4001	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.317533	1.378166	-2.939368	20774.637943
HLA A*2602	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.524847	1.585464	-2.939383	33484.770088
HLA A*2403	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.465109	1.525646	-2.939463	29181.614480
HLA B*4001	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.338446	1.398961	-2.939486	21799.484797
HLA A*2301	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.473840	1.534036	-2.939804	29774.193189
HLA A*3101	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.394879	1.454961	-2.939918	24824.385681
HLA A*0211	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.465652	1.525646	-2.940006	29218.105085
HLA B*4001	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.349982	1.409864	-2.940118	22386.293898
HLA B*0702	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.130211	1.190001	-2.940210	13496.195915
HLA B*4403	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.634944	1.694587	-2.940357	43146.362560
HLA A*8001	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.370817	1.430389	-2.940428	23486.453049
HLA A*0250	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.588890	1.648439	-2.940451	38805.169390
HLA A*0211	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.063115	1.122659	-2.940456	11564.178357
HLA B*1801	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.357672	1.417212	-2.940460	22786.208422
HLA A*2603	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.585577	1.645104	-2.940473	38510.291827
HLA B*2705	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.449730	1.509182	-2.940547	28166.286134
HLA B*1502	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.261996	1.321448	-2.940548	18280.847983
HLA B*3801	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.479683	1.538857	-2.940827	30177.493923
HLA B*1517	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.473302	1.532461	-2.940841	29737.329833
HLA B*0801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.814154	0.873256	-2.940898	6518.594300
HLA A*3001	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.211391	1.270418	-2.940973	16270.120888
HLA A*0250	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.601995	1.661000	-2.940995	39994.015527
HLA A*0216	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.450230	1.509182	-2.941048	28198.761032
HLA B*0702	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.335834	1.394783	-2.941051	21668.737197
HLA B*0803	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.466756	1.525646	-2.941110	29292.490966
HLA A*2602	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.589982	1.648439	-2.941543	38902.910501
HLA B*3901	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.471251	1.529572	-2.941679	29597.216510
HLA A*2403	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.451214	1.509182	-2.942032	28262.752891
HLA B*4001	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.353828	1.411765	-2.942063	22585.427119
HLA A*0250	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.559049	1.616917	-2.942131	36228.368330
HLA A*0301	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.345878	1.403484	-2.942394	22175.715987
HLA B*2705	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.314049	1.371517	-2.942532	20608.632625
HLA A*2501	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.413728	1.471168	-2.942560	25925.576841
HLA B*3801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.374396	1.431809	-2.942586	23680.763457
HLA A*0211	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.965700	1.022974	-2.942727	9240.605593
HLA A*0301	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.356594	1.413806	-2.942788	22729.697289

HLA A*2403	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-3.971706	1.028753	-2.942953	9369.269209
HLA A*8001	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.321201	1.378166	-2.943035	20950.819238
HLA B*3501	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.958135	1.014988	-2.943147	9081.029624
HLA A*2403	1:225-233	9	AYQHVREDP	0.311821	0.227808	-3.482783	0.539629	-2.943154	3039.363109
HLA A*2601	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.392935	1.449604	-2.943331	24713.569996
HLA B*0801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.205710	1.262230	-2.943479	16058.675600
HLA A*2602	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.840877	0.897363	-2.943514	6932.294351
HLA A*0206	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-3.742546	0.798791	-2.943755	5527.723976
HLA A*6901	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.357573	1.413806	-2.943768	22781.031634
HLA A*8001	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.408813	1.465019	-2.943795	25633.818533
HLA A*2501	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.375636	1.431809	-2.943827	23748.502398
HLA A*2603	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.588105	1.644220	-2.943885	38735.115523
HLA A*2403	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.415213	1.471168	-2.944045	26014.369389
HLA B*1517	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-3.158958	0.214737	-2.944221	1441.975126
HLA A*0301	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.105509	1.161199	-2.944310	12749.961949
HLA A*0219	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-3.959418	1.014988	-2.944430	9107.892819
HLA A*0203	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-3.731452	0.786863	-2.944589	5388.303882
HLA B*0802	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.390588	1.445980	-2.944608	24580.366292
HLA B*5301	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.588962	1.644220	-2.944742	38811.677817
HLA A*3002	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.605876	1.661000	-2.944877	40353.049495
HLA B*1517	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.229667	1.284672	-2.944996	16969.436600
HLA B*0801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.183751	1.238694	-2.945057	15266.920294
HLA B*5801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.352755	1.407681	-2.945074	22529.657699
HLA A*0202	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.606250	1.661000	-2.945250	40387.775006
HLA B*0803	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.889784	0.944464	-2.945320	7758.609158
HLA B*5801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.359202	1.413806	-2.945396	22866.599232
HLA A*3201	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.349066	1.403484	-2.945582	22339.111815
HLA A*3201	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.581472	1.635751	-2.945721	38148.042638
HLA B*4001	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.395619	1.449604	-2.946015	24866.725357
HLA B*7301	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.532838	1.586804	-2.946033	34106.560103
HLA B*4501	1:40-48	9	KVLRADLAR	0.915954	0.778633	-4.640635	1.694587	-2.946048	43715.418586
HLA B*4002	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-3.952759	1.006578	-2.946181	8969.319010
HLA B*0702	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.324805	1.378166	-2.946639	21125.408704
HLA B*1501	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.396359	1.449604	-2.946755	24909.137245
HLA B*1501	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-3.895893	0.949124	-2.946769	7868.510628
HLA A*6901	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-3.921093	0.974301	-2.946792	8338.599434
HLA A*6901	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.213280	1.266360	-2.946920	16341.042733
HLA B*1801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.476500	1.529572	-2.946928	29957.089641
HLA A*0301	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.346604	1.398961	-2.947643	22212.817151
HLA B*2705	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.346629	1.398961	-2.947669	22214.139048
HLA B*5301	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.525228	1.577554	-2.947674	33514.129072
HLA B*4402	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.365103	1.417212	-2.947892	23179.469199
HLA B*4801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.291943	1.343697	-2.948246	19585.870248
HLA B*4601	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.351834	1.403484	-2.948350	22481.930208
HLA A*2602	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.567152	1.618772	-2.948380	36910.688676
HLA A*2403	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.449591	1.501143	-2.948448	28157.297356
HLA B*1503	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.311601	1.363134	-2.948467	20492.786435
HLA A*6801	1:309-317	9	TDPLPRQDL	1.393424	0.324615	-4.666669	1.718039	-2.948630	46416.168125
HLA A*0101	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.365916	1.417212	-2.948705	23222.897663
HLA A*2403	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.198285	1.249564	-2.948722	15786.481771
HLA B*1501	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.231016	1.282160	-2.948856	17022.213291
HLA B*4501	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.394860	1.445980	-2.948880	24823.311327
HLA A*3201	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.593173	1.644220	-2.948952	39189.768197
HLA B*0802	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.414093	1.465019	-2.949074	25947.325405
HLA A*2501	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.389242	1.440103	-2.949139	24504.288415
HLA B*7301	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.597609	1.648439	-2.949170	39592.098600
HLA A*3101	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.036378	1.086732	-2.949646	10873.707389
HLA B*0802	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.389790	1.440103	-2.949686	24535.195648
HLA B*1801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.450949	1.501143	-2.949806	28245.480656
HLA A*0219	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.389956	1.440103	-2.949853	24544.621479
HLA A*6801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.262758	1.312789	-2.949968	18312.918827
HLA B*5801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.271514	1.321448	-2.950066	18685.903470
HLA B*7301	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-3.555584	0.605498	-2.950085	3594.046817
HLA B*0702	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.405315	1.454961	-2.950354	25428.159234
HLA A*2602	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.541301	1.590840	-2.950461	34777.692630

HLA B*1801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.396751	1.445980	-2.950771	24931.651611
HLA A*0211	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.422201	1.471168	-2.951033	26436.299968
HLA A*0301	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.360999	1.409864	-2.951135	22961.430240
HLA A*8001	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.452338	1.501143	-2.951194	28335.932885
HLA A*0250	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-3.735005	0.783751	-2.951254	5432.559627
HLA A*6901	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.338056	1.386802	-2.951254	21779.916740
HLA B*1502	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.536736	1.585464	-2.951271	34414.044461
HLA B*0702	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-3.867732	0.916314	-2.951417	7374.483504
HLA A*2301	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.071770	1.120342	-2.951428	11796.964813
HLA B*0802	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.406574	1.454961	-2.951614	25502.000289
HLA A*2301	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.369229	1.417212	-2.952018	23400.717958
HLA B*4601	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.133294	1.181170	-2.952124	13592.329635
HLA B*3801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.439399	1.487180	-2.952219	27504.192649
HLA B*4403	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.569140	1.616917	-2.952222	37080.007439
HLA A*0101	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.355736	1.403484	-2.952252	22684.859295
HLA A*0201	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.362138	1.409864	-2.952274	23021.755461
HLA B*1503	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.485049	1.532461	-2.952589	30552.685873
HLA B*0801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.265497	1.312789	-2.952708	18428.800553
HLA A*8001	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.392823	1.440103	-2.952719	24707.153341
HLA A*0203	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-3.846629	0.893801	-2.952828	7024.712170
HLA A*3001	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.162446	1.209597	-2.952849	14536.046655
HLA A*0216	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.285674	1.332686	-2.952989	19305.206306
HLA B*1801	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.383387	1.430389	-2.952998	24176.152075
HLA A*0219	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.347825	1.394783	-2.953042	22275.392944
HLA A*2902	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.424360	1.471168	-2.953192	26568.060270
HLA B*4402	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.383589	1.430389	-2.953200	24187.402658
HLA A*3201	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.543016	1.589799	-2.953217	34915.308917
HLA B*5301	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.589021	1.635751	-2.953270	38816.927344
HLA B*4001	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.356826	1.403484	-2.953342	22741.874098
HLA A*0301	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.223773	1.270418	-2.953354	16740.659603
HLA A*3002	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.179903	1.226371	-2.953532	15132.231676
HLA B*0803	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.483130	1.529572	-2.953558	30417.944674
HLA A*3301	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.361537	1.407681	-2.953856	22989.893972
HLA B*4601	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.348756	1.394783	-2.953973	22323.165030
HLA A*0212	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.053562	1.099547	-2.954015	11312.582913
HLA A*6801	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.508845	1.554751	-2.954094	32273.419194
HLA B*3901	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.357592	1.403484	-2.954108	22782.017599
HLA A*2602	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.541016	1.586804	-2.954212	34754.934721
HLA A*3002	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.215230	1.261014	-2.954215	16414.582395
HLA B*4001	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.400494	1.445980	-2.954514	25147.439914
HLA B*4501	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.615573	1.661000	-2.954573	41264.129210
HLA B*1503	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.073279	1.118640	-2.954638	11838.008662
HLA A*0301	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.332958	1.378166	-2.954792	21525.727234
HLA B*4501	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.563896	1.609050	-2.954846	36634.963407
HLA B*5401	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.539997	1.585042	-2.954955	34673.429612
HLA A*2602	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.529519	0.574537	-2.954981	3384.687235
HLA A*2603	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-3.978012	1.022974	-2.955038	9506.304813
HLA A*2403	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.211532	1.256417	-2.955115	16275.402918
HLA B*4801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.410117	1.454961	-2.955157	25710.899437
HLA B*1502	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.542006	1.586804	-2.955201	34834.181496
HLA A*8001	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.261949	1.306673	-2.955276	18278.870143
HLA A*0216	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.225488	1.270153	-2.955335	16806.902853
HLA A*2403	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.372598	1.417212	-2.955387	23582.961593
HLA B*0803	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.401523	1.445980	-2.955543	25207.098217
HLA B*1502	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.443062	1.487180	-2.955882	27737.144461
HLA A*3101	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.396218	1.440103	-2.956114	24901.053217
HLA B*5101	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.373442	1.417212	-2.956230	23628.807753
HLA A*8001	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.373512	1.417212	-2.956301	23632.642941
HLA B*4403	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.555137	1.598716	-2.956421	35903.507836
HLA B*0801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.297055	1.340547	-2.956508	19817.795949
HLA B*7301	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.541496	1.584939	-2.956557	34793.312044
HLA B*4601	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.406241	1.449604	-2.956637	25482.417067
HLA A*2902	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.218881	1.262230	-2.956650	16553.160956
HLA A*0206	1:14-22	9	GEILGFGGM	0.948298	0.046073	-3.951307	0.994371	-2.956937	8939.381855
HLA B*1509	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.495812	1.538857	-2.956956	31319.324437

HLA B*5801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.351885	1.394783	-2.957102	22484.606111
HLA B*4403	1:477-485	9	TSAITNVVI	1.425064	0.225264	-4.607681	1.650328	-2.957353	40521.056914
HLA A*1101	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.483057	1.525646	-2.957411	30412.843813
HLA A*3101	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.290202	1.332686	-2.957516	19507.512986
HLA A*2902	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.374988	1.417212	-2.957776	23713.069271
HLA B*7301	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.407411	1.449604	-2.957807	25551.162441
HLA A*0250	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.542889	1.585042	-2.957847	34905.110457
HLA A*3001	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.019635	1.061692	-2.957943	10462.493757
HLA A*2501	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.487606	1.529572	-2.958034	30733.048022
HLA A*1101	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.184522	1.226371	-2.958151	15294.034633
HLA A*3002	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.492955	1.534036	-2.958919	31113.968803
HLA A*0216	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.262020	1.303070	-2.958949	18281.836984
HLA B*4002	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.216160	1.257069	-2.959091	16449.785313
HLA B*1503	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.468417	1.509182	-2.959235	29404.743174
HLA B*3901	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.484937	1.525646	-2.959290	30544.753144
HLA A*3201	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.597620	1.638299	-2.959321	39593.169559
HLA B*0702	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.409015	1.449604	-2.959411	25645.747454
HLA A*6901	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.367105	1.407681	-2.959425	23286.555203
HLA B*0802	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.448520	1.488986	-2.959533	28087.921460
HLA A*6901	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.354601	1.394783	-2.959818	22625.661666
HLA A*0216	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.489549	1.529572	-2.959977	30870.855056
HLA A*0206	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-3.057014	0.096922	-2.960091	1140.285534
HLA B*0802	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.390976	1.430389	-2.960587	24602.317302
HLA B*5401	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.550520	1.589799	-2.960722	35523.859520
HLA A*6802	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.347673	1.386802	-2.960870	22267.561340
HLA A*2501	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.425939	1.465019	-2.960920	26664.822786
HLA B*4402	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.410832	1.449604	-2.961227	25753.218534
HLA A*0203	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.411153	1.449604	-2.961549	25772.312731
HLA A*2403	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.373345	1.411765	-2.961581	23623.567335
HLA B*1801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.444244	1.482642	-2.961602	27812.724851
HLA B*7301	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.580375	1.618772	-2.961603	38051.786371
HLA B*7301	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.570857	1.609050	-2.961808	37226.935442
HLA A*2301	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.433062	1.471168	-2.961894	27105.806908
HLA B*5801	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.246708	1.284672	-2.962037	17648.517842
HLA B*5401	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.516819	1.554751	-2.962068	32871.470385
HLA A*1101	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.392531	1.430389	-2.962142	24690.584692
HLA B*4403	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.606452	1.644220	-2.962232	40406.569809
HLA A*2301	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.488292	1.525910	-2.962382	30781.635004
HLA A*2603	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.402503	1.440103	-2.962399	25264.027699
HLA B*4402	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.361570	1.398961	-2.962609	22991.635256
HLA A*0203	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-3.882754	0.920120	-2.962634	7634.036211
HLA A*0201	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.143871	1.181170	-2.962701	13927.439474
HLA A*0202	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.095068	1.132158	-2.962910	12447.088497
HLA B*4002	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-3.442710	0.479739	-2.962971	2771.467382
HLA B*4402	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.409006	1.445980	-2.963026	25645.192498
HLA B*1502	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.403139	1.440103	-2.963036	25301.093948
HLA A*0101	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.295822	1.332686	-2.963136	19761.589463
HLA A*2603	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.488797	1.525646	-2.963150	30817.458759
HLA A*3301	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.595825	1.632662	-2.963164	39429.862559
HLA B*4601	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.096247	1.133041	-2.963207	12480.937798
HLA B*4403	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.572471	1.609050	-2.963422	37365.550269
HLA B*5801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.366945	1.403484	-2.963462	23277.990296
HLA A*0250	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.554380	1.590840	-2.963540	35841.018932
HLA B*4001	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.248482	1.284672	-2.963811	17720.750033
HLA A*2301	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.502732	1.538857	-2.963875	31822.303909
HLA B*1502	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.429040	1.465019	-2.964021	26855.919220
HLA B*5401	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.541618	1.577554	-2.964064	34803.101275
HLA A*3201	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.374057	1.409864	-2.964193	23662.322757
HLA A*2602	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.852206	0.887960	-2.964246	7115.512921
HLA B*4801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.297091	1.332686	-2.964405	19819.404195
HLA A*2603	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.503413	1.538857	-2.964556	31872.268082
HLA B*1509	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.359441	1.394783	-2.964658	22879.220702
HLA A*2402	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.297361	1.332686	-2.964675	19831.738421
HLA A*8001	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.363722	1.398961	-2.964761	23105.852114
HLA A*0201	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.077738	1.112976	-2.964762	11960.187164

HLA B*1502	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.609060	1.644220	-2.964840	40649.940315
HLA B*5401	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.550400	1.585464	-2.964936	35514.059684
HLA A*2402	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.491034	1.525910	-2.965124	30976.584696
HLA A*6802	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.539720	0.574537	-2.965183	3465.133789
HLA B*2705	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.377279	1.411765	-2.965514	23838.477671
HLA A*0101	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.360311	1.394783	-2.965528	22925.062965
HLA A*2601	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.379588	1.413806	-2.965782	23965.586490
HLA A*3201	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.383089	1.417212	-2.965877	24159.547412
HLA A*3301	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.383375	1.417212	-2.966164	24175.498133
HLA A*3001	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.215836	1.249564	-2.966272	16437.509067
HLA A*2501	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.467438	1.501143	-2.966294	29338.483082
HLA A*2403	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.224764	1.258359	-2.966405	16778.921739
HLA B*5801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.222842	1.256417	-2.966425	16704.834207
HLA B*3801	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.528550	1.561867	-2.966684	33771.481256
HLA A*0201	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-3.984717	1.017549	-2.967168	9654.219432
HLA A*0101	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.377109	1.409864	-2.967245	23829.194106
HLA B*5701	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.345542	1.378166	-2.967376	22158.567173
HLA B*4801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.345866	1.378166	-2.967700	22175.116154
HLA B*4403	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.535960	1.568231	-2.967730	34352.661135
HLA A*3201	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.280698	1.312789	-2.967909	19085.266904
HLA B*5101	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.506810	1.538857	-2.967954	32122.573017
HLA B*5101	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.500598	1.532461	-2.968138	31666.370345
HLA A*2402	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.385640	1.417212	-2.968429	24301.905904
HLA B*4002	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.629545	1.661000	-2.968545	42613.290627
HLA A*2301	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.423512	1.454961	-2.968551	26516.224280
HLA B*4403	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.555405	1.586804	-2.968600	35925.657341
HLA A*0219	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.378533	1.409864	-2.968669	23907.443761
HLA A*0202	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.271836	1.303070	-2.968766	18699.757751
HLA A*0206	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.873770	0.904921	-2.968849	7477.730087
HLA A*0101	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.382701	1.413806	-2.968895	24137.991456
HLA A*6801	1:575-583	9	EPRLRALGW	1.410483	0.250517	-4.629895	1.661000	-2.968895	42647.653918
HLA B*4501	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.433918	1.465019	-2.968899	27159.236243
HLA B*5101	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.378895	1.409864	-2.969031	23927.369900
HLA A*0216	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-3.798577	0.829510	-2.969067	6288.931538
HLA B*4801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.372577	1.403484	-2.969093	23581.813390
HLA B*1509	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.434148	1.465019	-2.969129	27173.639049
HLA A*3002	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.834275	0.865145	-2.969129	6827.708042
HLA B*0702	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.268403	1.298743	-2.969661	18552.540266
HLA A*2501	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.254370	1.284672	-2.969698	17962.629366
HLA A*2301	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.531604	1.561867	-2.969738	34009.828364
HLA A*0216	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.179377	1.209597	-2.969779	15113.905315
HLA A*3002	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.373371	1.403484	-2.969888	23624.973187
HLA B*4001	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.377676	1.407681	-2.969995	23860.282472
HLA A*1101	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.410148	1.440103	-2.970044	25712.707711
HLA B*2705	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.377763	1.407681	-2.970082	23865.058965
HLA B*4402	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.364920	1.394783	-2.970137	23169.690190
HLA A*3002	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.479328	1.509182	-2.970146	30152.852198
HLA B*4002	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.555710	1.585464	-2.970246	35950.932225
HLA A*0203	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-3.977030	1.006578	-2.970452	9484.832174
HLA B*4402	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.402340	1.431809	-2.970531	25254.598844
HLA A*3001	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.703521	0.732827	-2.970694	5052.675447
HLA A*2603	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.402829	1.431809	-2.971020	25283.032751
HLA A*2301	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.417076	1.445980	-2.971096	26126.211862
HLA B*4001	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.366116	1.394783	-2.971333	23233.578950
HLA B*4002	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.619837	1.648439	-2.971398	41671.295282
HLA B*5101	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.497321	1.525910	-2.971411	31428.290230
HLA B*7301	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.609769	1.638299	-2.971470	40716.407922
HLA A*2402	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.510372	1.538857	-2.971515	32387.106116
HLA A*2601	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.370559	1.398961	-2.971598	23472.480705
HLA B*4801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.225690	1.254080	-2.971609	16814.724092
HLA B*1503	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.040954	1.069099	-2.971855	10988.905503
HLA B*5301	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.588828	1.616917	-2.971911	38799.711550
HLA A*2403	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.358774	1.386802	-2.971972	22844.095863
HLA A*6901	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.312581	1.340547	-2.972034	20539.068784
HLA A*2602	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.459226	1.487180	-2.972047	28788.975176

HLA B*1801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.242615	1.270418	-2.972197	17482.978982
HLA B*0702	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.375683	1.403484	-2.972199	23751.072072
HLA A*2602	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.616440	1.644220	-2.972219	41346.584964
HLA B*0702	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.292342	1.319849	-2.972493	19603.891289
HLA A*3201	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.209384	1.236758	-2.972626	16195.125566
HLA A*6901	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.206325	1.233662	-2.972664	16081.453160
HLA A*3301	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.602021	1.629324	-2.972697	39996.395592
HLA A*0301	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.367693	1.394783	-2.972910	23318.070930
HLA B*1503	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.498665	1.525646	-2.973018	31525.694338
HLA B*3801	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.474369	1.501143	-2.973225	29810.457149
HLA B*4002	1:392-400	9	STIPPDHVI	1.394582	0.214468	-4.582410	1.609050	-2.973360	38230.475870
HLA A*2301	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.212208	1.238694	-2.973514	16300.780543
HLA B*5401	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.560322	1.586804	-2.973518	36334.751589
HLA B*5101	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.428481	1.454961	-2.973520	26821.363035
HLA B*5101	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.419762	1.445980	-2.973782	26288.263887
HLA B*3901	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.483048	1.509182	-2.973865	30412.185700
HLA A*0101	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.286696	1.312789	-2.973907	19350.690780
HLA A*0216	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.839082	0.865145	-2.973936	6903.701232
HLA A*0212	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.087009	1.112976	-2.974033	12218.251032
HLA B*1501	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.294121	1.319849	-2.974271	19684.339449
HLA B*4402	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.211203	1.236758	-2.974445	16263.080847
HLA B*1501	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.315210	1.340547	-2.974663	20663.782552
HLA A*3001	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.231780	1.257069	-2.974711	17052.168310
HLA B*3801	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.504386	1.529572	-2.974814	31943.732212
HLA B*3501	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.155999	1.181092	-2.974907	14321.856613
HLA A*2603	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.565858	1.590840	-2.975018	36800.827311
HLA B*5101	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.484267	1.509182	-2.975085	30497.694968
HLA B*5401	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.245381	1.270153	-2.975228	17594.655964
HLA A*2301	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.143928	1.168679	-2.975249	13929.247893
HLA B*5701	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.387059	1.411765	-2.975294	24381.444034
HLA B*0801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.181731	1.206278	-2.975453	15196.055852
HLA A*2602	1:155-163	9	MDFGIARAI	1.445600	0.187062	-4.608195	1.632662	-2.975534	40569.093324
HLA A*6901	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-3.629865	0.654207	-2.975658	4264.469847
HLA A*3002	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.195367	1.219563	-2.975804	15680.766652
HLA B*5101	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.505473	1.529572	-2.975901	32023.844481
HLA B*3501	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.447098	1.471168	-2.975930	27996.140453
HLA A*0101	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.383728	1.407681	-2.976047	24195.124109
HLA A*2902	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.379628	1.403484	-2.976144	23967.790662
HLA B*5401	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.130850	1.154698	-2.976153	13516.070049
HLA B*1801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.463502	1.487180	-2.976323	29073.831421
HLA A*3101	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.371125	1.394783	-2.976342	23503.103692
HLA B*0801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.157512	1.181170	-2.976342	14371.840533
HLA A*0202	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.386296	1.409864	-2.976432	24338.613902
HLA A*6801	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.561384	1.584939	-2.976445	36423.708581
HLA B*5301	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.408329	1.431809	-2.976520	25605.267166
HLA B*5101	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.388380	1.411765	-2.976615	24455.685148
HLA A*0250	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.079509	1.102823	-2.976687	12009.073079
HLA B*4801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.386806	1.409864	-2.976942	24367.202897
HLA B*1503	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.079989	1.102823	-2.977166	12022.333816
HLA A*6901	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.172084	1.194908	-2.977176	14862.227186
HLA A*6901	1:585-593	9	GMLDKGADV	0.832496	0.121837	-3.931652	0.954333	-2.977318	8543.812275
HLA B*2705	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.239707	1.262230	-2.977476	17366.278963
HLA A*2601	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.385196	1.407681	-2.977516	24277.070656
HLA A*3001	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.259746	1.282160	-2.977586	18186.349401
HLA B*1517	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.507170	1.529572	-2.977598	32149.172297
HLA B*4403	1:414-422	9	DEITVNVST	1.070685	-0.486156	-3.562425	0.584529	-2.977897	3651.114312
HLA B*4002	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.007075	1.029142	-2.977933	10164.238920
HLA A*0101	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.204380	1.226371	-2.978009	16009.579184
HLA B*1503	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-3.920275	0.942253	-2.978023	8322.915609
HLA A*0219	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.214901	1.236758	-2.978143	16402.154952
HLA A*3201	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.595304	1.616917	-2.978386	39382.535901
HLA B*1503	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.121725	1.143250	-2.978475	13235.033172
HLA B*2705	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.298409	1.319849	-2.978559	19879.646422
HLA B*4501	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.565524	1.586804	-2.978719	36772.567614
HLA A*0101	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.308497	1.329751	-2.978747	20346.857542

HLA B*4801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.424729	1.445980	-2.978749	26590.635507
HLA B*4403	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.614553	1.635751	-2.978802	41167.359143
HLA A*1101	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.508502	1.529572	-2.978930	32247.938298
HLA B*0802	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.382464	1.403484	-2.978980	24124.806089
HLA A*2603	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.608327	1.629324	-2.979003	40581.385746
HLA A*2902	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.365841	1.386802	-2.979039	23218.877746
HLA A*0212	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.282261	1.303070	-2.979190	19154.051262
HLA B*4601	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.386916	1.407681	-2.979236	24373.399406
HLA B*1517	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.504971	1.525646	-2.979324	31986.791407
HLA B*4801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.393149	1.413806	-2.979343	24725.739480
HLA A*0206	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.541254	1.561867	-2.979387	34773.929965
HLA A*0206	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.002432	1.022974	-2.979459	10056.162501
HLA B*4501	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.174391	1.194908	-2.979483	14941.393031
HLA B*0801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.419604	1.440103	-2.979501	26278.737102
HLA B*0803	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.396852	1.417212	-2.979641	24937.452017
HLA A*3301	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.628093	1.648439	-2.979654	42471.059018
HLA A*8001	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.312477	1.332686	-2.979792	20534.180346
HLA B*5701	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.213538	1.233662	-2.979877	16350.769983
HLA B*5701	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.383547	1.403484	-2.980063	24185.047452
HLA B*4501	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.628547	1.648439	-2.980108	42515.426574
HLA A*2403	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.379113	1.398961	-2.980153	23939.411260
HLA A*6801	1:239-247	9	RHEGLSADL	1.161744	0.529922	-4.671967	1.691666	-2.980301	46985.880868
HLA A*3301	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.570378	1.589799	-2.980579	37185.873811
HLA B*3901	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.313380	1.332686	-2.980694	20576.882339
HLA B*4501	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.548988	1.568231	-2.980758	35398.778792
HLA B*1517	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.482138	1.501143	-2.980995	30348.580530
HLA B*4801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.388765	1.407681	-2.981085	24477.392393
HLA B*1509	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.470076	1.488986	-2.981090	29517.265860
HLA A*2402	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.515233	1.534036	-2.981197	32751.653352
HLA A*0250	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-3.942572	0.961256	-2.981316	8761.371663
HLA B*1517	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.886307	0.904921	-2.981385	7696.736825
HLA B*5801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.368376	1.386802	-2.981574	23354.808961
HLA A*2603	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.470600	1.488986	-2.981614	29552.897134
HLA B*5801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.353222	1.371517	-2.981705	22553.925467
HLA A*0203	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.557022	0.574537	-2.982484	3605.965895
HLA A*2602	1:191-199	9	DSVDARSDV	0.837527	0.035965	-3.856125	0.873492	-2.982633	7180.011711
HLA B*4002	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.618387	1.635751	-2.982636	41532.432483
HLA B*4801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.264832	1.282160	-2.982672	18400.607672
HLA A*0206	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-3.876707	0.894030	-2.982676	7528.468563
HLA B*0801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.085862	1.103143	-2.982720	12186.037075
HLA B*3801	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.508636	1.525910	-2.982726	32257.883924
HLA A*2603	1:129-137	9	SHQNGIIHR	1.025550	0.610201	-4.618481	1.635751	-2.982730	41541.420889
HLA A*0203	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.927268	0.944464	-2.982804	8457.997617
HLA B*0702	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.422941	1.440103	-2.982837	26481.388872
HLA A*1101	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.400059	1.417212	-2.982848	25122.284205
HLA A*0216	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.484088	1.501143	-2.982945	30485.158370
HLA A*6901	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.346632	1.363134	-2.983498	22214.259225
HLA A*3001	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-3.902133	0.918327	-2.983806	7982.386790
HLA B*1503	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.397696	1.413806	-2.983890	24985.931356
HLA B*1501	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.238048	1.254080	-2.983968	17300.077020
HLA A*6802	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.203562	1.219563	-2.983999	15979.467241
HLA B*3901	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.305537	1.321448	-2.984089	20208.635623
HLA B*4403	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.613444	1.629324	-2.984120	41062.373718
HLA B*0803	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.493308	1.509182	-2.984125	31139.227518
HLA B*4002	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.601100	1.616917	-2.984182	39911.666048
HLA A*0203	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.254492	1.270153	-2.984339	17967.683220
HLA B*1502	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.510151	1.525646	-2.984505	32370.640501
HLA A*2402	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.455695	1.471168	-2.984527	28555.839300
HLA A*0206	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.857793	0.873256	-2.984537	7207.643322
HLA B*3901	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.536934	0.552387	-2.984547	3442.972217
HLA A*0201	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.398523	1.413806	-2.984717	25033.556922
HLA B*0801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.371581	1.386802	-2.984779	23527.783582
HLA B*1501	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.392820	1.407681	-2.985140	24707.019678
HLA A*0206	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.221531	1.236390	-2.985141	16654.483057
HLA A*1101	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.486379	1.501143	-2.985236	30646.381488

HLA B*5801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.325804	1.340547	-2.985257	21174.036185
HLA A*0301	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.350121	1.364704	-2.985417	22393.440373
HLA B*4501	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.108093	1.122659	-2.985434	12826.061623
HLA B*0702	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.350217	1.364704	-2.985513	22398.407911
HLA B*4601	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.399378	1.413806	-2.985572	25082.901562
HLA A*0201	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.393316	1.407681	-2.985636	24735.238513
HLA B*5801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.350346	1.364704	-2.985642	22405.073412
HLA B*4001	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.318349	1.332686	-2.985663	20813.673377
HLA A*0206	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.117938	1.132158	-2.985780	13120.115683
HLA A*0250	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.223961	1.238104	-2.985857	16747.906380
HLA B*4403	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.624456	1.638299	-2.986157	42116.869927
HLA B*0802	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.364483	1.378166	-2.986317	23146.387661
HLA A*2403	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.435957	1.449604	-2.986353	27287.070049
HLA A*8001	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.436215	1.449604	-2.986611	27303.313084
HLA A*6802	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.099616	1.112976	-2.986641	12578.138725
HLA B*5101	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.512348	1.525646	-2.986702	32534.793990
HLA A*3001	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.874686	0.887960	-2.986726	7493.523681
HLA B*7301	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.256886	1.270153	-2.986733	18067.006773
HLA B*5801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.349919	1.363134	-2.986785	22383.024238
HLA B*4002	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.631014	1.644220	-2.986793	42757.617724
HLA B*5301	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.458056	1.471168	-2.986888	28711.518470
HLA B*0803	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.488085	1.501143	-2.986942	30766.984271
HLA B*4001	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.327516	1.340547	-2.986970	21257.707427
HLA A*2403	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.390476	1.403484	-2.986992	24573.984222
HLA A*2501	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.396869	1.409864	-2.987005	24938.396397
HLA A*6901	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.358863	1.371517	-2.987346	22848.792538
HLA B*4402	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.308829	1.321448	-2.987380	20362.383932
HLA A*0216	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.419440	1.431809	-2.987631	26268.787432
HLA B*0801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.119968	1.132158	-2.987810	13181.584541
HLA B*1509	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.475083	1.487180	-2.987903	29859.523951
HLA A*2402	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.549827	1.561867	-2.987960	35467.211592
HLA A*0101	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.359603	1.371517	-2.988086	22887.762706
HLA A*2602	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.320851	1.332686	-2.988165	20933.938143
HLA B*5701	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.244605	1.256417	-2.988189	17563.272890
HLA B*4801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.309689	1.321448	-2.988240	20402.741789
HLA B*1501	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.055545	1.067242	-2.988303	11364.353661
HLA A*0201	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.328928	1.340547	-2.988382	21326.936015
HLA A*0201	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.309855	1.321448	-2.988407	20410.580031
HLA A*0212	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.438020	1.449604	-2.988416	27416.988735
HLA B*0802	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.383312	1.394783	-2.988529	24171.967148
HLA B*1501	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.244960	1.256417	-2.988543	17577.626071
HLA A*2603	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.522683	1.534036	-2.988647	33318.346903
HLA B*0802	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.398593	1.409864	-2.988729	25037.620115
HLA A*0203	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.398497	0.409720	-2.988778	2503.209295
HLA B*4501	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.618275	1.629324	-2.988950	41521.648962
HLA B*2705	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.227057	1.238104	-2.988953	16867.749617
HLA B*3901	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.476152	1.487180	-2.988972	29933.113690
HLA B*2705	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.353932	1.364704	-2.989227	22590.803884
HLA A*0301	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.273967	1.284672	-2.989295	18791.738631
HLA B*4601	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.243431	1.254080	-2.989350	17515.829405
HLA B*4501	1:615-623	9	NRDGIITLR	0.950398	0.693822	-4.633619	1.644220	-2.989399	43014.915986
HLA A*0211	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.016059	1.026649	-2.989411	10376.700827
HLA B*5301	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.523548	1.534036	-2.989512	33384.744446
HLA B*0803	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.228288	1.238694	-2.989594	16915.633847
HLA B*1502	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.606861	1.616917	-2.989943	40444.623258
HLA B*0702	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.422448	0.432298	-2.990150	2645.134823
HLA B*5301	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.577321	1.586804	-2.990516	37785.112480
HLA A*2902	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.256983	1.266360	-2.990622	18071.014578
HLA A*2301	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.440233	1.449604	-2.990629	27557.065498
HLA B*5401	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-3.170278	0.179592	-2.990686	1480.054091
HLA A*2301	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.520306	1.529572	-2.990734	33136.433781
HLA B*4402	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.402528	1.411765	-2.990763	25265.531176
HLA A*2602	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.499947	1.509182	-2.990765	31618.952583
HLA A*3002	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.159594	1.168679	-2.990915	14440.892446
HLA B*0801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.289756	1.298743	-2.991013	19487.471926

HLA B*0803	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.403052	1.411765	-2.991287	25296.030039
HLA A*2601	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.290143	1.298743	-2.991401	19504.874827
HLA A*0202	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-3.746329	0.754459	-2.991870	5576.080302
HLA A*0212	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.399683	1.407681	-2.992003	25100.548210
HLA B*2705	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.422429	1.430389	-2.992039	26450.176301
HLA A*2301	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.457076	1.465019	-2.992058	28646.820477
HLA A*0211	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.554199	1.561867	-2.992333	35826.092054
HLA B*5801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.305156	1.312789	-2.992367	20190.932492
HLA B*4002	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.577464	1.585042	-2.992422	37797.583747
HLA A*3001	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.228857	1.236390	-2.992467	16937.794182
HLA A*2603	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.641321	1.648439	-2.992882	43784.529864
HLA B*4501	1:342-350	9	LTVVVTIAI	1.320951	0.277765	-4.591622	1.598716	-2.992906	39050.089590
HLA A*0206	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.464115	1.471168	-2.992947	29114.912116
HLA A*3201	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.583918	1.590840	-2.993078	38363.486853
HLA B*5401	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.475762	1.482642	-2.993120	29906.244575
HLA A*0212	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.060577	1.067242	-2.993336	11496.809559
HLA B*2705	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.433619	1.440103	-2.993516	27140.582737
HLA B*1509	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.337279	1.343697	-2.993582	21740.950923
HLA A*3201	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-3.777507	0.783751	-2.993756	5991.101611
HLA B*0702	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.959446	0.965301	-2.994145	9108.484111
HLA A*3002	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.959484	0.965301	-2.994183	9109.272559
HLA A*0203	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.276366	1.282160	-2.994206	18895.821926
HLA A*2902	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.402042	1.407681	-2.994362	25237.253481
HLA A*0202	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-3.912804	0.918327	-2.994477	8180.957355
HLA B*1801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.301252	1.306673	-2.994578	20010.204758
HLA B*3501	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.316077	1.321448	-2.994629	20705.073810
HLA A*6802	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.408489	1.413806	-2.994683	25614.688371
HLA A*3201	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.123280	1.128536	-2.994744	13282.517391
HLA B*0803	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.477517	1.482642	-2.994875	30027.345839
HLA A*0206	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.520541	1.525646	-2.994894	33154.365074
HLA B*3901	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.324913	1.329751	-2.995162	21130.666519
HLA B*5101	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.338890	1.343697	-2.995194	21821.785494
HLA B*0801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.256900	1.261650	-2.995250	18067.593225
HLA B*4501	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.580417	1.585042	-2.995375	38055.491959
HLA B*2705	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.373686	1.378166	-2.995520	23642.105733
HLA A*1101	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.466691	1.471168	-2.995522	29288.054167
HLA B*1517	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.245108	1.249564	-2.995545	17583.617952
HLA A*0203	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.215141	1.219563	-2.995577	16411.208301
HLA A*3101	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.256628	1.261014	-2.995613	18056.258516
HLA B*4501	1:414-422	9	DEITVNVST	1.070685	-0.486156	-3.580235	0.584529	-2.995706	3803.947608
HLA A*6802	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.176830	1.181092	-2.995738	15025.531918
HLA A*2301	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.394773	1.398961	-2.995812	24818.343044
HLA B*7301	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.530117	1.534036	-2.996081	33893.562261
HLA B*4801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.395243	1.398961	-2.996282	24845.210473
HLA B*1503	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.019283	1.022881	-2.996402	10454.007061
HLA B*2705	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.451581	1.454961	-2.996620	28286.615103
HLA A*6901	1:140-148	9	KPANIMISA	1.205138	-0.289626	-3.912221	0.915512	-2.996710	8169.988712
HLA B*3501	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.246299	1.249564	-2.996736	17631.912743
HLA B*1509	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.309597	1.312789	-2.996807	20398.437557
HLA A*6802	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.003466	1.006578	-2.996888	10080.128212
HLA A*8001	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.406840	1.409864	-2.996976	25517.594873
HLA B*2705	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.318917	1.321448	-2.997469	20840.940341
HLA B*3501	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.360630	1.363134	-2.997496	22941.936170
HLA A*2602	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.582624	1.585042	-2.997582	38249.301364
HLA B*4002	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.616374	1.618772	-2.997602	41340.322386
HLA B*5701	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.405334	1.407681	-2.997653	25429.259766
HLA B*1501	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.235924	1.238104	-2.997820	17215.676854
HLA A*8001	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.409741	1.411765	-2.997976	25688.654168
HLA B*0802	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.405681	1.407681	-2.998001	25449.628202
HLA A*2301	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.480703	1.482642	-2.998061	30248.430660
HLA A*0202	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.236197	1.238104	-2.998093	17226.483894
HLA A*2301	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.530756	1.532461	-2.998296	33943.473007
HLA A*3002	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.560228	1.561867	-2.998362	36326.889761
HLA B*4403	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.646917	1.648439	-2.998479	44352.403956
HLA B*4002	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.637026	1.638299	-2.998727	43353.666480

HLA A*0101	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.385718	1.386802	-2.998916	24306.244822
HLA A*3201	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.393793	1.394783	-2.999010	24762.417859
HLA B*4501	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.617917	1.618772	-2.999145	41487.519613
HLA B*4801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.411050	1.411765	-2.999285	25766.178745
HLA B*5801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.265845	1.266360	-2.999485	18443.561732
HLA A*2902	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.168179	1.168679	-2.999500	14729.196349
HLA A*2403	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.343629	1.343697	-2.999933	22061.203140
HLA B*3501	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.343949	1.343697	-3.000252	22077.440531
HLA A*1101	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.455230	1.454961	-3.000269	28525.267859
HLA B*4601	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.387099	1.386802	-3.000297	24383.686453
HLA A*3101	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.001530	1.001026	-3.000504	10035.293539
HLA B*2705	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.285266	1.284672	-3.000594	19287.042466
HLA A*0211	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.239124	1.238104	-3.001020	17342.995074
HLA A*3002	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.533500	1.532461	-3.001040	34158.632398
HLA A*3002	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.322881	1.321448	-3.001433	21032.015424
HLA B*1501	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.388570	1.386802	-3.001768	24466.404002
HLA A*6802	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.012530	1.010656	-3.001874	10292.724993
HLA A*2402	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.534417	1.532461	-3.001956	34230.778301
HLA A*2601	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.396760	1.394783	-3.001978	24932.191127
HLA A*0101	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.365190	1.363134	-3.002057	23184.109402
HLA A*2403	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.323555	1.321448	-3.002107	21064.695898
HLA A*3001	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.163518	1.161155	-3.002363	14571.950033
HLA A*2501	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.416209	1.413806	-3.002404	26074.109457
HLA A*3002	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.593285	1.590840	-3.002446	39199.946109
HLA B*5301	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.343025	1.340547	-3.002479	22030.551846
HLA B*7301	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.580380	1.577554	-3.002825	38052.198085
HLA B*4403	1:338-346	9	VLAVLTVVV	1.399873	0.245231	-4.647949	1.645104	-3.002845	44457.863494
HLA B*3501	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.406342	1.403484	-3.002858	25488.345609
HLA A*0206	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.532857	1.529572	-3.003285	34108.036237
HLA B*4002	1:146-154	9	ISATNAVKV	1.443784	0.185540	-4.632902	1.629324	-3.003578	42943.999201
HLA A*8001	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.316446	1.312789	-3.003656	20722.667188
HLA A*0101	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.101482	1.097819	-3.003663	12632.283721
HLA B*7301	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.593511	1.589799	-3.003712	39220.309864
HLA B*4501	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.179151	1.175404	-3.003747	15106.057956
HLA B*1502	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.398828	1.394783	-3.004045	25051.168854
HLA B*0802	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.415829	1.411765	-3.004064	26051.268065
HLA A*2601	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.367209	1.363134	-3.004075	23292.098880
HLA A*6901	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.130451	1.126330	-3.004121	13503.645288
HLA A*0203	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.240564	1.236390	-3.004175	17400.604461
HLA B*3501	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.453799	1.449604	-3.004195	28431.442515
HLA A*2301	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.513614	1.509182	-3.004432	32629.801630
HLA A*0219	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.454116	1.449604	-3.004512	28452.214578
HLA B*4001	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.325961	1.321448	-3.004513	21181.712372
HLA A*6901	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-3.555499	0.550986	-3.004514	3593.346923
HLA A*3002	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.391568	1.386802	-3.004766	24635.880319
HLA A*1101	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.403861	1.398961	-3.004900	25343.149830
HLA B*5401	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.537384	1.532461	-3.004924	34465.467464
HLA A*6901	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.369676	1.364704	-3.004971	23424.783430
HLA A*2301	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.506359	1.501143	-3.005216	32089.224665
HLA B*1501	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.419290	1.413806	-3.005484	26259.693888
HLA B*0803	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.470527	1.465019	-3.005509	29547.941335
HLA A*0202	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.567389	1.561867	-3.005523	36930.862143
HLA B*4001	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.392395	1.386802	-3.005593	24682.838654
HLA B*0801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.195701	1.190001	-3.005699	15692.817312
HLA B*3501	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.419588	1.413806	-3.005782	26277.741965
HLA A*0206	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.180533	1.174655	-3.005878	15154.187059
HLA B*0801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.349576	1.343697	-3.005879	22365.352124
HLA A*3001	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.073443	1.067242	-3.006202	11842.492473
HLA B*5101	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.438245	1.431809	-3.006436	27431.231428
HLA B*5401	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.545307	1.538857	-3.006450	35099.961228
HLA B*0801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.167733	1.161155	-3.006578	14714.064297
HLA A*0211	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.216254	1.209597	-3.006657	16453.345359
HLA B*5801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.350485	1.343697	-3.006788	22412.225883
HLA A*8001	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.401849	1.394783	-3.007066	25226.060443
HLA A*3001	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.162023	1.154939	-3.007084	14521.898632

HLA A*6802	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.213364	1.206278	-3.007086	16344.225560
HLA B*4402	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-3.880236	0.873123	-3.007113	7589.891502
HLA B*5701	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.274286	1.266360	-3.007926	18805.569644
HLA B*7301	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.593149	1.585042	-3.008107	39187.648132
HLA A*2301	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.264536	1.256417	-3.008119	18388.069245
HLA A*3301	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.563280	1.554751	-3.008529	36583.074123
HLA B*1501	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.380110	1.371517	-3.008592	23994.386340
HLA B*0802	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.407688	1.398961	-3.008727	25567.478665
HLA A*2501	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.407758	1.398961	-3.008798	25571.628519
HLA A*0202	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.953399	0.944464	-3.008935	8982.526987
HLA B*5701	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.403762	1.394783	-3.008979	25337.392131
HLA A*1101	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.418843	1.409864	-3.008979	26232.715969
HLA B*0801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.422889	1.413806	-3.009083	26478.237310
HLA A*2601	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.352809	1.343697	-3.009112	22532.461181
HLA A*3002	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-3.903806	0.894591	-3.009215	8013.192968
HLA B*1509	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.266427	1.257069	-3.009359	18468.323189
HLA A*2403	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.190593	1.181170	-3.009423	15509.333634
HLA A*0201	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.396246	1.386802	-3.009444	24902.669813
HLA A*0202	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.480853	1.471168	-3.009685	30258.905475
HLA A*0203	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.122698	1.112976	-3.009722	13264.708818
HLA B*5101	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.342739	1.332686	-3.010053	22016.016337
HLA A*0211	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.216470	1.206278	-3.010192	16461.536389
HLA A*2601	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.381766	1.371517	-3.010249	24086.074992
HLA B*4403	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.354098	1.343697	-3.010402	22599.482726
HLA B*4002	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.578742	1.568231	-3.010511	37908.985114
HLA B*3501	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.159848	1.149326	-3.010521	14449.332263
HLA B*2705	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.427811	1.417212	-3.010600	26780.041227
HLA B*5101	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.414097	1.403484	-3.010614	25947.606151
HLA B*5801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.340493	1.329751	-3.010742	21902.446650
HLA B*0801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.330719	1.319849	-3.010869	21415.034261
HLA B*1801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.451261	1.440103	-3.011158	28265.811023
HLA A*2301	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.376031	1.364704	-3.011327	23770.096306
HLA A*3201	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.007315	0.995952	-3.011363	10169.849184
HLA B*7301	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.579614	1.568231	-3.011383	37985.147464
HLA A*2602	1:47-55	9	ARDPSFYLR	0.876085	0.740832	-4.628572	1.616917	-3.011655	42517.956690
HLA B*4501	1:372-380	9	DAIATLQNR	1.011737	0.626562	-4.650051	1.638299	-3.011752	44673.643802
HLA A*3201	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.482961	1.471168	-3.011793	30406.098826
HLA A*8001	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.415331	1.403484	-3.011847	26021.407084
HLA B*5401	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.541428	1.529572	-3.011856	34787.853861
HLA B*0803	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.466848	1.454961	-3.011887	29298.671915
HLA A*0206	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.909275	0.897363	-3.011912	8114.751079
HLA A*0250	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.220103	1.208137	-3.011965	16599.792914
HLA A*2902	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.406830	1.394783	-3.012047	25517.042690
HLA B*0801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-3.919308	0.907250	-3.012057	8304.385535
HLA A*0216	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.383634	1.371517	-3.012117	24189.888958
HLA B*3801	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.544661	1.532461	-3.012200	35047.781155
HLA A*2902	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.422208	1.409864	-3.012344	26436.729023
HLA A*0203	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.222034	1.209597	-3.012437	16673.775388
HLA B*4403	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.567317	1.554751	-3.012565	36924.669114
HLA B*3801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.495239	1.482642	-3.012597	31278.009797
HLA B*1503	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.110424	1.097819	-3.012605	12895.079124
HLA A*2301	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.538275	1.525646	-3.012628	34536.206160
HLA A*6901	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.294814	1.282160	-3.012654	19715.779108
HLA B*1502	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.273744	1.261014	-3.012729	18782.083296
HLA B*4001	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.377476	1.364704	-3.012772	23849.313069
HLA A*6801	1:460-468	9	TPELVGKVI	1.597950	0.050489	-4.661223	1.648439	-3.012785	45837.738038
HLA B*1501	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.273925	1.261014	-3.012910	18789.908818
HLA B*4801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.274585	1.261650	-3.012935	18818.494562
HLA A*3002	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.411898	1.398961	-3.012938	25816.548488
HLA B*0802	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.957477	0.944464	-3.013013	9067.284375
HLA A*0201	1:143-151	9	NIMISATNA	0.971550	-0.064300	-3.920290	0.907250	-3.013040	8323.185770
HLA B*1517	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.399906	1.386802	-3.013104	25113.451688
HLA B*1503	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.221371	1.208137	-3.013234	16648.357458
HLA A*2601	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.320123	1.306673	-3.013449	20898.859977
HLA A*2902	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.251647	1.238104	-3.013543	17850.354926

HLA A*0301	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.326555	1.312789	-3.013766	21210.723672
HLA B*1509	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.312647	1.298743	-3.013904	20542.180214
HLA B*4501	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.501085	1.487180	-3.013905	31701.851700
HLA A*2603	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.497046	1.482642	-3.014404	31408.403767
HLA A*0250	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.424414	1.409864	-3.014550	26571.366272
HLA A*2403	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.327420	1.312789	-3.014631	21252.992874
HLA A*3101	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.313462	1.298743	-3.014719	20580.778861
HLA A*2603	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.569525	1.554751	-3.014774	37112.920229
HLA A*0203	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.221118	1.206278	-3.014839	16638.633196
HLA A*2501	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.327726	1.312789	-3.014936	21267.945055
HLA B*4501	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.277198	1.262230	-3.014967	18932.044003
HLA A*6802	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-3.933193	0.918162	-3.015031	8574.187169
HLA B*4801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.378669	1.363134	-3.015536	23914.946462
HLA B*7301	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.545152	1.529572	-3.015579	35087.430930
HLA A*6901	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.225356	1.209597	-3.015759	16801.811910
HLA A*2603	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.328564	1.312789	-3.015775	21309.060175
HLA B*0801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.083038	1.067242	-3.015797	12107.052178
HLA A*2403	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.410763	1.394783	-3.015980	25749.178511
HLA B*5401	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.748115	0.732039	-3.016076	5599.053639
HLA A*2601	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.356704	1.340547	-3.016157	22735.477385
HLA B*1801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.481262	1.465019	-3.016243	30287.402220
HLA A*2603	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.130305	1.113773	-3.016533	13499.116748
HLA A*0203	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.424228	1.407681	-3.016548	26560.012595
HLA B*4403	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.601598	1.584939	-3.016659	39957.466858
HLA B*4601	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.388239	1.371517	-3.016722	24447.748283
HLA A*0301	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.360461	1.343697	-3.016764	22933.001750
HLA A*2601	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.254936	1.238104	-3.016832	17986.064015
HLA B*5101	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.424611	1.407681	-3.016931	26583.443860
HLA B*4501	1:289-297	9	TDAERTSLL	1.288079	0.301720	-4.606873	1.589799	-3.017074	40445.717277
HLA B*3801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.287274	1.270153	-3.017121	19376.460457
HLA B*5701	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.431018	1.413806	-3.017212	26978.530376
HLA A*3002	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.427132	1.409864	-3.017268	26738.204472
HLA B*0801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.299600	1.282160	-3.017440	19934.247437
HLA B*1503	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.116998	1.099547	-3.017451	13091.755031
HLA A*0250	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.825493	0.807959	-3.017534	6691.023684
HLA B*4402	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.395703	1.378166	-3.017537	24871.568772
HLA B*1502	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.316314	1.298743	-3.017572	20716.390129
HLA B*4801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.404572	1.386802	-3.017770	25384.726296
HLA A*1101	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.254556	1.236758	-3.017797	17970.307898
HLA A*0201	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.389385	1.371517	-3.017868	24512.376244
HLA B*4801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.389642	1.371517	-3.018124	24526.834914
HLA A*0203	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.197599	1.179436	-3.018163	15761.563747
HLA A*3002	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.489528	1.471168	-3.018359	30869.352021
HLA A*0212	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.432191	1.413806	-3.018385	27051.458246
HLA A*2601	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.915811	0.897363	-3.018449	8237.804283
HLA B*1501	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-3.936656	0.918162	-3.018494	8642.832583
HLA B*4001	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.348307	1.329751	-3.018556	22300.110666
HLA A*2902	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.019795	1.001026	-3.018769	10466.343328
HLA B*1502	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.396960	1.378166	-3.018794	24943.658596
HLA B*4001	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.390567	1.371517	-3.019050	24579.169528
HLA A*0211	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.551664	1.532461	-3.019204	35617.574646
HLA B*1502	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.465184	1.445980	-3.019204	29186.666735
HLA A*3001	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.280980	1.261650	-3.019330	19097.660828
HLA A*0202	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.255906	1.236390	-3.019517	18026.294921
HLA A*3001	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.088630	1.069099	-3.019531	12263.944837
HLA B*0801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.382673	1.363134	-3.019539	24136.424500
HLA B*3501	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-3.784052	0.764421	-3.019632	6082.083114
HLA A*6802	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-3.873070	0.853416	-3.019654	7465.684599
HLA A*3201	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.086896	1.067242	-3.019655	12215.078674
HLA B*4601	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.349465	1.329751	-3.019714	22359.666126
HLA B*0803	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.450143	1.430389	-3.019754	28193.117167
HLA A*0101	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.384912	1.364704	-3.020208	24261.184169
HLA B*1801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.423735	1.403484	-3.020251	26529.855516
HLA B*1801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.428298	1.407681	-3.020617	26810.047576
HLA A*3301	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.605717	1.584939	-3.020778	40338.207450

HLA A*0206	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.553685	1.532461	-3.021224	35783.671662
HLA B*4001	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.384437	1.363134	-3.021304	24234.686086
HLA B*1517	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.384489	1.363134	-3.021355	24237.570611
HLA B*7301	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.606924	1.585464	-3.021460	40450.531314
HLA A*0301	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.354153	1.332686	-3.021467	22602.294897
HLA A*0301	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.362030	1.340547	-3.021483	23016.027097
HLA A*0101	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.343143	1.321448	-3.021695	22036.511795
HLA A*3301	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.612709	1.590840	-3.021869	40992.901828
HLA B*1509	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.426124	1.403484	-3.022641	26676.221267
HLA B*1509	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.430478	1.407681	-3.022797	26944.982554
HLA A*3001	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-3.977485	0.954621	-3.022864	9494.791906
HLA A*6802	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-3.748866	0.725976	-3.022890	5608.754917
HLA A*0203	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.436789	1.413806	-3.022983	27339.377608
HLA B*4601	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.344637	1.321448	-3.023189	22112.463177
HLA B*4002	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-3.820686	0.797462	-3.023224	6617.371563
HLA B*5401	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.322044	1.298743	-3.023302	20991.548414
HLA A*0219	1:143-151	9	NIMISATNA	0.971550	-0.064300	-3.930552	0.907250	-3.023302	8522.208172
HLA A*0211	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.552895	1.529572	-3.023323	35718.685949
HLA B*1503	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.343249	1.319849	-3.023399	22041.877127
HLA A*0201	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.386554	1.363134	-3.023420	24353.101825
HLA A*0250	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.356112	1.332686	-3.023426	22704.503407
HLA B*3901	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.336459	1.312789	-3.023669	21699.941618
HLA B*4601	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.293834	1.270153	-3.023681	19671.351944
HLA A*2402	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.401911	1.378166	-3.023745	25229.608918
HLA B*1509	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.473377	1.449604	-3.023773	29742.478300
HLA B*1502	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.285479	1.261650	-3.023830	19296.539813
HLA A*6801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.073725	1.049687	-3.024038	11850.182957
HLA A*2501	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.473861	1.449604	-3.024257	29775.642900
HLA A*8001	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.344294	1.319849	-3.024445	22095.004680
HLA A*8001	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.432261	1.407681	-3.024581	27055.848964
HLA A*3001	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.278943	1.254080	-3.024863	19008.295401
HLA A*3301	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.513960	1.488986	-3.024974	32655.760922
HLA A*0212	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.365545	1.340547	-3.024998	23203.056083
HLA B*1801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.474622	1.449604	-3.025018	29827.879535
HLA A*2402	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.474683	1.449604	-3.025079	29832.075334
HLA B*3901	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.480059	1.454961	-3.025098	30203.626335
HLA A*0212	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.917296	0.892112	-3.025184	8266.017952
HLA B*0803	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.474801	1.449604	-3.025197	29840.145836
HLA A*0201	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.390027	1.364704	-3.025323	24548.605313
HLA A*3002	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-3.947154	0.921765	-3.025389	8854.287093
HLA A*3001	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-3.648750	0.623337	-3.025413	4453.999956
HLA B*4402	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.390208	1.364704	-3.025504	24558.833446
HLA B*1517	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.186726	1.161155	-3.025571	15371.841091
HLA A*0212	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.347184	1.321448	-3.025736	22242.518704
HLA B*4402	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.429287	1.403484	-3.025803	26871.178746
HLA A*3301	1:478-486	9	SAITNVVII	1.257201	0.311030	-4.594221	1.568231	-3.025990	39284.439850
HLA A*2902	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.389216	1.363134	-3.026082	24502.830238
HLA A*3301	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.456529	1.430389	-3.026140	28610.733789
HLA A*0203	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.346012	1.319849	-3.026162	22182.555227
HLA B*0702	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.339029	1.312789	-3.026239	21828.751759
HLA B*0803	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.404450	1.378166	-3.026284	25377.586216
HLA A*1101	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.325148	1.298743	-3.026406	21142.101068
HLA A*6802	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.296729	1.270153	-3.026576	19802.899071
HLA A*2601	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.207805	1.181170	-3.026635	16136.355961
HLA A*2601	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.391345	1.364704	-3.026641	24623.222221
HLA B*3901	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.476286	1.449604	-3.026682	29942.345398
HLA B*5401	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.552686	1.525910	-3.026776	35701.492251
HLA B*5101	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.339609	1.312789	-3.026820	21857.939764
HLA A*2402	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.413728	1.386802	-3.026926	25925.576841
HLA A*8001	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.391721	1.364704	-3.027017	24644.544872
HLA B*0803	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.346982	1.319849	-3.027133	22232.172769
HLA B*0802	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.311855	1.284672	-3.027183	20504.763213
HLA B*0802	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.398936	1.371517	-3.027419	25057.403736
HLA B*5101	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.312123	1.284672	-3.027451	20517.412962
HLA A*0211	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.536752	1.509182	-3.027570	34415.347719

HLA A*0101	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.312376	1.284672	-3.027705	20529.404133
HLA A*0219	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.399343	1.371517	-3.027825	25080.866209
HLA B*1517	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.340622	1.312789	-3.027832	21908.964559
HLA B*2705	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.294250	1.266360	-3.027890	19690.197276
HLA B*1503	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.196603	1.168679	-3.027924	15725.451415
HLA B*3501	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.925332	0.897363	-3.027969	8420.377902
HLA A*3101	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.357792	1.329751	-3.028041	22792.496104
HLA A*0211	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.843419	0.815296	-3.028123	6972.991531
HLA A*2501	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.160670	1.132158	-3.028512	14476.717431
HLA A*3201	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.289770	1.261014	-3.028755	19488.104486
HLA B*1501	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.253557	1.224706	-3.028851	17929.037976
HLA A*0101	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.372702	1.343697	-3.029005	23588.575835
HLA A*0202	1:352-360	9	TFGGITRDV	0.726621	0.189665	-3.945547	0.916286	-3.029261	8821.583551
HLA B*7301	1:479-487	9	AITNVVIII	1.197409	0.357342	-4.584155	1.554751	-3.029404	38384.454344
HLA A*0203	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.267522	1.238104	-3.029419	18514.940723
HLA A*3201	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-3.934114	0.904590	-3.029524	8592.389540
HLA A*2602	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-3.994937	0.965301	-3.029636	9884.106711
HLA B*4402	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.437432	1.407681	-3.029752	27379.933081
HLA A*0211	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.266157	1.236390	-3.029767	18456.836931
HLA B*5401	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.475785	1.445980	-3.029805	29907.862513
HLA A*2501	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.047416	1.017549	-3.029867	11153.611740
HLA B*5801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.349773	1.319849	-3.029924	22375.517936
HLA B*3501	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.359688	1.329751	-3.029937	22892.220669
HLA A*0101	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.349855	1.319849	-3.030006	22379.755055
HLA A*3001	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.163062	1.133041	-3.030021	14556.664524
HLA B*4402	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.417044	1.386802	-3.030241	26124.233178
HLA A*0216	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.479977	1.449604	-3.030373	30197.907937
HLA B*5701	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.395708	1.364704	-3.031004	24871.837879
HLA B*4001	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.337894	1.306673	-3.031221	21771.788199
HLA A*8001	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.394359	1.363134	-3.031225	24794.723741
HLA A*3301	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.618070	1.586804	-3.031266	41502.110966
HLA B*4001	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.313713	1.282160	-3.031553	20592.695661
HLA A*0301	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.361415	1.329751	-3.031664	22983.427497
HLA B*7301	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.622525	1.590840	-3.031685	41929.995020
HLA B*4403	1:376-384	9	TLQNRGFKI	1.335223	0.283549	-4.650723	1.618772	-3.031951	44742.817627
HLA A*0301	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.353417	1.321448	-3.031969	22564.054922
HLA A*2603	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.519272	1.487180	-3.032092	33057.651233
HLA B*1501	1:585-593	9	GMLDKGADV	0.832496	0.121837	-3.986639	0.954333	-3.032306	9697.036816
HLA B*0803	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.442550	1.409864	-3.032686	27704.451779
HLA A*2602	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.571628	1.538857	-3.032771	37293.051183
HLA A*2601	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.259163	1.226371	-3.032792	18161.966000
HLA A*3001	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.146742	1.113773	-3.032970	14019.817181
HLA A*2602	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.432141	1.398961	-3.033181	27048.385167
HLA A*2601	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.353037	1.319849	-3.033187	22544.288402
HLA A*3101	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.017558	0.984065	-3.033493	10412.577986
HLA A*0216	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.355005	1.321448	-3.033557	22646.724664
HLA B*4403	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.567763	1.534036	-3.033727	36962.642716
HLA B*5701	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.420728	1.386802	-3.033925	26346.779937
HLA B*1502	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.516641	1.482642	-3.033999	32857.958006
HLA A*0206	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.040593	1.006578	-3.034015	10979.754206
HLA B*5401	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.412211	1.378166	-3.034045	25835.130573
HLA B*1501	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.363814	1.329751	-3.034063	23110.727633
HLA A*0203	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.397216	1.363134	-3.034082	24958.371659
HLA A*2402	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.543624	1.509182	-3.034442	34964.265186
HLA B*3801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.499466	1.465019	-3.034447	31583.905739
HLA B*0702	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.229853	1.195398	-3.034455	16976.690569
HLA A*6901	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.354674	1.319849	-3.034825	22629.456456
HLA B*5101	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.375444	1.340547	-3.034897	23737.969640
HLA A*0250	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.467026	1.431809	-3.035217	29310.720586
HLA A*1101	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.443367	1.407681	-3.035687	27756.658456
HLA A*2902	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.407277	1.371517	-3.035760	25543.284605
HLA A*2603	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.620868	1.585042	-3.035826	41770.379777
HLA A*2603	1:63-71	9	AAALNHPAI	1.199473	0.385466	-4.620800	1.584939	-3.035862	41763.827070
HLA A*0202	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.561605	1.525646	-3.035959	36442.235825
HLA B*1503	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.210620	1.174655	-3.035965	16241.276075

HLA B*5301	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.588392	0.552387	-3.036005	3876.072919
HLA B*4001	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.449861	1.413806	-3.036055	28174.820510
HLA A*2403	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.407573	1.371517	-3.036056	25560.702019
HLA A*6901	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-3.719136	0.682948	-3.036188	5237.645251
HLA A*6802	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.293273	1.257069	-3.036204	19645.934040
HLA B*4601	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.379912	1.343697	-3.036216	23983.485032
HLA B*1801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.414492	1.378166	-3.036326	25971.199648
HLA A*2601	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.150182	1.113773	-3.036409	14131.296101
HLA B*4601	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.401130	1.364704	-3.036426	25184.335111
HLA A*2601	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.321161	1.284672	-3.036490	20948.892519
HLA B*3501	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.215963	1.179436	-3.036527	16442.311724
HLA A*2301	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.440115	1.403484	-3.036632	27549.612473
HLA A*2602	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.570702	1.534036	-3.036666	37213.645837
HLA A*2301	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.380429	1.343697	-3.036733	24012.046584
HLA A*2403	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.450822	1.413806	-3.037016	28237.230396
HLA B*5401	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.112839	1.075727	-3.037112	12966.993164
HLA B*4001	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.349931	1.312789	-3.037141	22383.629694
HLA B*5301	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.526351	1.488986	-3.037365	33600.906315
HLA B*3801	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.415575	1.378166	-3.037409	26036.051587
HLA A*0203	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.291663	1.254080	-3.037583	19573.265377
HLA A*2403	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.087282	1.049687	-3.037594	12225.920967
HLA A*6802	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.445418	1.407681	-3.037738	27888.058570
HLA B*5301	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.493385	1.454961	-3.038425	31144.787187
HLA B*3501	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-3.834322	0.795837	-3.038485	6828.446825
HLA A*0206	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.539908	1.501143	-3.038764	34666.302327
HLA B*0803	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.446480	1.407681	-3.038800	27956.335845
HLA A*6801	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.521448	1.482642	-3.038806	33223.670928
HLA A*3002	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.218270	1.179436	-3.038834	16529.894124
HLA B*3501	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.301228	1.262230	-3.038998	20009.122257
HLA B*0702	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.293169	1.254080	-3.039089	19641.258174
HLA B*5701	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.410702	1.371517	-3.039185	25745.556961
HLA A*6901	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.258792	1.219563	-3.039228	18146.448466
HLA A*6802	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-3.994040	0.954621	-3.039419	9863.701529
HLA A*0212	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.426324	1.386802	-3.039522	26688.490897
HLA A*2402	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.208242	1.168679	-3.039563	16152.601170
HLA A*2602	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.771619	0.732039	-3.039580	5910.427249
HLA B*0802	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.453432	1.413806	-3.039626	28407.458128
HLA A*0250	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.601600	1.561867	-3.039734	39957.683024
HLA B*1503	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.369643	1.329751	-3.039892	23423.009340
HLA B*0801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-3.652133	0.612002	-3.040132	4488.833189
HLA B*0803	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.404885	1.364704	-3.040181	25402.997567
HLA A*6802	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.772380	0.732039	-3.040341	5920.796155
HLA A*0211	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-3.214124	0.173777	-3.040347	1637.282714
HLA B*1801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.452131	1.411765	-3.040366	28322.446201
HLA B*5401	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.549735	1.509182	-3.040553	35459.729308
HLA A*0250	1:352-360	9	TFGGITRDV	0.726621	0.189665	-3.956862	0.916286	-3.040576	9054.441592
HLA B*3801	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.549766	1.509182	-3.040584	35462.223228
HLA A*2603	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.322780	1.282160	-3.040620	21027.123415
HLA A*6801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.154420	1.113773	-3.040648	14269.884812
HLA A*1101	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.370413	1.329751	-3.040662	23464.609047
HLA A*0203	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.297208	1.256417	-3.040791	19824.765959
HLA B*3801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.529868	1.488986	-3.040882	33874.131629
HLA B*4402	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.195865	1.154927	-3.040939	15698.761185
HLA A*2902	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-3.805480	0.764363	-3.041117	6389.688018
HLA A*0101	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.202552	1.161155	-3.041397	15942.338171
HLA A*3101	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.362904	1.321448	-3.041456	23062.393002
HLA A*0212	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.413101	1.371517	-3.041584	25888.155923
HLA A*0202	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.247890	1.206278	-3.041612	17696.607935
HLA A*0219	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.139149	1.097502	-3.041646	13776.814630
HLA B*5801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.344844	1.303070	-3.041773	22122.992769
HLA A*3001	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.117510	1.075727	-3.041783	13107.203977
HLA A*3001	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.221263	1.179436	-3.041827	16644.214948
HLA B*5301	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.449645	1.407681	-3.041965	28160.801114
HLA A*0203	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.413493	1.371517	-3.041976	25911.555184
HLA B*4402	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.405294	1.363134	-3.042160	25426.921193

HLA B*4001	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.951298	0.909118	-3.042180	8939.188413
HLA A*6901	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.299264	1.257069	-3.042195	19918.831984
HLA A*6802	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-3.960532	0.918327	-3.042205	9131.278045
HLA A*2403	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.450115	1.407681	-3.042434	28191.286966
HLA B*4601	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.268812	1.226371	-3.042441	18570.012378
HLA B*3901	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.057598	1.014994	-3.042604	11418.214321
HLA A*0216	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.147010	1.104337	-3.042673	14028.466253
HLA A*0212	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.407422	1.364704	-3.042718	25551.853595
HLA A*2402	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.572314	1.529572	-3.042742	37352.009109
HLA B*4002	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.474566	1.431809	-3.042757	29824.007014
HLA A*0211	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.203938	1.161155	-3.042783	15993.304772
HLA A*3101	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.204042	1.161199	-3.042842	15997.112194
HLA A*2902	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.325111	1.282160	-3.042951	21140.271125
HLA B*0702	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.406177	1.363134	-3.043043	25478.695198
HLA B*1801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.325259	1.282160	-3.043099	21147.477444
HLA B*0802	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.281882	1.238694	-3.043188	19137.375497
HLA A*0211	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-3.961537	0.918327	-3.043210	9152.445400
HLA B*0801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.349902	1.306673	-3.043229	22382.176626
HLA B*5801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.305542	1.262230	-3.043311	20208.854277
HLA B*4002	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.530564	1.487180	-3.043384	33928.418651
HLA A*8001	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.373249	1.329751	-3.043498	23618.328080
HLA B*3801	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.483602	1.440103	-3.043499	30451.038764
HLA A*2601	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.931656	0.887960	-3.043696	8543.904718
HLA A*0219	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.408496	1.364704	-3.043792	25615.104092
HLA A*2403	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.406927	1.363134	-3.043793	25522.703137
HLA A*3002	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.569459	1.525646	-3.043813	37107.298905
HLA A*0206	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.253599	1.209597	-3.044002	17930.783955
HLA A*0216	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.409159	1.364704	-3.044454	25654.212030
HLA B*5101	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.494142	1.449604	-3.044538	31199.088199
HLA A*2602	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.343314	1.298743	-3.044572	22045.216215
HLA B*2705	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-3.907471	0.862842	-3.044629	8081.105896
HLA A*0203	1:453-461	9	KQANSPSTP	0.696748	0.084681	-3.826174	0.781429	-3.044745	6701.529255
HLA A*0202	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.577215	1.532461	-3.044754	37775.915002
HLA A*0212	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.251038	1.206278	-3.044760	17825.361214
HLA B*0803	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.416759	1.371517	-3.045242	26107.137940
HLA A*2902	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.409955	1.364704	-3.045251	25701.303803
HLA A*3301	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-3.842183	0.796898	-3.045285	6953.177379
HLA B*5401	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.571172	1.525646	-3.045526	37253.931967
HLA B*1503	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.950678	0.904921	-3.045757	8926.430480
HLA B*0802	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.348836	1.303070	-3.045765	22327.271447
HLA A*2501	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.367281	1.321448	-3.045833	23296.005446
HLA A*1101	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.358628	1.312789	-3.045839	22836.434938
HLA A*2603	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.491856	1.445980	-3.045876	31035.293220
HLA A*0211	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.547026	1.501143	-3.045883	35239.234019
HLA B*1503	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.166299	1.120342	-3.045958	14665.587440
HLA B*4402	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.300251	1.254080	-3.046170	19964.142083
HLA B*0702	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.778240	0.732039	-3.046201	6001.222443
HLA B*0803	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.486412	1.440103	-3.046309	30648.702685
HLA B*0801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.227405	1.181092	-3.046313	16881.260418
HLA A*0202	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.241840	1.195398	-3.046442	17451.795103
HLA B*4001	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.281734	1.235214	-3.046521	19130.854150
HLA B*5401	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.533733	1.487180	-3.046554	34176.931945
HLA A*3301	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.580657	1.534036	-3.046621	38076.497105
HLA A*2402	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.547924	1.501143	-3.046781	35312.133933
HLA A*6901	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-3.965010	0.918162	-3.046848	9225.920024
HLA B*2705	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.359728	1.312789	-3.046938	22894.326120
HLA B*3501	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.012436	0.965301	-3.047135	10290.497934
HLA B*0803	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.350274	1.303070	-3.047203	22401.316250
HLA A*0101	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.387757	1.340547	-3.047210	24420.650093
HLA B*4403	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.632379	1.585042	-3.047337	42892.222572
HLA B*1509	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.461254	1.413806	-3.047448	28923.697500
HLA B*0801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.308537	1.261014	-3.047523	20348.728891
HLA A*0219	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.380211	1.332686	-3.047525	23999.968689
HLA A*0202	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.301733	1.254080	-3.047653	20032.408931
HLA A*0203	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-3.945124	0.897363	-3.047761	8812.997450

HLA B*2705	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.346904	1.298743	-3.048162	22228.204095
HLA A*6801	1:66-74	9	LNHPAIVAV	1.383003	0.151033	-4.582241	1.534036	-3.048204	38215.587540
HLA A*3301	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.535490	1.487180	-3.048311	34315.512418
HLA A*2402	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.287340	1.238694	-3.048646	19379.395765
HLA A*6801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.181717	1.133041	-3.048676	15195.562606
HLA A*0301	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.347567	1.298743	-3.048824	22262.141073
HLA A*0203	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-3.832630	0.783751	-3.048879	6801.900937
HLA B*5301	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.558144	1.509182	-3.048962	36152.990145
HLA A*2501	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.392663	1.343697	-3.048966	24698.065931
HLA A*3001	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.255408	1.206278	-3.049130	18005.632478
HLA B*0802	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.412401	1.363134	-3.049267	25846.454034
HLA B*0702	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.463086	1.413806	-3.049281	29046.005087
HLA A*0211	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.018390	0.968816	-3.049574	10432.538228
HLA B*1517	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.457394	1.407681	-3.049713	28667.749896
HLA A*0202	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.579327	1.529572	-3.049755	37960.085292
HLA A*0219	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.457478	1.407681	-3.049798	28673.333656
HLA B*3801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.495796	1.445980	-3.049816	31318.138421
HLA A*3002	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-3.937807	0.887960	-3.049847	8665.773792
HLA A*2603	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.636669	1.586804	-3.049864	43318.031277
HLA B*4002	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.640752	1.590840	-3.049912	43727.244963
HLA B*2705	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.356662	1.306673	-3.049988	22733.263557
HLA A*0206	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-3.748072	0.697848	-3.050224	5598.508441
HLA B*1502	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-3.994726	0.944464	-3.050262	9879.295409
HLA A*2902	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.383018	1.332686	-3.050333	24155.626716
HLA B*1801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.421938	1.371517	-3.050420	26420.286865
HLA A*0206	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.120156	1.069720	-3.050436	13187.290649
HLA A*2601	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.312679	1.262230	-3.050449	20543.736106
HLA A*0212	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.073429	1.022974	-3.050455	11842.108080
HLA A*0206	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.306895	1.256417	-3.050478	20271.925226
HLA A*2601	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.371962	1.321448	-3.050513	23548.412418
HLA A*2602	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-3.797313	0.746693	-3.050620	6270.654086
HLA A*0202	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-3.472680	0.421976	-3.050704	2969.475882
HLA A*0211	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.151411	0.100651	-3.050760	1417.134996
HLA B*7301	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.539912	1.488986	-3.050926	34666.677410
HLA B*4801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.370853	1.319849	-3.051003	23488.359013
HLA B*1517	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.305107	1.254080	-3.051027	20188.638777
HLA A*2902	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.464853	1.413806	-3.051047	29164.411799
HLA A*0201	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.118393	1.067242	-3.051152	13133.892715
HLA B*4601	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.391805	1.340547	-3.051259	24649.345013
HLA A*2301	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.372814	1.321448	-3.051366	23594.701986
HLA B*3901	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.465173	1.413806	-3.051367	29185.877263
HLA B*1502	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.613350	1.561867	-3.051484	41053.488964
HLA A*0250	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.560801	1.509182	-3.051619	36374.873388
HLA B*1517	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.310027	1.258359	-3.051668	20418.642208
HLA B*1517	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.446814	1.394783	-3.052031	27977.820272
HLA B*4601	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.917372	0.865145	-3.052226	8267.449059
HLA B*1801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.507219	1.454961	-3.052258	32152.824897
HLA A*6802	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-3.892387	0.839877	-3.052510	7805.255143
HLA A*2403	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.351265	1.298743	-3.052522	22452.516277
HLA B*7301	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.535223	1.482642	-3.052581	34294.355627
HLA A*3301	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.498672	1.445980	-3.052692	31526.205994
HLA A*2902	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.359385	1.306673	-3.052711	22876.250318
HLA A*2601	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.382579	1.329751	-3.052828	24131.202050
HLA A*1101	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.456444	1.403484	-3.052961	28605.162220
HLA B*0802	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.439768	1.386802	-3.052966	27527.563329
HLA B*2705	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.382779	1.329751	-3.053028	24142.301108
HLA B*5301	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.351960	1.298743	-3.053218	22488.498904
HLA A*0219	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.374898	1.321448	-3.053450	23708.194939
HLA B*4501	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.425013	1.371517	-3.053496	26608.047344
HLA B*1502	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.554679	1.501143	-3.053535	35865.652178
HLA B*1501	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.208247	1.154698	-3.053549	16152.775938
HLA B*1517	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.418582	1.364704	-3.053878	26216.968012
HLA A*2601	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.336480	1.282160	-3.054320	21700.998192
HLA A*0250	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.586925	1.532461	-3.054465	38630.062791
HLA A*0250	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.235637	1.181170	-3.054467	17204.318145

HLA A*3101	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.395038	1.340547	-3.054491	24833.519569
HLA B*0803	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.367281	1.312789	-3.054492	23296.005446
HLA B*4501	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.580507	1.525910	-3.054597	38063.316050
HLA B*3801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.387353	1.332686	-3.054667	24397.937224
HLA B*5301	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.167719	1.112976	-3.054743	14713.586696
HLA A*6802	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.426646	1.371517	-3.055129	26708.278532
HLA B*1501	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.316793	1.261650	-3.055144	20739.265717
HLA B*5101	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.384924	1.329751	-3.055173	24261.840429
HLA B*1503	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.104945	1.049687	-3.055258	12733.418480
HLA B*0702	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.210033	1.154698	-3.055335	16219.325046
HLA B*1801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.450291	1.394783	-3.055508	28202.727667
HLA B*5701	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.418958	1.363134	-3.055825	26239.670779
HLA B*5801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.338019	1.282160	-3.055859	21778.031591
HLA B*2705	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-3.948046	0.892112	-3.055934	8872.508086
HLA A*3001	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.176304	1.120342	-3.055962	15007.334779
HLA B*1503	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-3.465129	0.409024	-3.056104	2918.290743
HLA B*7301	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.618016	1.561867	-3.056150	41496.947285
HLA A*0202	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-3.474757	0.418508	-3.056249	2983.710943
HLA A*0206	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.565463	1.509182	-3.056280	36767.395655
HLA B*5701	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.355104	1.298743	-3.056361	22651.870932
HLA A*3101	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.313443	1.257069	-3.056374	20579.888162
HLA B*5301	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.585962	1.529572	-3.056390	38544.474160
HLA B*1517	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.377934	1.321448	-3.056486	23874.485661
HLA B*1502	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.588977	1.532461	-3.056516	38812.937639
HLA B*1509	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.341205	1.284672	-3.056533	21938.378504
HLA A*1101	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.389266	1.332686	-3.056580	24505.614106
HLA B*4002	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.634253	1.577554	-3.056699	43077.792496
HLA A*2902	1:352-360	9	TFGGITRDV	0.726621	0.189665	-3.973007	0.916286	-3.056722	9397.391767
HLA A*2602	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.237961	1.181170	-3.056791	17296.614481
HLA B*7301	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.206166	1.149326	-3.056839	16075.538324
HLA A*2501	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.451656	1.394783	-3.056873	28291.512405
HLA A*1101	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.451717	1.394783	-3.056934	28295.492088
HLA A*0203	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.039314	0.982334	-3.056981	10947.488514
HLA B*4402	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.386832	1.329751	-3.057081	24368.653002
HLA A*0211	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.124366	1.067242	-3.057124	13315.756822
HLA A*0203	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.183470	1.126330	-3.057140	15257.012428
HLA A*8001	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.470957	1.413806	-3.057151	29577.208569
HLA A*2602	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.586815	1.529572	-3.057243	38620.241775
HLA A*2601	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.389947	1.332686	-3.057261	24544.090350
HLA A*0206	1:453-461	9	KQANSPSTP	0.696748	0.084681	-3.838795	0.781429	-3.057366	6899.146248
HLA B*0801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.387327	1.329751	-3.057576	24396.485376
HLA A*0212	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.189794	1.132158	-3.057636	15480.832570
HLA B*3501	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.364450	1.306673	-3.057777	23144.634656
HLA A*6801	1:558-566	9	GNQFVMPDL	1.284685	0.302119	-4.644615	1.586804	-3.057810	44117.883426
HLA B*1801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.529029	1.471168	-3.057861	33808.772623
HLA A*0216	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.295979	1.238104	-3.057876	19768.753598
HLA A*2603	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.467757	1.409864	-3.057893	29360.076665
HLA A*3201	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.583556	1.525646	-3.057910	38331.538662
HLA B*2705	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.471725	1.413806	-3.057920	29629.577957
HLA B*0803	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.379428	1.321448	-3.057980	23956.771833
HLA A*0202	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.567253	1.509182	-3.058071	36919.276032
HLA A*6801	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.504137	1.445980	-3.058157	31925.419386
HLA B*1501	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.324565	1.266360	-3.058205	21113.754735
HLA B*1501	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.315285	1.257069	-3.058216	20667.360103
HLA A*2603	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.316584	1.258359	-3.058226	20729.282577
HLA B*5101	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.320099	1.261650	-3.058449	20897.729402
HLA A*6801	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.343187	1.284672	-3.058516	22038.776998
HLA B*3501	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.284904	1.226371	-3.058533	19270.980680
HLA A*3301	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.643597	1.585042	-3.058555	44014.659026
HLA B*5801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.308131	1.249564	-3.058567	20329.693204
HLA B*7301	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.591152	1.532461	-3.058692	39007.861108
HLA A*0202	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.675365	0.616515	-3.058850	4735.492733
HLA A*6802	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.422191	1.363134	-3.059057	26435.727904
HLA B*0702	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.430642	1.371517	-3.059125	26955.188342
HLA A*2602	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.379010	1.319849	-3.059161	23933.713517

HLA B*3501	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.135009	1.075727	-3.059282	13646.114857
HLA A*0216	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.446189	1.386802	-3.059387	27937.588289
HLA B*4402	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.400177	1.340547	-3.059630	25129.080563
HLA B*0702	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.446624	1.386802	-3.059821	27965.563048
HLA B*2705	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.293663	1.233662	-3.060001	19663.584830
HLA B*7301	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.586124	1.525910	-3.060214	38558.864817
HLA B*0803	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.459238	1.398961	-3.060277	28789.753912
HLA A*3201	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.622161	1.561867	-3.060294	41894.850080
HLA B*1801	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.345020	1.284672	-3.060349	22131.970811
HLA A*0201	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.363586	1.303070	-3.060515	23098.603246
HLA A*0206	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.380601	1.319849	-3.060751	24021.531340
HLA A*3001	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.296059	1.235214	-3.060845	19772.390123
HLA A*6801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-3.926135	0.865145	-3.060990	8435.971555
HLA A*0212	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.424313	1.363134	-3.061179	26565.185820
HLA B*3501	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.215878	1.154698	-3.061181	16439.109797
HLA A*0101	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.343596	1.282160	-3.061436	22059.532322
HLA A*2602	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.587435	1.525910	-3.061525	38675.439026
HLA A*3201	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.594256	1.532461	-3.061795	39287.627847
HLA A*2501	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.084772	1.022974	-3.061799	12155.486184
HLA B*4601	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.374598	1.312789	-3.061808	23691.783507
HLA A*6801	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.549021	1.487180	-3.061842	35401.459942
HLA B*0702	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.332110	1.270153	-3.061957	21483.729159
HLA A*2402	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.587654	1.525646	-3.062007	38694.902297
HLA B*3901	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.300131	1.238104	-3.062027	19958.634649
HLA A*3002	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.425260	1.363134	-3.062126	26623.166030
HLA A*2603	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.588152	1.525910	-3.062242	38739.306803
HLA A*6802	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.328639	1.266360	-3.062279	21312.749443
HLA B*1503	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.046419	0.984065	-3.062354	11128.056983
HLA A*3002	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.591996	1.529572	-3.062424	39083.693849
HLA A*0216	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.470118	1.407681	-3.062438	29520.140332
HLA A*0202	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.344630	1.282160	-3.062470	22112.104302
HLA B*5301	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.594963	1.532461	-3.062502	39351.655018
HLA A*2402	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.369229	1.306673	-3.062556	23400.717958
HLA B*1503	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.403229	1.340547	-3.062682	25306.295775
HLA B*1502	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.480207	1.417212	-3.062996	30213.922181
HLA B*4801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.403550	1.340547	-3.063004	25325.058610
HLA B*4402	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.395767	1.332686	-3.063081	24875.201953
HLA B*4501	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.654344	1.590840	-3.063504	45117.381486
HLA B*0801	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.283247	1.219563	-3.063684	19197.621686
HLA A*0250	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.283294	1.219563	-3.063731	19199.698938
HLA B*5801	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.283417	1.219563	-3.063853	19205.100847
HLA B*5301	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.602796	1.538857	-3.063940	40067.863470
HLA A*2403	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.330618	1.266360	-3.064258	21410.053163
HLA B*3901	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.435809	1.371517	-3.064292	27277.771572
HLA B*0702	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.385784	1.321448	-3.064335	24309.926935
HLA A*3002	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.020100	0.955683	-3.064417	10473.706745
HLA A*0203	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.165217	0.100651	-3.064565	1462.907266
HLA A*0202	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.190899	1.126330	-3.064569	15520.244961
HLA A*3002	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-3.861468	0.796898	-3.064570	7268.886397
HLA A*0201	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.225803	1.161155	-3.064647	16819.091017
HLA B*3501	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.178484	1.113773	-3.064711	15082.866700
HLA B*1502	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.301736	1.236758	-3.064977	20032.517304
HLA B*4001	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.363731	1.298743	-3.064989	23106.352120
HLA B*0702	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.326104	1.261014	-3.065090	21188.703559
HLA A*3101	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.301867	1.236758	-3.065109	20038.587151
HLA B*5101	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.178883	1.113773	-3.065111	15096.744509
HLA B*4001	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.246412	1.181170	-3.065242	17636.491899
HLA A*0203	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-3.953619	0.888375	-3.065244	8987.096029
HLA A*8001	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.405808	1.340547	-3.065261	25457.063990
HLA A*0250	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.536590	1.471168	-3.065422	34402.503474
HLA A*3002	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-3.839317	0.773768	-3.065549	6907.437069
HLA B*5401	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.505779	1.440103	-3.065675	32046.374311
HLA B*5401	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.515304	1.449604	-3.065700	32756.969268
HLA B*4402	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.372408	1.306673	-3.065735	23572.629779
HLA A*0201	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.061832	0.995952	-3.065880	11530.070492

HLA B*3501	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-3.995163	0.929186	-3.065977	9889.241349
HLA B*0803	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.315623	1.249564	-3.066060	20683.466746
HLA A*0301	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.301463	1.235214	-3.066249	20019.949899
HLA B*0801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.323353	1.257069	-3.066284	21054.897818
HLA A*0219	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.480144	1.413806	-3.066338	30209.509246
HLA A*2902	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.081361	1.014988	-3.066373	12060.376945
HLA B*0801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.437912	1.371517	-3.066394	27410.166732
HLA B*5301	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.592364	1.525910	-3.066455	39116.903787
HLA B*0702	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.316072	1.249564	-3.066508	20704.849787
HLA A*1101	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.153321	1.086732	-3.066589	14233.801613
HLA A*1101	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.351305	1.284672	-3.066633	22454.581287
HLA B*1503	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.051978	0.985326	-3.066652	11271.409345
HLA B*7301	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-3.462492	0.395731	-3.066761	2900.630674
HLA B*2705	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.316401	1.249564	-3.066837	20720.537258
HLA A*0206	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.407502	1.340547	-3.066955	25556.553939
HLA B*4403	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.644631	1.577554	-3.067077	44119.554168
HLA A*2902	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.396873	1.329751	-3.067122	24938.666226
HLA A*8001	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.454083	1.386802	-3.067281	28450.059733
HLA A*2403	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.374003	1.306673	-3.067330	23659.378698
HLA B*4501	1:138-146	9	DVKPANIMI	1.366995	0.210559	-4.644941	1.577554	-3.067387	44151.071430
HLA B*4403	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.652939	1.585464	-3.067474	44971.657471
HLA B*3901	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.408045	1.340547	-3.067498	25588.511530
HLA A*2403	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.305748	1.238104	-3.067645	20218.477401
HLA A*0250	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.597305	1.529572	-3.067733	39564.477876
HLA A*0201	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.387633	1.319849	-3.067783	24413.649107
HLA B*4801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.186538	1.118640	-3.067898	15365.189734
HLA A*0211	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.439429	1.371517	-3.067912	27506.127047
HLA A*1101	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.482061	1.413806	-3.068255	30343.162992
HLA B*4501	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.412131	1.343697	-3.068434	25830.378994
HLA B*4601	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.350755	1.282160	-3.068595	22426.173702
HLA B*1509	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.371706	1.303070	-3.068635	23534.530533
HLA B*5701	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.412436	1.343697	-3.068740	25848.551516
HLA B*4501	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.551385	1.482642	-3.068743	35594.652257
HLA A*0301	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.330075	1.261014	-3.069061	21383.314065
HLA B*2705	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.455982	1.386802	-3.069179	28574.692560
HLA B*3901	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.318823	1.249564	-3.069260	20836.430942
HLA A*6801	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.479124	1.409864	-3.069260	30138.663785
HLA B*5701	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.331600	1.262230	-3.069369	21458.523220
HLA B*3801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.464198	1.394783	-3.069415	29120.425434
HLA B*0702	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.413136	1.343697	-3.069440	25890.256789
HLA A*8001	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.368217	1.298743	-3.069474	23346.218950
HLA B*4501	1:288-296	9	LTDAERTSL	1.232510	0.352954	-4.654964	1.585464	-3.069500	45181.864651
HLA B*1517	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.351714	1.282160	-3.069554	22475.728201
HLA B*4801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.434303	1.364704	-3.069599	27183.343202
HLA A*6802	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.352160	1.282160	-3.070000	22498.842406
HLA B*5701	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.410571	1.340547	-3.070024	25737.758428
HLA A*0203	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.686568	0.616515	-3.070052	4859.230706
HLA A*6801	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.559061	1.488986	-3.070074	36229.348300
HLA A*6901	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.307015	1.236758	-3.070257	20277.519110
HLA B*0803	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.465182	1.394783	-3.070399	29186.508839
HLA A*2603	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.632329	1.561867	-3.070463	42887.349963
HLA A*0216	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.336874	1.266360	-3.070514	21720.730357
HLA A*0216	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.251727	1.181170	-3.070557	17853.638555
HLA B*2705	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.403276	1.332686	-3.070590	25309.034009
HLA A*2402	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.373677	1.303070	-3.070606	23641.594134
HLA B*1502	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.579814	1.509182	-3.070631	38002.618593
HLA B*4002	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.979774	0.909118	-3.070655	9544.954210
HLA B*3801	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.520397	1.449604	-3.070793	33143.425832
HLA A*3301	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.390645	1.319849	-3.070795	24583.557949
HLA B*0803	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.484617	1.413806	-3.070811	30522.288262
HLA A*6901	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.170402	1.099547	-3.070854	14804.769988
HLA A*2301	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.403647	1.332686	-3.070961	25330.676470
HLA A*2902	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.055282	0.984065	-3.071217	11357.469999
HLA B*0803	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.458075	1.386802	-3.071273	28712.761106
HLA A*6801	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.662158	1.590840	-3.071318	45936.539244

HLA A*2403	1:352-360	9	TFGGITRDV	0.726621	0.189665	-3.987786	0.916286	-3.071500	9722.671067
HLA A*0216	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.240294	1.168679	-3.071615	17389.782264
HLA B*1509	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.470633	1.398961	-3.071672	29555.135509
HLA B*4001	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.328755	1.257069	-3.071686	21318.399873
HLA B*5801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.342104	1.270418	-3.071686	21983.881676
HLA B*0802	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.401495	1.329751	-3.071744	25205.461859
HLA B*5101	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.485656	1.413806	-3.071850	30595.359601
HLA A*0203	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.333526	1.261650	-3.071877	21553.927025
HLA A*6802	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-3.726095	0.654207	-3.071888	5322.249804
HLA B*4601	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.267287	1.195398	-3.071889	18504.927054
HLA B*1517	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.375155	1.303070	-3.072084	23722.179260
HLA A*0201	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.278382	1.206278	-3.072103	18983.734250
HLA B*0702	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.401856	1.329751	-3.072106	25226.469857
HLA B*3501	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.392137	1.319849	-3.072287	24668.154567
HLA A*6901	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.342739	1.270418	-3.072321	22016.016337
HLA A*2902	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.253710	1.181170	-3.072540	17935.343702
HLA B*1501	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.278974	1.206278	-3.072695	19009.632274
HLA B*5801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.299153	1.226371	-3.072782	19913.767970
HLA A*0301	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.309550	1.236758	-3.072792	20396.230610
HLA B*4601	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.334581	1.261650	-3.072931	21606.346019
HLA A*0101	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.376031	1.303070	-3.072961	23770.096306
HLA B*2705	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.343415	1.270418	-3.072997	22050.345085
HLA A*0101	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.087991	1.014988	-3.073003	12245.911838
HLA B*4002	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.335338	1.262230	-3.073107	21644.016736
HLA A*2602	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.574671	1.501143	-3.073527	37555.236418
HLA A*0212	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.149299	1.075727	-3.073571	14102.580588
HLA B*4001	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.327765	1.254080	-3.073685	21269.901118
HLA B*1501	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-3.947055	0.873256	-3.073799	8852.275492
HLA B*1509	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.323445	1.249564	-3.073881	21059.340568
HLA A*0202	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.978862	0.904921	-3.073941	9524.940011
HLA B*5301	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.380643	1.306673	-3.073969	24023.870623
HLA B*3501	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.445606	1.371517	-3.074089	27900.130887
HLA B*4001	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.394059	1.319849	-3.074209	24777.560185
HLA A*0206	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.202829	1.128536	-3.074293	15952.518481
HLA A*2601	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.323985	1.249564	-3.074422	21085.560478
HLA A*3001	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.255594	1.181092	-3.074502	18013.329392
HLA B*4403	1:235-243	9	PPSARHEGL	1.512930	0.077910	-4.665382	1.590840	-3.074542	46278.765633
HLA A*6802	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.235800	1.161155	-3.074644	17210.741412
HLA A*0216	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.437895	1.363134	-3.074761	27409.128749
HLA A*3201	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.144116	1.069099	-3.075016	13935.277653
HLA A*8001	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.195522	1.120342	-3.075181	15686.366512
HLA A*2501	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.407977	1.332686	-3.075291	25584.497345
HLA B*4801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.382351	1.306673	-3.075678	24118.542301
HLA A*0216	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.489577	1.413806	-3.075771	30872.859216
HLA B*1503	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.336797	1.261014	-3.075782	21716.852980
HLA A*2403	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.405590	1.329751	-3.075839	25444.259261
HLA B*5801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.285543	1.209597	-3.075946	19299.358606
HLA A*3201	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.208191	1.132158	-3.076033	16150.678841
HLA B*3501	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.462924	1.386802	-3.076122	29035.164750
HLA A*0211	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.342579	1.266360	-3.076219	22007.918740
HLA A*3001	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.173752	1.097502	-3.076250	14919.423092
HLA B*5401	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.488195	1.411765	-3.076430	30774.808227
HLA A*2402	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.486311	1.409864	-3.076447	30641.573853
HLA B*7301	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.615359	1.538857	-3.076502	41243.819882
HLA B*4501	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.454772	1.378166	-3.076606	28495.191612
HLA B*4002	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.602538	1.525910	-3.076628	40044.026666
HLA A*3201	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.245451	1.168679	-3.076772	17597.511750
HLA B*1517	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.448383	1.371517	-3.076866	28079.109595
HLA B*0802	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.420622	1.343697	-3.076925	26340.366725
HLA B*4801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.375679	1.298743	-3.076936	23750.815092
HLA A*6901	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.179823	1.102823	-3.077000	15129.448567
HLA B*1517	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.406760	1.329751	-3.077009	25512.901695
HLA B*5401	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.480494	1.403484	-3.077010	30233.870147
HLA A*0216	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.099922	1.022881	-3.077041	12586.987860
HLA A*2902	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.331226	1.254080	-3.077146	21440.073128

HLA B*5701	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.398635	1.321448	-3.077187	25040.058347
HLA A*2403	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.303629	1.226371	-3.077258	20120.057219
HLA B*5301	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.523548	1.445980	-3.077568	33384.744446
HLA A*2501	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-3.731776	0.654207	-3.077569	5392.328101
HLA A*8001	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.421322	1.343697	-3.077625	26382.865516
HLA A*2601	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.331884	1.254080	-3.077804	21472.574495
HLA A*0216	1:226-234	9	YQHVREDPI	0.574108	0.335010	-3.987081	0.909118	-3.077962	9706.904293
HLA B*4601	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.397844	1.319849	-3.077994	24994.448588
HLA A*2501	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.384816	1.306673	-3.078142	24255.803503
HLA A*6801	1:366-374	9	RGQSSADAI	1.357283	0.227759	-4.663265	1.585042	-3.078223	46053.737451
HLA A*2501	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.485940	1.407681	-3.078259	30615.393775
HLA A*3201	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.095824	1.017549	-3.078276	12468.790026
HLA B*1801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.268307	1.190001	-3.078306	18548.425667
HLA B*1801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.492208	1.413806	-3.078402	31060.488066
HLA B*3901	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.381578	1.303070	-3.078508	24075.653008
HLA B*5701	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.363402	1.284672	-3.078731	23088.858353
HLA B*4801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.337112	1.258359	-3.078753	21732.601781
HLA A*0212	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.348951	1.270153	-3.078798	22333.190846
HLA B*5401	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-3.874644	0.795837	-3.078807	7492.794012
HLA B*0801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.107595	1.028753	-3.078842	12811.359890
HLA B*4402	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-3.853343	0.774481	-3.078862	7134.168496
HLA B*4403	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.544087	1.465019	-3.079069	35001.548151
HLA A*0206	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.672485	0.593391	-3.079094	4704.188391
HLA A*1101	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.341400	1.262230	-3.079169	21948.231504
HLA B*3501	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.315647	1.236390	-3.079257	20684.585729
HLA B*4801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.409025	1.329751	-3.079274	25646.302423
HLA B*4001	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.382372	1.303070	-3.079302	24119.716637
HLA A*3201	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.269573	1.190001	-3.079572	18602.590515
HLA A*0206	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-3.702986	0.623337	-3.079649	5046.447043
HLA B*0802	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.386333	1.306673	-3.079660	24340.720700
HLA B*4001	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.316443	1.236758	-3.079685	20722.555081
HLA B*1509	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.386362	1.306673	-3.079688	24342.300919
HLA A*0101	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.340749	1.261014	-3.079734	21915.365848
HLA A*6802	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.313457	1.233662	-3.079796	20580.556182
HLA A*6802	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.333956	1.254080	-3.079876	21575.276188
HLA A*0101	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.213068	1.133041	-3.080028	16333.088379
HLA A*0250	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.316822	1.236758	-3.080063	20740.612127
HLA A*0101	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.342302	1.262230	-3.080071	21993.874096
HLA B*1517	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.493900	1.413806	-3.080094	31181.708330
HLA A*0201	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.316530	1.236390	-3.080140	20726.703445
HLA A*2501	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.451710	1.371517	-3.080193	28295.032865
HLA A*6802	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.445066	1.364704	-3.080362	27865.437054
HLA B*4403	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-3.953831	0.873123	-3.080708	8991.472822
HLA A*0250	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.022962	0.942253	-3.080709	10542.948440
HLA B*0702	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.337819	1.257069	-3.080750	21768.019470
HLA A*0216	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.421310	1.340547	-3.080763	26382.151883
HLA B*5301	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.606473	1.525646	-3.080827	40408.537213
HLA A*0219	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.384108	1.303070	-3.081038	24216.338060
HLA A*8001	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.402575	1.321448	-3.081127	25268.264998
HLA B*5401	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.511533	1.430389	-3.081143	32473.775939
HLA B*4402	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.338383	1.257069	-3.081314	21796.300844
HLA B*5701	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.262605	1.181170	-3.081435	18306.480353
HLA B*4002	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.643398	1.561867	-3.081531	43994.423953
HLA B*1502	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.611339	1.529572	-3.081767	40863.815310
HLA A*8001	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.366443	1.284672	-3.081771	23251.056581
HLA B*4601	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.338935	1.257069	-3.081866	21824.028625
HLA A*0301	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.344127	1.262230	-3.081897	22086.519572
HLA B*3501	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-3.674078	0.592081	-3.081996	4721.474589
HLA B*4601	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.318499	1.236390	-3.082109	20820.881003
HLA B*5701	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.394944	1.312789	-3.082155	24828.146287
HLA B*4403	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.644025	1.561867	-3.082158	44058.017194
HLA B*3801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.468995	1.386802	-3.082193	29443.902020
HLA B*4801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.352656	1.270418	-3.082238	22524.539197
HLA A*0206	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.531976	1.449604	-3.082372	34038.911117
HLA B*5101	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.453930	1.371517	-3.082413	28440.057233

HLA B*5701	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.385901	1.303070	-3.082831	24316.503525
HLA B*0803	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.336938	1.254080	-3.082857	21723.903270
HLA A*0101	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.349505	1.266360	-3.083145	22361.722597
HLA B*0803	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.426853	1.343697	-3.083156	26720.996576
HLA B*4002	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.622038	1.538857	-3.083182	41883.066120
HLA A*6802	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-3.255865	0.172544	-3.083321	1802.455815
HLA B*3501	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.448029	1.364704	-3.083324	28056.181326
HLA B*1501	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.353802	1.270418	-3.083384	22584.083128
HLA B*1517	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-3.833908	0.750403	-3.083505	6821.948278
HLA B*4801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.263094	1.179436	-3.083657	18327.091442
HLA A*1101	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.318889	1.235214	-3.083675	20839.587419
HLA A*0216	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.186576	1.102823	-3.083753	15366.519775
HLA B*0702	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.387050	1.303070	-3.083980	24380.916436
HLA B*4402	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.404002	1.319849	-3.084152	25351.377383
HLA A*0219	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.424712	1.340547	-3.084165	26589.628559
HLA A*0219	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.470974	1.386802	-3.084171	29578.328656
HLA A*0301	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.366344	1.282160	-3.084184	23245.774185
HLA A*0211	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.187191	1.102823	-3.084368	15388.315584
HLA B*5401	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.494243	1.409864	-3.084379	31206.346739
HLA A*6901	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.091041	1.006578	-3.084463	12332.205698
HLA A*0202	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.534100	1.449604	-3.084496	34205.787492
HLA A*0201	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.216734	1.132158	-3.084575	16471.513581
HLA A*6901	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.342960	1.258359	-3.084601	22027.214980
HLA A*2501	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.404455	1.319849	-3.084606	25377.860797
HLA B*1503	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.346312	1.261650	-3.084662	22197.921207
HLA B*5701	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.414523	1.329751	-3.084772	25973.026229
HLA A*0206	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.456301	1.371517	-3.084784	28595.723981
HLA B*2705	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.425436	1.340547	-3.084889	26633.970350
HLA A*0201	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.323029	1.238104	-3.084925	21039.184840
HLA A*6802	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.388093	1.303070	-3.085023	24439.549563
HLA A*0219	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.367195	1.282160	-3.085035	23291.342847
HLA B*4801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.388319	1.303070	-3.085248	24452.245524
HLA A*2402	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.406699	1.321448	-3.085251	25509.313376
HLA B*5801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.343975	1.258359	-3.085616	22078.754372
HLA B*4801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.352242	1.266360	-3.085882	22503.102878
HLA B*0802	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.426434	1.340547	-3.085888	26695.277703
HLA A*0206	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.340152	1.254080	-3.086072	21885.272365
HLA A*0201	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.368264	1.282160	-3.086104	23348.745096
HLA A*0201	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.229430	1.143250	-3.086180	16960.167053
HLA B*4501	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.625116	1.538857	-3.086260	42180.943791
HLA A*8001	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.458120	1.371517	-3.086602	28715.712582
HLA B*3901	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.449755	1.363134	-3.086622	28167.962325
HLA B*0702	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.324730	1.238104	-3.086626	21121.751864
HLA A*2902	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.320299	1.233662	-3.086637	20907.341236
HLA A*0216	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.343582	1.256417	-3.087165	22058.816296
HLA B*3501	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.325395	1.238104	-3.087291	21154.114004
HLA B*4402	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.369474	1.282160	-3.087314	23413.887573
HLA B*5801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.348333	1.261014	-3.087318	22301.437758
HLA B*4402	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.386101	1.298743	-3.087358	24327.687811
HLA A*3002	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.452067	1.364704	-3.087363	28318.309528
HLA B*5701	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.407267	1.319849	-3.087418	25542.731866
HLA B*5801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.357583	1.270153	-3.087430	22781.524611
HLA B*3901	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.474286	1.386802	-3.087484	29804.813189
HLA A*2603	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.314059	1.226371	-3.087688	20609.078592
HLA B*3501	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.043379	0.955683	-3.087696	11050.428204
HLA B*5401	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.558924	1.471168	-3.087756	36217.982272
HLA B*1801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.400743	1.312789	-3.087953	25161.864805
HLA B*5801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.342057	1.254080	-3.087977	21981.503197
HLA A*3002	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.420702	1.332686	-3.088016	26345.212119
HLA A*6801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.495711	1.407681	-3.088031	31312.039619
HLA B*1502	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.350323	1.262230	-3.088092	22403.861356
HLA B*0802	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.407946	1.319849	-3.088097	25582.698088
HLA B*3901	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.395043	1.306673	-3.088369	24833.788263
HLA B*4501	1:49-57	9	DPSFYLRFR	1.131679	0.430188	-4.650270	1.561867	-3.088403	44696.125647
HLA A*2601	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.391632	1.303070	-3.088561	24639.479071

HLA B*0803	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.326694	1.238104	-3.088590	21217.494865
HLA A*2603	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.543747	1.454961	-3.088786	34974.102515
HLA A*0202	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.590001	1.501143	-3.088858	38904.594221
HLA A*2902	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.350135	1.261014	-3.089120	22394.167261
HLA A*1101	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.284110	1.194908	-3.089202	19235.775070
HLA B*0802	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.387971	1.298743	-3.089228	24432.675336
HLA A*2402	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.187125	1.097819	-3.089306	15385.984786
HLA B*1501	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.116025	1.026649	-3.089377	13062.466316
HLA B*7301	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.433114	1.343697	-3.089417	27109.033167
HLA A*0203	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.244314	1.154698	-3.089616	17551.494937
HLA B*5401	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.411083	1.321448	-3.089635	25768.130310
HLA A*0216	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.360061	1.270418	-3.089643	22911.920396
HLA A*2602	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.503495	1.413806	-3.089689	31878.303543
HLA A*2301	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.476622	1.386802	-3.089820	29965.518182
HLA B*4002	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.411316	1.321448	-3.089867	25781.934876
HLA A*0211	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.454586	1.364704	-3.089882	28483.015903
HLA A*3002	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.591025	1.501143	-3.089882	38996.467249
HLA B*4601	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.392954	1.303070	-3.089884	24714.639600
HLA B*3801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.402716	1.312789	-3.089927	25276.468240
HLA B*3801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.501705	1.411765	-3.089940	31747.160973
HLA A*3002	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.419938	1.329751	-3.090187	26298.932296
HLA A*0101	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.360475	1.270153	-3.090322	22933.746152
HLA A*0219	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.352581	1.262230	-3.090350	22520.640166
HLA B*4001	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.105777	1.014994	-3.090783	12757.827625
HLA A*0250	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.591993	1.501143	-3.090850	39083.482411
HLA A*2902	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.310450	1.219563	-3.090887	20438.535158
HLA A*6802	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.286332	1.195398	-3.090934	19334.471392
HLA A*2601	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.352188	1.261014	-3.091174	22500.303048
HLA B*4402	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.404006	1.312789	-3.091217	25351.651680
HLA A*0203	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.153152	1.061692	-3.091460	14228.258456
HLA A*2402	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.404302	1.312789	-3.091513	25368.938424
HLA A*3101	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.281793	1.190001	-3.091792	19133.441720
HLA B*5801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.353572	1.261650	-3.091922	22572.112917
HLA A*2601	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.362108	1.270153	-3.091955	23020.136431
HLA A*0206	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.478957	1.386802	-3.092155	30127.089683
HLA B*3501	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.115255	1.022974	-3.092281	13039.308258
HLA A*2402	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.495789	1.403484	-3.092305	31317.630142
HLA B*0803	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.377084	1.284672	-3.092412	23827.776102
HLA B*4601	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.362980	1.270418	-3.092561	23066.385827
HLA B*1503	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-3.633333	0.540737	-3.092596	4298.657937
HLA B*4402	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.377326	1.284672	-3.092654	23841.057081
HLA B*1502	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.547684	1.454961	-3.092724	35292.653766
HLA A*6901	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.349357	1.256417	-3.092940	22354.102506
HLA B*2705	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.312766	1.219563	-3.093203	20547.848673
HLA A*0206	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.457922	1.364704	-3.093218	28702.666246
HLA A*2602	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.618902	1.525646	-3.093255	41581.667846
HLA A*2501	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.319723	1.226371	-3.093352	20879.648525
HLA B*1502	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.564751	1.471168	-3.093583	36707.176041
HLA A*6901	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.363760	1.270153	-3.093607	23107.852202
HLA B*2705	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.363783	1.270153	-3.093630	23109.102345
HLA A*0211	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.055070	0.961256	-3.093814	11351.941506
HLA B*0802	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.415277	1.321448	-3.093829	26018.169508
HLA A*0203	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-3.998800	0.904921	-3.093879	9972.406632
HLA A*3002	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.392682	1.298743	-3.093939	24699.134865
HLA A*0219	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.364100	1.270153	-3.093947	23125.985897
HLA A*0211	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.313669	1.219563	-3.094105	20590.579090
HLA A*0216	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-3.191085	0.096922	-3.094162	1552.689538
HLA A*0201	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.364375	1.270153	-3.094222	23140.628286
HLA A*0211	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.543850	1.449604	-3.094246	34982.428571
HLA A*8001	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.320696	1.226371	-3.094325	20926.464958
HLA A*2902	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.343897	1.249564	-3.094333	22074.813084
HLA A*2501	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.238978	1.144551	-3.094428	17337.178981
HLA A*0219	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.457640	1.363134	-3.094507	28684.038903
HLA A*0201	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.350927	1.256417	-3.094510	22435.032038
HLA B*4501	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.627005	1.532461	-3.094545	42364.811533

HLA B*5301	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.438360	1.343697	-3.094664	27438.503988
HLA B*5401	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.357012	1.262230	-3.094781	22751.595626
HLA A*6901	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.255977	1.161155	-3.094822	18029.220766
HLA B*1502	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.289812	1.194908	-3.094904	19490.002291
HLA A*0216	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.239610	1.144551	-3.095060	17362.427455
HLA B*1801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.321431	1.226371	-3.095060	20961.929660
HLA A*1101	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.353631	1.258359	-3.095272	22575.165939
HLA A*2402	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.365792	1.270418	-3.095374	23216.240053
HLA A*2603	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.955574	0.860149	-3.095426	9027.638371
HLA B*1501	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.305166	1.209597	-3.095568	20191.369419
HLA A*2301	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.315278	1.219563	-3.095715	20667.024681
HLA B*4001	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.365940	1.270153	-3.095787	23224.154030
HLA B*0802	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.408665	1.312789	-3.095876	25625.083427
HLA A*2501	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.345471	1.249564	-3.095908	22154.971203
HLA A*0301	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.345485	1.249564	-3.095922	22155.690351
HLA A*3201	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.605106	1.509182	-3.095923	40281.508774
HLA A*6901	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.399000	1.303070	-3.095929	25061.064063
HLA A*3101	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.366126	1.270153	-3.095973	23234.081719
HLA A*0212	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.352527	1.256417	-3.096110	22517.838154
HLA A*0206	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.064943	0.968816	-3.096127	11612.953328
HLA A*0301	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.366405	1.270153	-3.096252	23249.044098
HLA A*3101	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.193939	1.097502	-3.096436	15629.274008
HLA A*2902	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.440205	1.343697	-3.096508	27555.276589
HLA B*4801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.346073	1.249564	-3.096509	22185.675580
HLA B*0802	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.350713	1.254080	-3.096632	22423.989992
HLA B*4402	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.353069	1.256417	-3.096653	22545.995936
HLA B*3801	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.504334	1.407681	-3.096653	31939.930573
HLA B*4002	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.561772	1.465019	-3.096753	36456.236054
HLA A*2403	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.416663	1.319849	-3.096814	26101.347876
HLA B*4601	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.353236	1.256417	-3.096819	22554.657564
HLA B*4001	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.323240	1.226371	-3.096869	21049.431104
HLA B*7301	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.622534	1.525646	-3.096888	41930.902376
HLA A*2501	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.426723	1.329751	-3.096973	26713.047089
HLA A*0206	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.012709	0.915512	-3.097197	10296.957733
HLA A*0301	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.355626	1.258359	-3.097267	22679.092067
HLA A*2301	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.492051	1.394783	-3.097268	31049.231842
HLA A*2402	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.353791	1.256417	-3.097374	22583.472249
HLA A*0201	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.367930	1.270418	-3.097512	23330.815378
HLA A*3201	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.627153	1.529572	-3.097581	42379.252897
HLA B*3501	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.364006	1.266360	-3.097646	23120.982078
HLA A*6802	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.417565	1.319849	-3.097716	26155.627110
HLA A*0101	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.354817	1.257069	-3.097749	22636.925483
HLA B*1503	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.334248	1.236390	-3.097858	21589.754305
HLA B*5801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.336031	1.238104	-3.097927	21678.586374
HLA B*5401	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.355031	1.257069	-3.097962	22648.072383
HLA A*0203	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.200968	1.102823	-3.098146	15884.314027
HLA B*5101	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.259330	1.161155	-3.098175	18168.943390
HLA B*1509	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.317780	1.219563	-3.098217	20786.442087
HLA B*5801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.355511	1.257069	-3.098442	22673.080987
HLA A*2301	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.364916	1.266360	-3.098555	23169.439501
HLA B*1502	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.369004	1.270418	-3.098585	23388.567966
HLA B*7301	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.607782	1.509182	-3.098599	40530.484231
HLA A*8001	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.380789	1.282160	-3.098629	24031.929896
HLA A*2301	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.397463	1.298743	-3.098720	24972.552999
HLA A*0101	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.360388	1.261650	-3.098738	22929.156058
HLA A*2501	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.462093	1.363134	-3.098959	28979.612694
HLA A*6801	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.510725	1.411765	-3.098960	32413.398380
HLA A*0250	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.539095	1.440103	-3.098991	34601.473884
HLA A*2403	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-3.829698	0.730675	-3.099023	6756.132298
HLA A*6901	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.084359	0.985326	-3.099033	12143.917962
HLA B*4001	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.335486	1.236390	-3.099096	21651.394772
HLA B*7301	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.529509	1.430389	-3.099119	33846.105169
HLA A*6801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.360832	1.261650	-3.099182	22952.612400
HLA A*6801	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.531001	1.431809	-3.099191	33962.575944
HLA B*3801	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.513001	1.413806	-3.099195	32583.761480

HLA A*0203	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.198774	1.099547	-3.099227	15804.255617
HLA B*0803	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.431979	1.332686	-3.099293	27038.290367
HLA B*1503	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.332977	1.233662	-3.099315	21526.658869
HLA A*0203	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.365677	1.266360	-3.099317	23210.086601
HLA B*1503	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.020801	0.921444	-3.099356	10490.605518
HLA B*0702	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.335838	1.236390	-3.099449	21668.971649
HLA A*0212	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-3.943672	0.844164	-3.099508	8783.582055
HLA A*3002	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.015914	0.916314	-3.099599	10373.220929
HLA A*3101	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.358165	1.258359	-3.099807	22812.110014
HLA A*0203	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-3.854321	0.754459	-3.099862	7150.242121
HLA A*2601	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.149581	1.049687	-3.099893	14111.738768
HLA A*0101	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.319493	1.219563	-3.099930	20868.581713
HLA B*4403	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.540034	1.440103	-3.099931	34676.431012
HLA B*3801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.443933	1.343697	-3.100237	27792.870724
HLA A*0202	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.366640	1.266360	-3.100280	23261.624976
HLA A*3301	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.532368	1.431809	-3.100559	34069.677518
HLA A*0202	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.310194	1.209597	-3.100596	20426.486558
HLA B*4601	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.367089	1.266360	-3.100729	23285.673375
HLA A*0216	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.420695	1.319849	-3.100845	26344.784548
HLA A*6802	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-3.242224	0.141319	-3.100904	1746.720903
HLA B*3501	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.296491	1.195398	-3.101093	19792.081747
HLA B*4601	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.362138	1.261014	-3.101124	23021.755461
HLA A*8001	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.404286	1.303070	-3.101215	25367.977740
HLA B*4403	1:337-345	9	AVLAVLTVV	1.202640	0.286346	-4.590224	1.488986	-3.101238	38924.593966
HLA A*1101	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.215136	1.113773	-3.101363	16411.030736
HLA B*0702	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.046058	0.944464	-3.101594	11118.789804
HLA A*3002	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.339983	1.238104	-3.101879	21876.749448
HLA B*1517	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.338735	1.236758	-3.101977	21813.995358
HLA B*7301	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.589381	1.487180	-3.102201	38849.069921
HLA A*3101	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.384372	1.282160	-3.102212	24231.015369
HLA A*3001	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.277672	1.175404	-3.102268	18952.744203
HLA A*0101	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.360632	1.258359	-3.102274	22942.060284
HLA B*5101	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.489100	1.386802	-3.102298	30838.973021
HLA A*2403	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.222720	1.120342	-3.102378	16700.135560
HLA A*3001	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.234846	1.132158	-3.102688	17172.980966
HLA B*1801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.422558	1.319849	-3.102708	26458.047561
HLA B*4002	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.635212	1.532461	-3.102751	43172.980310
HLA A*0202	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.064097	0.961256	-3.102841	11590.358413
HLA B*5101	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.215949	1.112976	-3.102973	16441.778026
HLA B*3901	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.088315	0.985326	-3.102989	12255.057617
HLA A*0203	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.172718	1.069720	-3.102999	14883.951858
HLA B*4801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.373165	1.270153	-3.103012	23613.728717
HLA A*0212	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.357129	1.254080	-3.103049	22757.750639
HLA B*4501	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.506566	1.403484	-3.103082	32104.505027
HLA B*1501	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.298531	1.195398	-3.103133	19885.239636
HLA B*0702	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.361734	1.258359	-3.103376	23000.343659
HLA B*4403	1:443-451	9	KLTAAGFGR	0.811746	0.727111	-4.642284	1.538857	-3.103427	43881.754124
HLA B*4002	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.633375	1.529572	-3.103803	42990.721376
HLA A*0301	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.360358	1.256417	-3.103941	22927.543540
HLA B*5101	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.386120	1.282160	-3.103960	24328.740715
HLA A*2601	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.374483	1.270418	-3.104064	23685.504013
HLA A*0219	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.358161	1.254080	-3.104080	22811.863193
HLA B*4601	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.353657	1.249564	-3.104093	22576.509400
HLA A*0211	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.358375	1.254080	-3.104294	22823.096236
HLA A*3201	1:459-467	9	STPELVGKV	0.780846	0.079303	-3.964516	0.860149	-3.104368	9215.444622
HLA A*3101	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.354195	1.249564	-3.104631	22604.495971
HLA B*1501	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.312936	1.208137	-3.104798	20555.853866
HLA A*0301	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.366483	1.261650	-3.104833	23253.195035
HLA A*6901	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.341233	1.236390	-3.104843	21939.802761
HLA B*5401	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.559871	1.454961	-3.104910	36297.030323
HLA A*0203	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.279606	1.174655	-3.104951	19037.316373
HLA B*4002	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.545065	1.440103	-3.104961	35080.408326
HLA A*6802	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.313140	1.208137	-3.105003	20565.530968
HLA B*1501	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.034338	0.929186	-3.105153	10822.766507
HLA B*4002	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.387351	1.282160	-3.105191	24397.805234

HLA A*2601	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.371567	1.266360	-3.105207	23527.019899
HLA B*5701	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.387391	1.282160	-3.105231	24400.049157
HLA B*1503	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.140051	1.034768	-3.105283	13805.464298
HLA B*3901	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.079599	0.974301	-3.105298	12011.542107
HLA A*0202	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.470100	1.364704	-3.105395	29518.862755
HLA B*1509	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.470116	1.364704	-3.105412	29519.980632
HLA A*0211	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.260406	1.154939	-3.105466	18214.016929
HLA B*5701	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.375671	1.270153	-3.105519	23750.429628
HLA A*2501	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.446297	1.340547	-3.105750	27944.541560
HLA A*2603	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.606941	1.501143	-3.105797	40452.063173
HLA B*3501	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.362879	1.257069	-3.105810	23061.020628
HLA B*3801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.509313	1.403484	-3.105829	32308.182432
HLA B*0803	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.367965	1.261650	-3.106315	23332.708712
HLA B*3801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.436126	1.329751	-3.106375	27297.700761
HLA B*4801	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.419264	1.312789	-3.106474	26258.131252
HLA B*5801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.343310	1.236758	-3.106551	22044.977692
HLA A*2602	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.360748	1.254080	-3.106667	22948.142676
HLA B*4002	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.450552	1.343697	-3.106855	28219.668426
HLA B*1509	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.493820	1.386802	-3.107018	31175.973412
HLA B*5401	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.524345	1.417212	-3.107133	33446.026656
HLA B*3501	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-3.628206	0.521039	-3.107168	4248.213273
HLA B*7301	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.608423	1.501143	-3.107280	40590.387917
HLA A*0301	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.364460	1.257069	-3.107391	23145.135501
HLA A*0250	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.472454	1.364704	-3.107750	29679.310394
HLA B*2705	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.130634	1.022881	-3.107753	13509.344642
HLA B*5401	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.539666	1.431809	-3.107856	34646.991000
HLA A*0201	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.374344	1.266360	-3.107984	23677.945199
HLA A*2603	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.357571	1.249564	-3.108007	22780.908392
HLA B*0702	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.448599	1.340547	-3.108053	28093.088321
HLA A*2402	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.406804	1.298743	-3.108062	25515.524247
HLA B*0802	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.472881	1.364704	-3.108177	29708.547029
HLA B*1801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.448813	1.340547	-3.108266	28106.921951
HLA B*1509	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.374689	1.266360	-3.108329	23696.782661
HLA A*0206	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.343566	1.235214	-3.108352	22057.980962
HLA B*0802	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.370044	1.261650	-3.108395	23444.687782
HLA B*4001	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.364852	1.256417	-3.108435	23166.055457
HLA A*2601	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.342130	1.233662	-3.108469	21985.189949
HLA A*0206	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.370160	1.261650	-3.108510	23450.903431
HLA B*5801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.345095	1.236390	-3.108705	22135.802550
HLA B*3901	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.213045	1.104337	-3.108708	16332.204801
HLA A*3001	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.283410	1.174655	-3.108755	19204.789157
HLA B*4403	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.638414	1.529572	-3.108842	43492.500576
HLA A*0219	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.290035	1.181170	-3.108865	19500.021547
HLA B*4403	1:151-159	9	AVKVMDFGI	1.072624	0.414556	-4.596048	1.487180	-3.108869	39450.132330
HLA B*3501	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-3.804244	0.695361	-3.108882	6371.531357
HLA A*2402	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.520670	1.411765	-3.108905	33164.231421
HLA B*1509	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.288379	1.179436	-3.108942	19425.790661
HLA A*3301	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.591601	1.482642	-3.108959	39048.188326
HLA A*0101	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.363146	1.254080	-3.109066	23075.247377
HLA A*1101	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.452798	1.343697	-3.109101	28365.994494
HLA A*2603	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.638788	1.529572	-3.109216	43529.927718
HLA B*4601	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.258637	1.149326	-3.109310	18139.970384
HLA B*0702	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.290561	1.181170	-3.109391	19523.666293
HLA A*0216	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.345812	1.236390	-3.109422	22172.357133
HLA A*3002	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.146136	1.036678	-3.109458	14000.262652
HLA A*2601	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.124925	1.014988	-3.109937	13332.912615
HLA B*4402	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.380255	1.270153	-3.110102	24002.435722
HLA B*4001	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.380568	1.270418	-3.110150	24019.712055
HLA A*2301	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.521941	1.411765	-3.110176	33261.437015
HLA A*3201	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.329807	1.219563	-3.110244	21370.130456
HLA A*2301	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.488501	1.378166	-3.110335	30796.459319
HLA B*1501	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.253635	1.143250	-3.110384	17932.239067
HLA B*4403	1:21-29	9	GMSEVHLAR	0.922376	0.603534	-4.636359	1.525910	-3.110449	43287.108681
HLA A*2601	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.368900	1.258359	-3.110542	23383.001328
HLA B*1501	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.380822	1.270153	-3.110669	24033.750106

HLA B*3901	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.430577	1.319849	-3.110727	26951.105563
HLA B*0802	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.377189	1.266360	-3.110829	23833.577561
HLA B*4402	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.373162	1.262230	-3.110932	23613.600970
HLA B*0801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.265941	1.154927	-3.111015	18447.653068
HLA A*0206	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.292528	1.181092	-3.111436	19612.271415
HLA A*0203	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.319636	1.208137	-3.111499	20875.469549
HLA B*0801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.381656	1.270153	-3.111503	24079.951530
HLA B*5301	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.373216	1.261650	-3.111566	23616.539333
HLA A*2602	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.414910	1.303070	-3.111840	25996.220926
HLA A*6801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-3.877162	0.765110	-3.112052	7536.373977
HLA B*3501	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.320275	1.208137	-3.112138	20906.210202
HLA A*0201	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.373982	1.261650	-3.112332	23658.226775
HLA B*1801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.382523	1.270153	-3.112370	24128.069122
HLA B*1502	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.231040	1.118640	-3.112399	17023.134199
HLA B*1501	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.347696	1.235214	-3.112482	22268.766023
HLA A*3201	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.613693	1.501143	-3.112550	41085.927617
HLA B*3901	1:452-460	9	FKQANSPST	0.861933	-0.283110	-3.691412	0.578823	-3.112589	4913.739819
HLA B*5801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.351300	1.238694	-3.112606	22454.338335
HLA A*0301	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.366908	1.254080	-3.112827	23275.975481
HLA A*2403	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.383007	1.270153	-3.112854	24154.973328
HLA A*0212	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.432776	1.319849	-3.112926	27087.922802
HLA A*2301	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.523010	1.409864	-3.113146	33343.410876
HLA B*4001	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.371548	1.258359	-3.113189	23526.001692
HLA B*0801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.383627	1.270418	-3.113209	24189.496367
HLA B*1801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.370489	1.257069	-3.113420	23468.671509
HLA A*0201	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.211240	1.097819	-3.113422	16264.488612
HLA B*4001	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.268453	1.154939	-3.113513	18554.648096
HLA B*5101	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.211052	1.097502	-3.113550	16257.451008
HLA A*3201	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.294819	1.181170	-3.113649	19715.992429
HLA A*2603	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.433523	1.319849	-3.113673	27134.563476
HLA A*0219	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.433577	1.319849	-3.113728	27137.939970
HLA B*4002	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.509042	1.394783	-3.114259	32288.088559
HLA B*1509	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.217161	1.102823	-3.114339	16487.739417
HLA A*0206	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.227320	1.112976	-3.114345	16877.973011
HLA B*3501	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.320649	1.206278	-3.114371	20924.200883
HLA A*2301	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.485912	1.371517	-3.114394	30613.406329
HLA B*1501	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.283130	1.168679	-3.114451	19192.429538
HLA B*0802	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.385027	1.270418	-3.114609	24267.616287
HLA A*0216	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.339511	1.224706	-3.114805	21852.973869
HLA B*1502	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.447650	1.332686	-3.114964	28031.755251
HLA A*3301	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.580001	1.465019	-3.114983	38019.069349
HLA A*0212	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.351390	1.236390	-3.115000	22458.954878
HLA A*8001	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.371433	1.256417	-3.115016	23519.766139
HLA B*4501	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.526962	1.411765	-3.115197	33648.201635
HLA B*5801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.348967	1.233662	-3.115306	22334.036603
HLA B*1501	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.290721	1.175404	-3.115317	19530.849833
HLA A*0202	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.244013	1.128536	-3.115477	17539.345333
HLA A*0212	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.397839	1.282160	-3.115679	24994.178155
HLA B*4402	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.340490	1.224706	-3.115785	21902.328161
HLA B*5801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.351216	1.235214	-3.116002	22449.965643
HLA A*6901	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.150793	1.034768	-3.116024	14151.186760
HLA B*4001	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.377375	1.261014	-3.116360	23843.765762
HLA A*3001	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.203341	1.086732	-3.116610	15971.343275
HLA A*0250	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.023958	0.907250	-3.116708	10567.159538
HLA A*2902	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.229893	1.112976	-3.116917	16978.251955
HLA A*3101	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.323226	1.206278	-3.116948	21048.747864
HLA A*0202	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.296506	1.179436	-3.117069	19792.724195
HLA B*4501	1:285-293	9	PKVLTDAER	0.972118	0.557454	-4.646818	1.529572	-3.117246	44342.327554
HLA A*3001	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.221973	1.104337	-3.117636	16671.430268
HLA B*5301	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.439138	1.321448	-3.117690	27487.681402
HLA B*1501	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.298836	1.181092	-3.117744	19899.229558
HLA A*0101	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.355917	1.238104	-3.117813	22694.310901
HLA A*3101	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.312729	1.194908	-3.117821	20546.070165
HLA B*4002	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.516800	1.398961	-3.117840	32870.047767
HLA A*2601	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.262426	1.144551	-3.117876	18298.955162

HLA B*3801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.516857	1.398961	-3.117896	32874.315804
HLA A*0101	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.388382	1.270418	-3.117964	24455.817451
HLA B*7301	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.563964	1.445980	-3.117984	36640.711399
HLA B*0801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.376383	1.258359	-3.118025	23789.393172
HLA A*2902	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.250263	1.132158	-3.118105	17793.566638
HLA A*8001	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.379184	1.261014	-3.118169	23943.296862
HLA A*0201	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.328163	1.209597	-3.118565	21289.356470
HLA A*6802	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.355327	1.236758	-3.118569	22663.515614
HLA A*0216	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.279871	1.161155	-3.118716	19048.957776
HLA B*3501	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.352997	1.233662	-3.119335	22542.215141
HLA A*0201	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.373432	1.254080	-3.119352	23628.296441
HLA B*0803	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.449445	1.329751	-3.119694	28147.854612
HLA B*4601	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.378141	1.258359	-3.119782	23885.854299
HLA B*5101	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.376858	1.257069	-3.119789	23815.404374
HLA B*4403	1:24-32	9	EVHLARDLR	0.880960	0.651501	-4.652316	1.532461	-3.119856	44907.231367
HLA B*5101	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.483226	1.363134	-3.120092	30424.692289
HLA A*2603	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.441607	1.321448	-3.120159	27644.415840
HLA A*0101	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.356981	1.236758	-3.120223	22749.995595
HLA A*0201	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.378608	1.258359	-3.120250	23911.582891
HLA A*3101	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.381902	1.261650	-3.120252	24093.633751
HLA B*5301	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.569955	1.449604	-3.120351	37149.680574
HLA B*1503	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.224741	1.104337	-3.120403	16778.014043
HLA A*1101	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.485118	1.364704	-3.120413	30557.479562
HLA A*0206	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.378930	1.258359	-3.120572	23929.311645
HLA B*4801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.345330	1.224706	-3.120625	22147.781014
HLA A*0211	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.086154	0.965301	-3.120853	12194.214531
HLA B*4001	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.387292	1.266360	-3.120932	24394.505722
HLA B*0802	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.370533	1.249564	-3.120970	23471.083928
HLA A*2902	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.391218	1.270153	-3.121065	24616.029991
HLA A*0206	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.275908	1.154698	-3.121210	18875.898698
HLA B*7301	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.553128	1.431809	-3.121319	35737.821252
HLA B*5701	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.370907	1.249564	-3.121343	23491.281792
HLA A*3002	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.329553	1.208137	-3.121416	21357.648219
HLA A*0101	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.357825	1.236390	-3.121435	22794.222437
HLA A*2902	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.424522	1.303070	-3.121452	26577.979509
HLA B*5101	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.486203	1.364704	-3.121499	30633.949496
HLA A*3201	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.204168	1.082637	-3.121531	16001.786177
HLA B*0803	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.388027	1.266360	-3.121667	24435.847816
HLA A*0219	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.197407	1.075727	-3.121679	15754.573296
HLA B*4801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.357047	1.235214	-3.121833	22753.441955
HLA A*0212	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.360064	1.238104	-3.121960	22912.044347
HLA B*4501	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.486776	1.364704	-3.122072	30674.413406
HLA A*2602	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.593436	1.471168	-3.122268	39213.520770
HLA B*1503	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.297716	1.175404	-3.122312	19847.945453
HLA B*4402	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.392816	1.270418	-3.122398	24706.752355
HLA A*0203	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.347306	1.224706	-3.122600	22248.776721
HLA B*0801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.360778	1.238104	-3.122674	22949.756642
HLA B*3901	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.140483	1.017549	-3.122935	13819.213369
HLA A*3301	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.407876	1.284672	-3.123204	25578.546438
HLA B*5301	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.518234	1.394783	-3.123451	32978.699167
HLA B*0702	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.349839	1.226371	-3.123468	22378.907567
HLA B*0803	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.393763	1.270153	-3.123610	24760.676415
HLA B*7301	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.588699	1.465019	-3.123681	38788.168650
HLA A*8001	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.361901	1.238104	-3.123797	23009.179837
HLA B*0803	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.405985	1.282160	-3.123825	25467.395078
HLA A*3201	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.150478	1.026649	-3.123829	14140.931926
HLA B*4403	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.533822	1.409864	-3.123958	34183.958617
HLA B*1509	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.443814	1.319849	-3.123964	27785.203608
HLA A*0206	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.427142	1.303070	-3.124071	26738.783081
HLA B*4402	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.385173	1.261014	-3.124158	24275.757329
HLA A*0211	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.098507	0.974301	-3.124206	12546.061826
HLA B*1501	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.012263	0.887960	-3.124303	10286.379145
HLA B*0803	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.488111	1.363134	-3.124977	30768.815232
HLA A*0202	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.154171	1.029142	-3.125030	14261.704117
HLA B*1517	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.344618	1.219563	-3.125055	22111.506190

HLA A*0219	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.395550	1.270418	-3.125132	24862.824402
HLA A*0203	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.210587	1.085412	-3.125176	16240.046032
HLA B*3801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.446774	1.321448	-3.125326	27975.247323
HLA A*3101	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.268577	1.143250	-3.125327	18559.968924
HLA B*1517	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.469101	1.343697	-3.125405	29451.070864
HLA A*8001	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.391789	1.266360	-3.125429	24648.411579
HLA B*4002	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.651095	1.525646	-3.125448	44781.078459
HLA B*5701	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.382534	1.257069	-3.125465	24128.721782
HLA B*1509	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.362218	1.236390	-3.125829	23025.990385
HLA B*3801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.490613	1.364704	-3.125909	30946.602415
HLA B*1501	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.359592	1.233662	-3.125930	22887.143613
HLA A*3001	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.127044	1.001026	-3.126018	13398.132494
HLA A*6802	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.384442	1.258359	-3.126083	24234.948301
HLA B*1509	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.387113	1.261014	-3.126099	24384.477944
HLA A*0211	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.540095	1.413806	-3.126290	34681.308842
HLA B*2705	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.307586	1.181170	-3.126416	20304.193528
HLA A*3001	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.275746	1.149326	-3.126419	18868.853973
HLA A*3101	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.307628	1.181170	-3.126458	20306.170806
HLA A*2403	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.387487	1.261014	-3.126473	24405.461822
HLA B*5401	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.540547	1.413806	-3.126741	34717.350988
HLA B*1801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.448383	1.321448	-3.126935	28079.109595
HLA A*3002	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.470736	1.343697	-3.127040	29562.171507
HLA A*2603	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.526095	1.398961	-3.127134	33581.098443
HLA A*0212	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.322573	1.195398	-3.127175	21017.115410
HLA A*2602	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.088179	0.960920	-3.127259	12251.212907
HLA A*0101	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.360928	1.233662	-3.127267	22957.703979
HLA B*4002	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.573331	1.445980	-3.127351	37439.608078
HLA A*0301	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.353727	1.226371	-3.127356	22580.173790
HLA B*5801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.333656	1.206278	-3.127377	21560.341218
HLA A*0301	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.363800	1.236390	-3.127410	23109.977486
HLA B*3901	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.492128	1.364704	-3.127424	31054.775442
HLA A*3201	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.471150	1.343697	-3.127453	29590.332252
HLA A*2301	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.541266	1.413806	-3.127460	34774.870593
HLA A*0203	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.164194	1.036678	-3.127516	14594.671527
HLA B*1509	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.389353	1.261650	-3.127703	24510.519785
HLA B*0702	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.288952	1.161155	-3.127797	19451.449888
HLA B*4402	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.354373	1.226371	-3.128002	22613.791756
HLA B*5701	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.398429	1.270418	-3.128010	25028.140357
HLA A*0101	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.318222	1.190001	-3.128220	20807.593883
HLA A*2601	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.347844	1.219563	-3.128281	22276.357024
HLA A*3002	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.337880	1.209597	-3.128283	21771.081513
HLA A*0219	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.145882	1.017549	-3.128334	13992.085135
HLA B*1502	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.536026	1.407681	-3.128346	34357.865164
HLA B*0802	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.410606	1.282160	-3.128446	25739.847089
HLA A*2601	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.261573	1.133041	-3.128533	18263.055123
HLA A*0202	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.135155	1.006578	-3.128577	13650.692711
HLA A*8001	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.390880	1.262230	-3.128649	24596.860979
HLA B*4001	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.353436	1.224706	-3.128730	22565.031496
HLA B*1801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.366844	1.238104	-3.128741	23272.575878
HLA B*1502	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.542588	1.413806	-3.128782	34880.948229
HLA B*4002	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.538662	1.409864	-3.128798	34567.048036
HLA B*5701	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.226348	1.097502	-3.128845	16840.213815
HLA B*2705	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.387306	1.258359	-3.128947	24395.297564
HLA A*0212	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.353687	1.224706	-3.128982	22578.097229
HLA A*2501	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.310182	1.181170	-3.129012	20425.934040
HLA A*2501	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.493766	1.364704	-3.129062	31172.094506
HLA B*1501	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.214492	1.085412	-3.129081	16386.722528
HLA B*5301	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.461804	1.332686	-3.129118	28960.335600
HLA A*3001	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.242329	1.112976	-3.129353	17471.443909
HLA A*2603	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.179085	1.049687	-3.129398	15103.769910
HLA B*1502	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.528388	1.398961	-3.129427	33758.877310
HLA A*2601	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.386528	1.257069	-3.129460	24351.652644
HLA B*3901	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.366236	1.236758	-3.129478	23239.990079
HLA B*5701	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.355868	1.226371	-3.129497	22691.732800
HLA B*1801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.284589	1.154927	-3.129662	19257.015724

HLA A*6901	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.084307	0.954621	-3.129686	12142.472708
HLA A*2301	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.537403	1.407681	-3.129722	34466.959131
HLA B*0801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.366537	1.236758	-3.129778	23256.088551
HLA A*1101	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.470414	1.340547	-3.129868	29540.269479
HLA A*6901	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.046194	0.916314	-3.129879	11122.279134
HLA B*7301	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.585344	1.454961	-3.130383	38489.672045
HLA B*1801	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.517207	1.386802	-3.130405	32900.825601
HLA B*3501	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.233530	1.102823	-3.130707	17121.033497
HLA B*4001	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.320726	1.190001	-3.130725	20927.936738
HLA A*3301	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.429477	1.298743	-3.130734	26882.956304
HLA B*1503	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.004274	0.873492	-3.130782	10098.904816
HLA B*4402	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.366055	1.235214	-3.130841	23230.311211
HLA B*0803	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.471460	1.340547	-3.130913	29611.470413
HLA B*5801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.244714	1.113773	-3.130941	17567.644141
HLA B*4501	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.640144	1.509182	-3.130961	43666.018944
HLA A*6801	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.530002	1.398961	-3.131041	33884.578792
HLA B*1509	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.494598	1.363134	-3.131464	31231.849408
HLA A*2501	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.392482	1.261014	-3.131468	24687.779811
HLA A*6802	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-3.895930	0.764421	-3.131510	7869.191742
HLA B*7301	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.535004	1.403484	-3.131520	34277.105802
HLA A*0203	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.049934	0.918327	-3.131607	11218.483937
HLA B*4801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.369763	1.238104	-3.131659	23429.472742
HLA A*3001	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.276255	1.144551	-3.131705	18891.017995
HLA B*1801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.464503	1.332686	-3.131817	29140.912612
HLA B*3801	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.416635	1.284672	-3.131963	26099.653467
HLA A*0206	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.539708	1.407681	-3.132027	34650.365019
HLA B*5701	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.393142	1.261014	-3.132128	24725.338192
HLA A*6801	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.587221	1.454961	-3.132261	38656.403797
HLA B*1509	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.390701	1.258359	-3.132342	24586.750020
HLA B*3901	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.246405	1.113773	-3.132632	17636.205667
HLA A*0216	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.340890	1.208137	-3.132752	21922.480585
HLA A*0250	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.369170	1.236390	-3.132781	23397.553290
HLA A*3101	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.182483	1.049687	-3.132795	15222.385509
HLA B*3501	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.435950	1.303070	-3.132879	27286.627192
HLA B*0702	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.352494	1.219563	-3.132931	22516.132753
HLA A*0211	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.519944	1.386802	-3.133142	33108.838555
HLA B*4403	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.642336	1.509182	-3.133153	43886.977134
HLA A*2603	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.598269	1.465019	-3.133250	39652.331442
HLA B*2705	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.371978	1.238694	-3.133284	23549.304195
HLA A*6901	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.339684	1.206278	-3.133406	21861.724060
HLA A*2902	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.323494	1.190001	-3.133493	21061.733207
HLA A*0212	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.404018	1.270418	-3.133600	25352.337438
HLA B*5801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.314700	1.181092	-3.133608	20639.538622
HLA B*5801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.358332	1.224706	-3.133627	22820.873877
HLA B*0702	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.440419	1.306673	-3.133745	27568.845388
HLA A*2602	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.394853	1.261014	-3.133838	24822.908456
HLA B*1509	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.404279	1.270418	-3.133861	25367.566030
HLA A*0212	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.256616	1.122659	-3.133957	18055.770110
HLA B*1517	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.474587	1.340547	-3.134040	29825.459150
HLA A*2403	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.391110	1.257069	-3.134041	24609.904933
HLA A*0201	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.157028	1.022974	-3.134055	14355.832941
HLA A*3001	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.237245	1.103143	-3.134102	17268.098320
HLA A*0202	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.505699	1.371517	-3.134182	32040.480363
HLA B*4501	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.566229	1.431809	-3.134419	36832.296725
HLA A*2501	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.248423	1.113773	-3.134651	17718.353513
HLA A*1101	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.456289	1.321448	-3.134841	28594.950493
HLA B*0803	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.433612	1.298743	-3.134870	27140.142258
HLA B*4002	1:594-602	9	DAGGSQHNR	1.030117	0.479065	-4.644147	1.509182	-3.134965	44070.413085
HLA B*4402	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.393335	1.258359	-3.134976	24736.309055
HLA A*2902	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.152546	1.017549	-3.134997	14208.413197
HLA A*0216	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-3.881735	0.746693	-3.135042	7616.133344
HLA A*0206	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.548946	1.413806	-3.135140	35395.331897
HLA B*1801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.498524	1.363134	-3.135390	31515.462968
HLA A*8001	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.389491	1.254080	-3.135411	24518.344386
HLA A*0203	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.393894	1.258359	-3.135535	24768.178892

HLA A*6802	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.391972	1.256417	-3.135555	24658.814697
HLA A*2603	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.304327	1.168679	-3.135648	20152.410846
HLA A*0212	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.397545	1.261650	-3.135895	24977.281902
HLA B*3901	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-3.927385	0.791452	-3.135933	8460.285768
HLA B*4501	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.661644	1.525646	-3.135997	45882.147435
HLA B*3801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.439075	1.303070	-3.136004	27483.666652
HLA B*5701	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.394404	1.258359	-3.136045	24797.272469
HLA A*0211	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.043360	0.907250	-3.136110	11049.949962
HLA B*1517	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.101637	0.965301	-3.136336	12636.794918
HLA B*7301	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-3.444246	0.307875	-3.136371	2781.290387
HLA B*3801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.476934	1.340547	-3.136387	29987.086588
HLA B*4402	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.439573	1.303070	-3.136502	27515.205656
HLA B*4801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.375371	1.238694	-3.136677	23733.988960
HLA B*0802	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.374929	1.238104	-3.136825	23709.862360
HLA B*1509	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.269879	1.133041	-3.136838	18615.678050
HLA A*0201	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.356464	1.219563	-3.136901	22722.935212
HLA A*0206	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.163635	1.026649	-3.136987	14575.892197
HLA B*0803	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.407408	1.270418	-3.136990	25551.024212
HLA B*2705	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.398699	1.261650	-3.137049	25043.716140
HLA B*4601	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.375242	1.238104	-3.137138	23726.928107
HLA A*0203	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.091783	0.954621	-3.137162	12353.305942
HLA A*2501	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.010670	0.873492	-3.137178	10248.718794
HLA B*5701	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.391375	1.254080	-3.137295	24624.953997
HLA B*4801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.119639	0.982334	-3.137305	13171.604793
HLA A*0211	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.545020	1.407681	-3.137339	35076.802670
HLA B*5401	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.500554	1.363134	-3.137420	31663.115593
HLA A*6901	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.292511	1.154939	-3.137572	19611.528728
HLA B*4403	1:316-324	9	DLDDTDRDR	1.107860	0.417786	-4.663321	1.525646	-3.137675	46059.717334
HLA A*2602	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.587292	1.449604	-3.137688	38662.678112
HLA A*3001	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.098996	0.961256	-3.137740	12560.187315
HLA B*1502	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.357303	1.219563	-3.137740	22766.863114
HLA A*0211	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.292460	1.154698	-3.137762	19609.194750
HLA B*4002	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.620493	1.482642	-3.137851	41734.239720
HLA B*7301	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.578211	1.440103	-3.138108	37862.664587
HLA A*2601	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.011609	0.873492	-3.138117	10270.920581
HLA B*0801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.394599	1.256417	-3.138182	24808.409460
HLA A*2403	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.362921	1.224706	-3.138215	23063.266373
HLA A*2902	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.237808	1.099547	-3.138261	17290.533320
HLA A*0101	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.387893	1.249564	-3.138330	24428.313850
HLA A*6901	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.333764	1.195398	-3.138366	21565.707283
HLA B*3501	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.394921	1.256417	-3.138504	24826.803148
HLA A*2902	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.394935	1.256417	-3.138518	24827.609022
HLA B*4801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.364932	1.226371	-3.138561	23170.316926
HLA B*0702	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.333599	1.194908	-3.138691	21557.542063
HLA A*0301	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.271796	1.133041	-3.138755	18698.038048
HLA B*4501	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.395917	1.257069	-3.138848	24883.816058
HLA A*3002	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.206100	1.067242	-3.138858	16073.103436
HLA A*0219	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.400541	1.261650	-3.138891	25150.160959
HLA B*1503	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.224670	1.085412	-3.139258	16775.291248
HLA B*1501	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.288597	1.149326	-3.139271	19435.566618
HLA B*5101	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.405658	1.266360	-3.139298	25448.251442
HLA B*1501	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.057669	0.918327	-3.139342	11420.067610
HLA A*0212	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.405787	1.266360	-3.139427	25455.824541
HLA B*0801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.294379	1.154698	-3.139682	19696.056846
HLA B*5101	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.283022	1.143250	-3.139772	19187.654002
HLA A*3101	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.376362	1.236390	-3.139972	23788.234919
HLA B*4402	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.319462	1.179436	-3.140026	20867.114108
HLA B*4402	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.378883	1.238694	-3.140189	23926.722686
HLA A*3101	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.062025	0.921765	-3.140260	11535.186492
HLA B*4403	1:410-418	9	VSAGDEITV	1.272421	0.210221	-4.622927	1.482642	-3.140285	41968.802030
HLA B*4801	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.360012	1.219563	-3.140449	22909.317574
HLA B*1801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.505168	1.364704	-3.140464	32001.330490
HLA B*1801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.244826	1.104337	-3.140489	17572.206605
HLA B*3901	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.398978	1.258359	-3.140620	25059.843895
HLA B*1517	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.410839	1.270153	-3.140686	25753.636504

HLA B*0803	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.049892	0.909118	-3.140774	11217.391556
HLA B*5101	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.367305	1.226371	-3.140934	23297.265768
HLA A*0202	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.243764	1.102823	-3.140942	17529.290310
HLA A*8001	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.411377	1.270418	-3.140958	25785.561544
HLA A*0211	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.336538	1.195398	-3.141140	21703.933390
HLA B*2705	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.169974	1.028753	-3.141221	14790.200388
HLA A*0201	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.376550	1.235214	-3.141336	23798.532484
HLA B*1801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.440108	1.298743	-3.141366	27549.165356
HLA B*5301	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.553135	1.411765	-3.141370	35738.401269
HLA A*0211	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.310205	1.168679	-3.141526	20427.039091
HLA B*2705	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.402566	1.261014	-3.141552	25267.718210
HLA B*4001	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.380385	1.238694	-3.141691	24009.578563
HLA A*0219	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.398248	1.256417	-3.141831	25017.716770
HLA B*5401	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.239437	1.097502	-3.141934	17355.478114
HLA B*4001	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.380208	1.238104	-3.142105	23999.838852
HLA A*3101	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.396208	1.254080	-3.142128	24900.514375
HLA A*2501	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.445348	1.303070	-3.142277	27883.532799
HLA B*4002	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.572669	1.430389	-3.142279	37382.534180
HLA B*4002	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.613531	1.471168	-3.142363	41070.593827
HLA B*4801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.398896	1.256417	-3.142479	25055.099360
HLA B*4402	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.404133	1.261650	-3.142483	25359.058842
HLA A*0211	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.505732	1.363134	-3.142598	32042.907151
HLA B*5401	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.111420	0.968816	-3.142604	12924.691715
HLA B*1801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.322171	1.179436	-3.142735	20997.681655
HLA A*3301	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.613961	1.471168	-3.142793	41111.274248
HLA B*3901	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.379325	1.236390	-3.142935	23951.069958
HLA B*1517	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.297690	1.154698	-3.142992	19846.764361
HLA A*6901	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.381696	1.238694	-3.143002	24082.166219
HLA B*0802	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.362817	1.219563	-3.143254	23057.777159
HLA A*2403	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.425572	1.282160	-3.143412	26642.328697
HLA B*1801	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.363024	1.219563	-3.143461	23068.756894
HLA A*0206	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.506613	1.363134	-3.143479	32107.978851
HLA A*2301	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.400964	1.257069	-3.143895	25174.663612
HLA B*0802	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.401020	1.257069	-3.143951	25177.932435
HLA A*2402	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.538747	1.394783	-3.143964	34573.780832
HLA B*0801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.213082	1.069099	-3.143983	16333.618549
HLA A*0206	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.410688	1.266360	-3.144328	25744.721291
HLA A*2301	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.451132	1.306673	-3.144459	28257.401955
HLA B*1517	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.339541	1.194908	-3.144633	21854.510811
HLA B*4001	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.378385	1.233662	-3.144724	23899.296942
HLA A*2902	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.339750	1.194908	-3.144842	21865.035857
HLA A*0219	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.354660	1.209597	-3.145063	22628.721931
HLA A*6802	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.415495	1.270418	-3.145077	26031.263055
HLA A*2602	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.452197	1.306673	-3.145523	28326.736722
HLA B*1502	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.326755	1.181092	-3.145663	21220.479467
HLA A*3001	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.300605	1.154927	-3.145679	19980.457319
HLA B*0801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.353908	1.208137	-3.145771	22589.581779
HLA B*1509	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.517338	1.371517	-3.145821	32910.794541
HLA B*4001	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.395405	1.249564	-3.145841	24854.486483
HLA A*0301	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.335848	1.190001	-3.145846	21669.440561
HLA A*2601	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.402291	1.256417	-3.145874	25251.729890
HLA A*0201	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.370615	1.224706	-3.145910	23475.528507
HLA B*0803	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.452610	1.306673	-3.145937	28353.720600
HLA A*8001	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.416174	1.270153	-3.146021	26071.993672
HLA A*2501	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.428373	1.282160	-3.146213	26814.689238
HLA A*3301	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.517731	1.371517	-3.146213	32940.541283
HLA A*0216	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.400294	1.254080	-3.146214	25135.878759
HLA A*6801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.163781	1.017549	-3.146232	14580.781963
HLA A*6802	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-3.836822	0.690572	-3.146250	6867.865539
HLA A*0212	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.381496	1.235214	-3.146282	24071.094808
HLA B*0801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.412648	1.266360	-3.146287	25861.139983
HLA A*0101	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.341719	1.195398	-3.146321	21964.385746
HLA B*4501	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.545297	1.398961	-3.146337	35099.201689
HLA A*2403	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.400567	1.254080	-3.146486	25151.657659
HLA B*4002	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.647697	1.501143	-3.146554	44432.136145

HLA A*0101	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.352867	1.206278	-3.146589	22535.508840
HLA A*0216	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.246163	1.099547	-3.146616	17626.381183
HLA B*1501	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.385335	1.238694	-3.146641	24284.820732
HLA B*1501	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-3.259032	0.112336	-3.146696	1815.648324
HLA A*3002	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.054812	0.908065	-3.146747	11345.188114
HLA B*4402	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.396354	1.249564	-3.146790	24908.867735
HLA A*2601	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.385509	1.238694	-3.146815	24294.544665
HLA B*2705	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.373270	1.226371	-3.146899	23619.478061
HLA A*0250	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.596558	1.449604	-3.146954	39496.471848
HLA B*5101	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.409192	1.262230	-3.146961	25656.155114
HLA B*7301	1:42-50	9	LRADLARDP	0.607027	0.163019	-3.917057	0.770046	-3.147011	8261.457949
HLA A*3002	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.541806	1.394783	-3.147023	34818.167008
HLA A*3001	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.102953	0.955683	-3.147269	12675.136616
HLA B*5101	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.401408	1.254080	-3.147327	25200.417090
HLA B*4501	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.602401	1.454961	-3.147441	40031.463880
HLA B*1503	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.353753	1.206278	-3.147475	22581.517548
HLA A*3201	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.534581	1.386802	-3.147779	34243.743686
HLA B*4002	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.551373	1.403484	-3.147889	35593.689454
HLA A*3201	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.064191	0.916286	-3.147905	11592.866786
HLA A*3001	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.276563	1.128536	-3.148027	18904.410719
HLA B*0801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.036406	0.888375	-3.148031	10874.413318
HLA A*0101	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.357649	1.209597	-3.148051	22784.975747
HLA A*0219	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.414661	1.266360	-3.148301	25981.317712
HLA B*0802	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.404772	1.256417	-3.148355	25396.401908
HLA A*2501	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.368031	1.219563	-3.148468	23336.243346
HLA B*3501	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.163475	1.014994	-3.148482	14570.531114
HLA B*1801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.478384	1.329751	-3.148633	30087.347770
HLA B*3801	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.455310	1.306673	-3.148636	28530.515172
HLA B*5701	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.410385	1.261650	-3.148735	25726.760943
HLA B*5801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.343864	1.194908	-3.148956	22073.141235
HLA A*2902	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.406217	1.257069	-3.149148	25481.038533
HLA B*1509	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.382859	1.233662	-3.149197	24146.742160
HLA B*5701	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.368811	1.219563	-3.149248	23378.194843
HLA A*0212	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.328717	1.179436	-3.149281	21316.554670
HLA A*2402	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.520910	1.371517	-3.149392	33182.536782
HLA A*6901	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.318137	1.168679	-3.149458	20803.541873
HLA B*3501	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.325026	1.175404	-3.149622	21136.154331
HLA A*3001	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-3.941308	0.791452	-3.149856	8735.908586
HLA A*0219	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.386392	1.236390	-3.150002	24344.012938
HLA A*2902	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.225803	1.075727	-3.150075	16819.091017
HLA B*1509	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.479892	1.329751	-3.150141	30192.027286
HLA B*4001	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-3.924810	0.774481	-3.150329	8410.271137
HLA B*4501	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.651642	1.501143	-3.150499	44837.560786
HLA A*0206	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.375232	1.224706	-3.150526	23726.414672
HLA B*1502	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.111594	0.960920	-3.150674	12929.866916
HLA A*3002	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.168268	1.017549	-3.150720	14732.224626
HLA B*1801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.412413	1.261650	-3.150763	25847.153176
HLA A*2501	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.218012	1.067242	-3.150770	16520.060312
HLA B*4001	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.312090	1.161155	-3.150935	20515.859064
HLA B*5701	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.341106	1.190001	-3.151104	21933.394334
HLA B*1501	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.254436	1.103143	-3.151293	17965.350495
HLA A*3001	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.277625	1.126330	-3.151295	18950.693670
HLA B*4801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.384978	1.233662	-3.151316	24264.859456
HLA A*2602	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.413569	1.262230	-3.151338	25916.041289
HLA A*0202	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.538190	1.386802	-3.151388	34529.480681
HLA A*8001	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.401015	1.249564	-3.151452	25177.660017
HLA A*0211	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.056085	0.904590	-3.151495	11378.502838
HLA B*4601	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.388347	1.236758	-3.151589	24453.832982
HLA B*3501	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.306557	1.154927	-3.151630	20256.139059
HLA B*4402	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-3.949165	0.797462	-3.151703	8895.385189
HLA A*0219	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.296261	1.144551	-3.151711	19781.591377
HLA B*1503	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.306761	1.154939	-3.151822	20265.675064
HLA A*0203	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.332930	1.181092	-3.151837	21524.329858
HLA A*2402	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.565684	1.413806	-3.151878	36786.097718
HLA B*0702	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.418301	1.266360	-3.151940	26199.953829

HLA B*4402	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.418308	1.266360	-3.151947	26200.379049
HLA B*4403	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.582360	1.430389	-3.151971	38226.132842
HLA B*5801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.285017	1.133041	-3.151976	19275.985516
HLA B*4801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.358257	1.206278	-3.151979	22816.923550
HLA A*0211	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-3.578266	0.426123	-3.152142	3786.741492
HLA A*6802	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.067724	0.915512	-3.152213	11687.576617
HLA A*0216	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.387487	1.235214	-3.152273	24405.461822
HLA B*3801	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.523849	1.371517	-3.152332	33407.870246
HLA A*2501	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.414581	1.262230	-3.152351	25976.539246
HLA A*0202	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.360534	1.208137	-3.152396	22936.848088
HLA B*3901	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.285461	1.133041	-3.152420	19295.704693
HLA A*3201	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.515597	1.363134	-3.152464	32779.128206
HLA B*7301	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.474178	1.321448	-3.152730	29797.397038
HLA A*1101	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.413757	1.261014	-3.152742	25927.259949
HLA A*0203	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.297415	1.144551	-3.152864	19834.206187
HLA B*4402	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.391023	1.238104	-3.152919	24604.979362
HLA B*4601	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.359199	1.206278	-3.152921	22866.475526
HLA B*4002	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.566753	1.413806	-3.152947	36876.758216
HLA A*3301	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.531184	1.378166	-3.153018	33976.910203
HLA A*2501	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.386857	1.233662	-3.153196	24370.103194
HLA B*3501	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.322192	1.168679	-3.153513	20998.704036
HLA A*0301	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.363170	1.209597	-3.153572	23076.495756
HLA A*0101	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.285999	1.132158	-3.153841	19319.624273
HLA A*0216	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.072221	0.918327	-3.153894	11809.224671
HLA A*0203	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.424397	1.270418	-3.153979	26570.360054
HLA A*2403	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.416294	1.262230	-3.154064	26079.188041
HLA A*3101	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.287169	1.133041	-3.154128	19371.743928
HLA A*6901	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.389468	1.235214	-3.154254	24517.018007
HLA A*3001	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.063430	0.909118	-3.154311	11572.564560
HLA A*2902	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.298947	1.144551	-3.154396	19904.289874
HLA B*3501	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.185598	1.031103	-3.154495	15331.976094
HLA A*0203	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.962641	0.807959	-3.154683	9175.746456
HLA B*5101	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.413313	1.258359	-3.154954	25900.763677
HLA B*5801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.363177	1.208137	-3.155040	23076.870283
HLA B*2705	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.363212	1.208137	-3.155075	23078.743008
HLA B*4501	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.381684	1.226371	-3.155313	24081.514819
HLA A*3301	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.610291	1.454961	-3.155330	40765.337516
HLA A*0216	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.334938	1.179436	-3.155502	21624.120292
HLA B*0801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.350600	1.194908	-3.155692	22418.167805
HLA A*2601	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.392108	1.236390	-3.155719	24666.553195
HLA A*8001	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.310666	1.154939	-3.155726	20448.710149
HLA B*3801	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.417720	1.261650	-3.156070	26164.967714
HLA B*1801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.414560	1.258359	-3.156201	25975.274505
HLA B*4601	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.337384	1.181092	-3.156292	21746.244293
HLA B*5301	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.061263	0.904921	-3.156342	11514.985279
HLA A*0211	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.497006	1.340547	-3.156459	31405.515328
HLA B*3801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.438797	1.282160	-3.156638	27466.127587
HLA A*2403	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.393455	1.236758	-3.156697	24743.134852
HLA B*4001	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.366384	1.209597	-3.156787	23247.912153
HLA A*2602	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.500704	1.343697	-3.157007	31674.080304
HLA B*0801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.270908	1.113773	-3.157135	18659.840787
HLA B*3501	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.418251	1.261014	-3.157237	26196.977482
HLA A*0101	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.392564	1.235214	-3.157350	24692.454789
HLA B*1503	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.072969	0.915512	-3.157457	11829.558094
HLA A*0212	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.415848	1.258359	-3.157489	26052.395565
HLA A*0101	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.413968	1.256417	-3.157551	25939.886747
HLA A*3001	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.255634	1.097819	-3.157815	18014.986120
HLA A*0211	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.243276	1.085412	-3.157864	17509.576448
HLA B*0702	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.393156	1.235214	-3.157943	24726.140773
HLA A*0216	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.419691	1.261650	-3.158042	26283.997735
HLA A*0101	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.352961	1.194908	-3.158054	22540.385952
HLA B*5701	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.396272	1.238104	-3.158168	24904.151784
HLA B*4402	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.394768	1.236390	-3.158378	24818.074516
HLA B*5101	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.414873	1.256417	-3.158456	25993.970837
HLA B*1501	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.313478	1.154939	-3.158539	20581.558253

HLA B*1501	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.258106	1.099547	-3.158558	18117.805375
HLA B*1502	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.261733	1.102823	-3.158911	18269.774834
HLA B*0803	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.394138	1.235214	-3.158925	24782.118096
HLA B*1801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.354402	1.195398	-3.159004	22615.259861
HLA B*4002	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.613994	1.454961	-3.159033	41114.388070
HLA A*0201	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.392853	1.233662	-3.159192	24708.891020
HLA B*1517	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.088400	0.929186	-3.159214	12257.444596
HLA A*0201	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.398046	1.238694	-3.159352	25006.079973
HLA A*0219	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.397524	1.238104	-3.159420	24976.065813
HLA B*3501	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.429580	1.270153	-3.159427	26889.356153
HLA A*2403	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.421183	1.261650	-3.159534	26374.445885
HLA A*0301	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.365928	1.206278	-3.159650	23223.525838
HLA A*0211	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.418042	1.258359	-3.159683	26184.367194
HLA B*5301	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.441936	1.282160	-3.159777	27665.361222
HLA B*1509	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.397930	1.238104	-3.159827	24999.452125
HLA B*5801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.355269	1.195398	-3.159870	22660.450644
HLA B*4403	1:608-616	9	PPAGTGVNR	1.129131	0.372012	-4.661070	1.501143	-3.159927	45821.622361
HLA A*6802	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.339393	1.179436	-3.159957	21847.063560
HLA A*0212	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.321286	1.161155	-3.160130	20954.899933
HLA B*4001	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.379703	1.219563	-3.160140	23971.940240
HLA A*0201	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.304867	1.144551	-3.160317	20177.501584
HLA A*2902	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.121471	0.960920	-3.160551	13227.302624
HLA B*5701	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.397371	1.236758	-3.160613	24967.284703
HLA B*1509	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.329349	1.168679	-3.160670	21347.598386
HLA A*2301	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.490531	1.329751	-3.160780	30940.743350
HLA A*3001	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.279453	1.118640	-3.160813	19030.623215
HLA B*1502	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.356314	1.195398	-3.160916	22715.069146
HLA B*0802	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.394634	1.233662	-3.160973	24810.422703
HLA A*1101	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.294201	1.133041	-3.161160	19687.960445
HLA A*1101	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.410916	1.249564	-3.161353	25758.234617
HLA A*0250	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.188192	1.026649	-3.161543	15423.820590
HLA B*4001	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.294624	1.133041	-3.161583	19707.141526
HLA A*0201	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.316542	1.154939	-3.161603	20727.264099
HLA B*4601	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.395297	1.233662	-3.161635	24848.302091
HLA A*2601	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.396883	1.235214	-3.161669	24939.205894
HLA A*8001	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.400372	1.238694	-3.161678	25140.366576
HLA A*3301	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.502248	1.340547	-3.161701	31786.859705
HLA A*2402	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.420138	1.258359	-3.161779	26311.028393
HLA B*3801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.397042	1.235214	-3.161829	24948.382029
HLA A*6801	1:64-72	9	AALNHPAIV	1.169288	0.295731	-4.626869	1.465019	-3.161850	42351.520661
HLA A*2403	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.381663	1.219563	-3.162099	24080.342342
HLA B*0802	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.424348	1.262230	-3.162118	26567.341629
HLA B*4403	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.561220	1.398961	-3.162259	36409.917817
HLA B*3501	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.357374	1.194908	-3.162466	22770.558400
HLA A*6801	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.566006	1.403484	-3.162522	36813.372017
HLA A*2301	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.465666	1.303070	-3.162596	29219.053500
HLA A*6801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.260107	1.097502	-3.162605	18201.507179
HLA A*8001	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.420977	1.258359	-3.162618	26361.892784
HLA A*0203	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.157005	0.994371	-3.162634	14355.056327
HLA B*0803	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.382231	1.219563	-3.162668	24111.888808
HLA A*0202	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.737213	0.574537	-3.162676	5460.256162
HLA A*0206	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.382299	1.219563	-3.162736	24115.671941
HLA B*5701	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.401551	1.238694	-3.162857	25208.734681
HLA A*0203	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.192026	1.029142	-3.162885	15560.599480
HLA A*0216	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.421355	1.258359	-3.162996	26384.863789
HLA A*8001	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.396713	1.233662	-3.163052	24929.493665
HLA A*0101	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.344491	1.181170	-3.163321	22105.047610
HLA A*3301	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.466402	1.303070	-3.163331	29268.571899
HLA A*0202	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.526511	1.363134	-3.163377	33613.269437
HLA A*8001	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.425206	1.261650	-3.163556	26619.853583
HLA B*7301	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-3.722223	0.558588	-3.163635	5275.010195
HLA B*4001	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.369962	1.206278	-3.163684	23440.249041
HLA A*0202	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.124634	0.960920	-3.163714	13323.971547
HLA A*2601	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.343225	1.179436	-3.163789	22040.684718
HLA A*2301	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.132711	0.968816	-3.163895	13574.105680

HLA A*2902	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.422342	1.258359	-3.163983	26444.882407
HLA B*1801	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.467081	1.303070	-3.164010	29314.367871
HLA A*0219	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.213740	1.049687	-3.164053	16358.378956
HLA B*4801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.179198	1.014994	-3.164204	15107.692486
HLA A*3002	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.354261	1.190001	-3.164259	22607.920289
HLA B*7301	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.581533	1.417212	-3.164322	38153.408810
HLA B*5301	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.542530	1.378166	-3.164364	34876.230996
HLA A*3201	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.504917	1.340547	-3.164370	31982.811620
HLA B*1501	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-3.296530	0.132130	-3.164399	1979.381531
HLA B*1502	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.278173	1.113773	-3.164400	18974.596159
HLA A*0203	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.199225	1.034768	-3.164457	15820.680005
HLA B*0802	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.434622	1.270153	-3.164469	27203.350568
HLA B*0702	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.434914	1.270418	-3.164496	27221.605412
HLA B*4002	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.581717	1.417212	-3.164505	38169.511852
HLA A*0250	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.536285	1.371517	-3.164767	34378.317195
HLA B*5301	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.568273	1.403484	-3.164789	37006.060341
HLA A*6801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-3.847770	0.682948	-3.164822	7043.205888
HLA A*2402	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.572554	1.407681	-3.164873	37372.625961
HLA A*0202	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.435311	1.270418	-3.164893	27246.504724
HLA A*3002	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.346094	1.181092	-3.165001	22186.755805
HLA A*0211	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.484937	1.319849	-3.165087	30544.753144
HLA A*6901	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.389818	1.224706	-3.165112	24536.788492
HLA A*2603	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.427471	1.262230	-3.165240	26759.042292
HLA B*1503	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-3.434665	0.269402	-3.165263	2720.602764
HLA B*4601	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.403978	1.238694	-3.165284	25350.005938
HLA A*0212	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.384919	1.219563	-3.165356	24261.577923
HLA B*4601	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.384926	1.219563	-3.165363	24261.971684
HLA B*1501	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.180396	1.014988	-3.165408	15149.432822
HLA A*0101	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.390121	1.224706	-3.165415	24553.918097
HLA A*3101	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.130742	0.965301	-3.165441	13512.706927
HLA B*3501	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.297734	1.132158	-3.165576	19848.804473
HLA A*8001	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.422711	1.257069	-3.165642	26467.352978
HLA B*4002	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.615293	1.449604	-3.165689	41237.572870
HLA A*0203	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.288639	1.122659	-3.165981	19437.459307
HLA B*4403	1:421-429	9	STGPEQREI	1.260733	0.194228	-4.620955	1.454961	-3.165995	41778.741619
HLA B*1502	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.615655	1.449604	-3.166051	41271.943153
HLA B*1509	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.194902	1.028753	-3.166149	15663.979065
HLA A*0216	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.263993	1.097819	-3.166175	18365.104314
HLA B*1517	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.372775	1.206278	-3.166496	23592.532125
HLA A*3201	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.531203	1.364704	-3.166498	33978.380725
HLA A*2601	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.356547	1.190001	-3.166545	22727.238119
HLA B*3901	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.437021	1.270418	-3.166603	27354.023927
HLA B*0702	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.346291	1.179436	-3.166855	22196.840439
HLA A*8001	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.348244	1.181170	-3.167074	22296.853594
HLA A*0301	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.348251	1.181170	-3.167081	22297.215467
HLA A*0211	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.449246	1.282160	-3.167086	28134.914062
HLA B*2705	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.341794	1.174655	-3.167140	21968.188472
HLA A*2902	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.373432	1.206278	-3.167154	23628.296441
HLA B*3901	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.264705	1.097502	-3.167203	18395.233014
HLA B*5101	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.416818	1.249564	-3.167254	26110.669097
HLA A*0250	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.488839	1.321448	-3.167391	30820.459848
HLA A*0250	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.554362	1.386802	-3.167559	35839.467798
HLA A*3301	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.480374	1.312789	-3.167584	30225.529641
HLA B*4601	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.281415	1.113773	-3.167642	19116.783898
HLA A*0219	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.387367	1.219563	-3.167804	24398.729178
HLA A*1101	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.437994	1.270153	-3.167841	27415.357232
HLA B*4501	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.608038	1.440103	-3.167934	40554.391211
HLA A*2603	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.617553	1.449604	-3.167949	41452.745548
HLA B*0702	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.404728	1.236758	-3.167969	25393.791599
HLA B*1502	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.394491	1.226371	-3.168120	24802.236534
HLA A*1101	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.289006	1.120342	-3.168664	19453.870333
HLA A*2501	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.376827	1.208137	-3.168690	23813.729530
HLA B*4403	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.618300	1.449604	-3.168696	41524.119938
HLA B*4402	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.358720	1.190001	-3.168718	22841.253607
HLA B*0802	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.349982	1.181170	-3.168812	22386.293898

HLA B*1502	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.533545	1.364704	-3.168841	34162.143672
HLA B*4403	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.640092	1.471168	-3.168924	43660.822230
HLA B*2705	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.151267	0.982334	-3.168934	14166.659596
HLA B*5801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.337645	1.168679	-3.168966	21759.306784
HLA B*4002	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.547207	1.378166	-3.169041	35253.916384
HLA A*3001	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.272031	1.102823	-3.169208	18708.156216
HLA A*2501	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.439368	1.270153	-3.169215	27502.258386
HLA A*8001	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.378848	1.209597	-3.169251	23924.781151
HLA B*5101	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.219027	1.049687	-3.169339	16558.714034
HLA B*0702	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.425821	1.256417	-3.169404	26657.611075
HLA B*0801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.403109	1.233662	-3.169447	25299.314621
HLA A*2602	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.577201	1.407681	-3.169520	37774.688841
HLA B*4601	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.324260	1.154698	-3.169562	21098.910956
HLA B*1509	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.314117	1.144551	-3.169567	20611.866101
HLA A*2402	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.513314	1.343697	-3.169617	32607.214430
HLA A*0202	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.314178	1.144551	-3.169628	20614.765510
HLA A*3101	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.114207	0.944464	-3.169743	13007.884802
HLA B*1517	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.407899	1.238104	-3.169796	25579.930246
HLA B*5801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.349259	1.179436	-3.169822	22349.023887
HLA B*2705	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.269395	1.099547	-3.169848	18594.943603
HLA A*8001	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.406607	1.236758	-3.169849	25503.931844
HLA B*3801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.436333	1.266360	-3.169973	27310.699478
HLA A*6901	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.349472	1.179436	-3.170036	22360.029019
HLA B*4501	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.641213	1.471168	-3.170044	43773.635225
HLA A*1101	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.406621	1.236390	-3.170231	25504.759698
HLA A*2902	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.319613	1.149326	-3.170286	20874.340240
HLA A*3002	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.426733	1.256417	-3.170316	26713.625154
HLA A*3001	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.253129	1.082637	-3.170492	17911.393736
HLA A*0219	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.376978	1.206278	-3.170699	23821.976054
HLA A*8001	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.360705	1.190001	-3.170704	22945.908140
HLA A*2601	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.395452	1.224706	-3.170746	24857.175829
HLA A*0219	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.166976	0.995952	-3.171024	14688.454940
HLA A*0212	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.379325	1.208137	-3.171188	23951.069958
HLA B*5101	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.491111	1.319849	-3.171262	30982.115326
HLA A*3002	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.585253	1.413806	-3.171447	38481.552132
HLA B*1517	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.340258	1.168679	-3.171579	21890.600874
HLA B*4403	1:555-563	9	VSKGNQFVM	1.277715	0.154094	-4.603560	1.431809	-3.171750	40138.373315
HLA B*0802	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.380070	1.208137	-3.171932	23992.179723
HLA B*4001	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.351411	1.179436	-3.171974	22460.048408
HLA B*5701	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.407427	1.235214	-3.172213	25552.130062
HLA B*1801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.275363	1.103143	-3.172220	18852.222527
HLA A*0202	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.154566	0.982334	-3.172232	14274.671921
HLA A*0101	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.380432	1.208137	-3.172294	24012.176487
HLA A*2601	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.378639	1.206278	-3.172361	23913.264617
HLA B*7301	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-3.996004	0.823629	-3.172375	9908.412800
HLA A*6901	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.066583	0.894030	-3.172552	11656.887930
HLA B*3801	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.492462	1.319849	-3.172613	31078.641019
HLA B*1501	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-3.870466	0.697848	-3.172618	7421.067965
HLA A*0101	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.411452	1.238694	-3.172758	25790.025835
HLA A*0211	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.429195	1.256417	-3.172778	26865.509910
HLA B*1502	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.559620	1.386802	-3.172817	36276.025572
HLA A*0301	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.368235	1.195398	-3.172837	23347.229375
HLA A*2601	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.409734	1.236758	-3.172976	25688.237253
HLA A*0203	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.411851	1.238694	-3.173157	25813.755346
HLA A*2902	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-3.938305	0.765110	-3.173195	8675.718239
HLA A*2902	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.410054	1.236758	-3.173296	25707.144198
HLA B*4001	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.368830	1.195398	-3.173432	23379.206652
HLA B*0802	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.434526	1.261014	-3.173512	27197.317386
HLA A*0206	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.072461	0.898882	-3.173579	11815.742902
HLA A*0203	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.407422	1.233662	-3.173761	25551.853595
HLA B*3501	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.273363	1.099547	-3.173816	18765.629851
HLA A*6901	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.382046	1.208137	-3.173908	24101.586041
HLA B*2705	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.410486	1.236390	-3.174096	25732.746333
HLA B*3501	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.410886	1.236758	-3.174127	25756.423141
HLA B*4402	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.243229	1.069099	-3.174129	17507.682053

HLA A*3201	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.707107	0.532852	-3.174255	5094.560416
HLA B*0801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.116678	0.942253	-3.174425	13082.126381
HLA A*2601	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.384069	1.209597	-3.174471	24214.111031
HLA B*4801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.382652	1.208137	-3.174515	24135.249350
HLA B*5401	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.546058	1.371517	-3.174541	35160.777662
HLA B*1503	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.148885	0.974301	-3.174584	14089.159340
HLA A*2301	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.382830	1.208137	-3.174693	24145.174636
HLA A*2403	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.408393	1.233662	-3.174731	25609.007524
HLA B*1501	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-3.990083	0.815296	-3.174787	9774.248796
HLA A*3001	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.082912	0.908065	-3.174847	12103.515813
HLA A*3201	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.288010	1.112976	-3.175034	19409.298321
HLA B*5801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.288381	1.112976	-3.175405	19425.895753
HLA A*3101	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.431845	1.256417	-3.175428	27029.954025
HLA B*5701	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.411835	1.236390	-3.175445	25812.777818
HLA A*2601	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.356542	1.181092	-3.175450	22726.992216
HLA A*3001	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.206715	1.031103	-3.175612	16095.901460
HLA B*5301	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.505422	1.329751	-3.175671	32020.033308
HLA A*6801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.198685	1.022974	-3.175711	15801.006979
HLA B*4801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.436838	1.261014	-3.175823	27342.483748
HLA A*3002	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.583643	1.407681	-3.175963	38339.212097
HLA B*4601	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.355428	1.179436	-3.175992	22668.788333
HLA B*5301	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.430090	1.254080	-3.176010	26920.941340
HLA B*4801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.412413	1.236390	-3.176023	25847.153176
HLA A*0206	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.005585	0.829510	-3.176076	10129.436623
HLA A*0206	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.150379	0.974301	-3.176078	14137.719255
HLA A*3301	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.575124	1.398961	-3.176163	37594.468641
HLA B*4402	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.302532	1.126330	-3.176202	20069.289697
HLA B*2705	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.331327	1.154939	-3.176388	21445.061210
HLA A*6801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.357646	1.181170	-3.176476	22784.852483
HLA B*5801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.351928	1.175404	-3.176524	22486.795724
HLA A*6801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.402942	1.226371	-3.176571	25289.598967
HLA B*5801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.351242	1.174655	-3.176587	22451.301653
HLA B*5101	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.138341	0.961636	-3.176705	13751.199795
HLA B*5401	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.520524	1.343697	-3.176828	33153.109568
HLA B*1501	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.192003	1.014994	-3.177009	15559.757691
HLA B*1503	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.338432	1.161199	-3.177233	21798.777211
HLA B*4601	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.244554	1.067242	-3.177312	17561.182677
HLA A*3301	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.572098	1.394783	-3.177315	37333.423274
HLA A*2601	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.385676	1.208137	-3.177538	24303.878043
HLA A*3101	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-3.942732	0.765110	-3.177621	8764.595323
HLA B*5401	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.564434	1.386802	-3.177632	36680.377292
HLA A*0202	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.434211	1.256417	-3.177794	27177.608511
HLA A*0219	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.402519	1.224706	-3.177813	25264.984447
HLA B*4501	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.184414	1.006578	-3.177836	15290.229111
HLA B*4601	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.413056	1.235214	-3.177843	25885.495070
HLA A*2403	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.322510	1.144551	-3.177959	21014.045727
HLA A*1101	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.460143	1.282160	-3.177983	28849.779912
HLA B*1801	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.444380	1.266360	-3.178020	27821.453118
HLA A*2402	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.444420	1.266360	-3.178060	27824.011922
HLA B*4601	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.402994	1.224706	-3.178288	25292.609052
HLA A*2301	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.541456	1.363134	-3.178322	34790.112316
HLA B*5801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.322890	1.144551	-3.178340	21032.470552
HLA B*4001	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.386503	1.208137	-3.178365	24350.203550
HLA B*1503	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.388051	1.209597	-3.178454	24437.169804
HLA A*2902	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.386613	1.208137	-3.178476	24356.395737
HLA B*5301	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.093996	0.915512	-3.178485	12416.420500
HLA B*5401	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.448917	1.270418	-3.178499	28113.613182
HLA A*2403	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.414910	1.236390	-3.178520	25996.220926
HLA A*2902	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.440423	1.261650	-3.178773	27569.143679
HLA A*3001	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.175044	0.995952	-3.179092	14963.881033
HLA A*2603	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.522895	1.343697	-3.179198	33334.573223
HLA A*2402	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.499111	1.319849	-3.179262	31558.115595
HLA B*7301	1:336-344	9	VAVLAVLTV	1.159979	0.238982	-4.578246	1.398961	-3.179286	37865.737203
HLA B*2705	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.374234	1.194908	-3.179326	23671.925496
HLA A*2501	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.445787	1.266360	-3.179427	27911.755427

HLA A*6901	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-3.825474	0.645932	-3.179542	6690.734109
HLA A*0201	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.358997	1.179436	-3.179561	22855.839363
HLA A*0301	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.334598	1.154939	-3.179658	21607.164250
HLA B*5701	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.389277	1.209597	-3.179680	24506.276978
HLA A*0202	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.265154	1.085412	-3.179742	18414.250426
HLA A*3101	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.096064	0.916314	-3.179750	12475.672311
HLA A*2603	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.509663	1.329751	-3.179912	32334.235700
HLA A*3101	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.216865	1.036678	-3.180187	16476.504444
HLA A*1101	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.437263	1.257069	-3.180194	27369.270345
HLA B*0801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.389818	1.209597	-3.180220	24536.788492
HLA B*1502	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.438609	1.258359	-3.180251	27454.243063
HLA A*3001	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.102379	0.921765	-3.180615	12658.416310
HLA B*4403	1:328-336	9	SVGRWVAVV	1.311571	0.134409	-4.626655	1.445980	-3.180675	42330.676142
HLA B*4801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.285028	1.104337	-3.180691	19276.506927
HLA A*2501	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.349402	1.168679	-3.180723	22356.400355
HLA A*0201	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.376264	1.195398	-3.180865	23782.830481
HLA B*0802	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.407296	1.226371	-3.180924	25544.390120
HLA B*5101	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.442035	1.261014	-3.181021	27671.647931
HLA B*1509	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.443254	1.262230	-3.181024	27749.451690
HLA A*2603	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.447469	1.266360	-3.181109	28020.080734
HLA A*2601	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.142086	0.960920	-3.181166	13870.294145
HLA A*3001	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.303843	1.122659	-3.181184	20129.964760
HLA B*4501	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.591251	1.409864	-3.181387	39016.725300
HLA A*6802	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.417781	1.236390	-3.181392	26168.648262
HLA A*0219	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.350081	1.168679	-3.181402	22391.380985
HLA A*2601	1:117-125	9	EVIADACQA	1.033905	-0.225946	-3.989393	0.807959	-3.181434	9758.715138
HLA A*2403	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.284321	1.102823	-3.181499	19245.143057
HLA A*2501	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.443386	1.261650	-3.181736	27757.859765
HLA B*0801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.326445	1.144551	-3.181894	21205.331218
HLA B*5401	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.294929	1.112976	-3.181953	19721.006149
HLA A*2301	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.098272	0.916286	-3.181987	12539.276381
HLA B*3801	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.545184	1.363134	-3.182051	35090.088498
HLA A*0216	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.156450	0.974301	-3.182149	14336.740436
HLA A*0203	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.417372	1.235214	-3.182159	26144.026761
HLA B*7301	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.593936	1.411765	-3.182171	39258.732805
HLA B*1801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.415836	1.233662	-3.182174	26051.690872
HLA A*0203	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.131452	0.949124	-3.182328	13534.801850
HLA A*2601	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.377744	1.195398	-3.182346	23864.026129
HLA B*1502	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.545560	1.363134	-3.182427	35120.475005
HLA B*0802	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.417661	1.235214	-3.182448	26161.429214
HLA A*0219	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.440893	1.258359	-3.182535	27598.989024
HLA B*1502	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.485728	1.303070	-3.182658	30600.491074
HLA A*2603	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.577452	1.394783	-3.182669	37796.561357
HLA A*3301	1:408-416	9	TSVSAGDEI	1.105720	0.334383	-4.622976	1.440103	-3.182872	41973.570279
HLA B*1503	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.337680	1.154698	-3.182983	21761.072587
HLA A*3002	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.378261	1.194908	-3.183353	23892.445420
HLA B*4002	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.490115	1.306673	-3.183441	30911.130210
HLA B*1501	1:520-528	9	FSQASVDSP	0.682951	0.050091	-3.916540	0.733042	-3.183498	8251.631212
HLA B*1517	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.440581	1.257069	-3.183512	27579.138273
HLA B*0802	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.441889	1.258359	-3.183531	27662.368053
HLA A*2501	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.378954	1.195398	-3.183556	23930.606229
HLA B*5701	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.408632	1.224706	-3.183927	25623.142696
HLA A*3101	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.393589	1.209597	-3.183991	24750.765913
HLA B*3801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.433666	1.249564	-3.184103	27143.519447
HLA B*4801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.379558	1.195398	-3.184159	23963.901085
HLA A*3201	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.454588	1.270418	-3.184170	28483.169994
HLA B*3501	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.258028	1.073598	-3.184430	18114.571158
HLA B*4402	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.267125	1.082637	-3.184488	18498.020781
HLA B*5701	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.390797	1.206278	-3.184519	24592.204100
HLA B*0803	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.410893	1.226371	-3.184522	25756.841162
HLA A*0201	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.392703	1.208137	-3.184566	24700.337470
HLA B*5801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.339285	1.154698	-3.184587	21841.627488
HLA B*4801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.365938	1.181170	-3.184768	23224.028391
HLA A*0219	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.380204	1.195398	-3.184806	23999.579181
HLA A*0250	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.598628	1.413806	-3.184822	39685.165780

HLA A*0216	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.404401	1.219563	-3.184838	25374.703291
HLA A*2602	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.317982	1.133041	-3.184942	20796.115239
HLA A*0202	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.598774	1.413806	-3.184968	39698.478939
HLA A*0301	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.366079	1.181092	-3.184986	23231.567979
HLA B*5101	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.455472	1.270418	-3.185054	28541.167098
HLA B*4002	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.596951	1.411765	-3.185186	39532.171118
HLA A*3002	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.318349	1.133041	-3.185308	20813.673377
HLA B*1503	1:520-528	9	FSQASVDSP	0.682951	0.050091	-3.918457	0.733042	-3.185415	8288.138307
HLA A*2301	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.455601	1.270153	-3.185448	28549.660612
HLA A*6801	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.518184	1.332686	-3.185498	32974.952747
HLA B*0802	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.410244	1.224706	-3.185538	25718.411563
HLA A*8001	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.405240	1.219563	-3.185677	25423.757582
HLA B*1501	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.267729	1.081848	-3.185881	18523.757234
HLA A*6901	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.259605	1.073598	-3.186006	18180.447191
HLA B*1801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.335343	1.149326	-3.186016	21644.250920
HLA B*0801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.329302	1.143250	-3.186052	21345.288748
HLA B*4801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.376097	1.190001	-3.186095	23773.697199
HLA A*2402	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.448501	1.262230	-3.186270	28086.705866
HLA B*4402	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.419976	1.233662	-3.186314	26301.208783
HLA A*2403	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.376362	1.190001	-3.186361	23788.234919
HLA B*5801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.347670	1.161199	-3.186471	22267.440875
HLA B*0801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.365933	1.179436	-3.186497	23223.777113
HLA B*5401	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.551321	1.364704	-3.186617	35589.453432
HLA B*4501	1:543-551	9	TTVPVDSVI	1.197271	0.233118	-4.617114	1.430389	-3.186725	41410.831114
HLA B*1801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.436305	1.249564	-3.186741	27308.926561
HLA A*3002	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.453261	1.266360	-3.186901	28396.241616
HLA B*0803	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.445479	1.258359	-3.187121	27891.981500
HLA A*6901	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.368242	1.181092	-3.187150	23347.608296
HLA B*0702	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.395348	1.208137	-3.187211	24851.259652
HLA B*1517	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.047378	0.860149	-3.187229	11152.646345
HLA A*0203	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.356002	1.168679	-3.187323	22698.731185
HLA B*0702	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.421007	1.233662	-3.187346	26363.746844
HLA B*0801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.198074	1.010656	-3.187418	15778.797361
HLA A*2301	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.500380	1.312789	-3.187590	31650.442378
HLA B*4402	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.397259	1.209597	-3.187661	24960.802173
HLA A*0250	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-3.601826	0.414162	-3.187664	3997.848146
HLA A*0202	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.222537	1.034768	-3.187768	16693.090068
HLA A*0206	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.287390	1.099547	-3.187842	19381.597538
HLA A*3101	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.156671	0.968816	-3.187855	14344.032946
HLA A*0101	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.301813	1.113773	-3.188040	20036.093956
HLA A*0216	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.117233	0.929186	-3.188047	13098.839442
HLA B*3501	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-3.570028	0.381799	-3.188230	3715.594950
HLA B*4601	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.383178	1.194908	-3.188270	24164.514540
HLA B*2705	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.321333	1.133041	-3.188292	20957.167329
HLA A*0250	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.596006	1.407681	-3.188326	39446.290942
HLA A*6801	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.509820	1.321448	-3.188372	32345.957774
HLA A*0211	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.450051	1.261650	-3.188402	28187.169450
HLA B*5101	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.264158	1.075727	-3.188431	18372.060354
HLA A*2603	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.449471	1.261014	-3.188457	28149.529707
HLA A*0250	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.357139	1.168679	-3.188460	22758.243112
HLA B*2705	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.378479	1.190001	-3.188478	23904.469204
HLA B*1502	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.424879	1.236390	-3.188489	26599.843654
HLA B*4601	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.308840	1.120342	-3.188499	20362.934730
HLA B*5401	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.518257	1.329751	-3.188506	32980.483327
HLA A*3002	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.217279	1.028753	-3.188525	16492.199862
HLA B*1801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.449570	1.261014	-3.188555	28155.926438
HLA A*0216	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.153899	0.965301	-3.188598	14252.757033
HLA A*3101	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.349818	1.161155	-3.188663	22377.817987
HLA A*0101	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.369779	1.181092	-3.188687	23430.360014
HLA A*2902	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.424010	1.235214	-3.188796	26546.653090
HLA B*0702	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.413555	1.224706	-3.188849	25915.200085
HLA A*3101	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.343747	1.154698	-3.189049	22067.171380
HLA B*3501	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.302297	1.112976	-3.189321	20058.435370
HLA B*1501	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.293853	1.104337	-3.189516	19672.203321
HLA A*2603	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.496282	1.306673	-3.189609	31353.229591

HLA B*5401	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.522326	1.332686	-3.189641	33290.960383
HLA A*0203	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.292833	1.103143	-3.189690	19626.069295
HLA B*4402	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.384600	1.194908	-3.189692	24243.734155
HLA A*0203	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.088687	0.898882	-3.189805	12265.537259
HLA B*7301	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.554517	1.364704	-3.189812	35852.266661
HLA A*0203	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.344905	1.154939	-3.189966	22126.104744
HLA B*5301	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.603966	1.413806	-3.190160	40175.956837
HLA A*0301	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.365689	1.175404	-3.190284	23210.714430
HLA B*3901	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.425584	1.235214	-3.190370	26643.049367
HLA B*0802	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.400014	1.209597	-3.190417	25119.702071
HLA B*4402	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.396782	1.206278	-3.190503	24933.405080
HLA A*2403	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.386167	1.195398	-3.190769	24331.373173
HLA A*3001	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.085402	0.894591	-3.190811	12173.122601
HLA A*2902	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.288327	1.097502	-3.190825	19423.478789
HLA B*3901	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.317226	1.126330	-3.190896	20759.920267
HLA B*1509	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.399148	1.208137	-3.191010	25069.606907
HLA A*0301	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.345744	1.154698	-3.191046	22168.878856
HLA B*1503	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.120245	0.929186	-3.191059	13190.001915
HLA B*0801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.426369	1.235214	-3.191155	26691.234292
HLA B*1509	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.289377	1.097819	-3.191558	19470.505880
HLA B*1517	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.452652	1.261014	-3.191638	28356.481763
HLA A*0212	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.430396	1.238694	-3.191702	26939.881109
HLA B*5701	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.399866	1.208137	-3.191729	25111.142157
HLA A*3301	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.603588	1.411765	-3.191823	40140.979129
HLA B*1801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.454121	1.262230	-3.191890	28452.522426
HLA A*0206	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.261082	1.069099	-3.191983	18242.417362
HLA A*0101	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.366645	1.174655	-3.191990	23261.876663
HLA A*3001	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.207096	1.014988	-3.192108	16110.014125
HLA B*3501	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.147208	0.954621	-3.192586	14034.842667
HLA A*2403	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.400738	1.208137	-3.192601	25161.592561
HLA B*4801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.373785	1.181092	-3.192692	23647.478193
HLA B*4601	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.400999	1.208137	-3.192862	25176.706577
HLA B*5801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.336151	1.143250	-3.192901	21684.568415
HLA A*0201	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.135188	0.942253	-3.192935	13651.726633
HLA A*2601	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.387915	1.194908	-3.193007	24429.503269
HLA A*0202	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.229714	1.036678	-3.193036	16971.272755
HLA A*0101	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.260324	1.067242	-3.193082	18210.568502
HLA A*2402	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.556234	1.363134	-3.193100	35994.329792
HLA B*3501	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.111486	0.918327	-3.193159	12926.649656
HLA B*5401	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.158753	0.965301	-3.193452	14412.951253
HLA A*0301	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.368151	1.174655	-3.193496	23342.682805
HLA B*4801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.403198	1.209597	-3.193601	25304.516083
HLA A*2402	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.463777	1.270153	-3.193624	29092.239732
HLA A*0212	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.362416	1.168679	-3.193737	23036.456479
HLA A*3201	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.291287	1.097502	-3.193785	19556.330436
HLA B*7301	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.348598	1.154698	-3.193901	22315.075185
HLA B*0803	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.451144	1.257069	-3.194075	28258.166312
HLA A*6802	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.348977	1.154698	-3.194279	22334.519907
HLA B*3901	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.455328	1.261014	-3.194314	28531.749974
HLA B*4601	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.403924	1.209597	-3.194327	25346.851898
HLA B*4001	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.375491	1.181092	-3.194398	23740.538174
HLA A*0202	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.602195	1.407681	-3.194514	40012.410627
HLA B*3801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.450947	1.256417	-3.194530	28245.327852
HLA B*4501	1:50-58	9	PSFYLRFRR	1.008376	0.441228	-4.644185	1.449604	-3.194581	44074.227906
HLA A*0212	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.323118	1.128536	-3.194582	21043.510432
HLA A*2602	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.384990	1.190001	-3.194988	24265.515816
HLA A*0212	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.102253	0.907250	-3.195002	12654.718896
HLA A*0212	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.349956	1.154939	-3.195017	22384.961756
HLA A*2902	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.404829	1.209597	-3.195231	25399.699523
HLA A*2402	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.338611	1.143250	-3.195360	21807.741656
HLA B*7301	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.609201	1.413806	-3.195395	40663.137157
HLA B*0803	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.420128	1.224706	-3.195423	26310.459040
HLA A*0101	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.374957	1.179436	-3.195521	23711.401623
HLA A*0219	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.430753	1.235214	-3.195539	26962.042969
HLA B*0802	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.432299	1.236758	-3.195541	27058.190971

HLA A*2403	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.390476	1.194908	-3.195568	24573.984222
HLA B*3901	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.462048	1.266360	-3.195688	28976.634094
HLA A*3201	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.567270	1.371517	-3.195752	36920.674163
HLA B*4002	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.560508	1.364704	-3.195804	36350.283699
HLA A*3201	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.083800	0.887960	-3.195840	12128.292078
HLA A*3002	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.453096	1.257069	-3.196028	28385.490215
HLA B*1503	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.191989	0.995952	-3.196037	15559.252640
HLA A*0202	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.370745	1.174655	-3.196090	23482.514547
HLA A*0101	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.357310	1.161199	-3.196111	22767.232615
HLA B*0702	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.402390	1.206278	-3.196111	25257.468123
HLA A*1101	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.457939	1.261650	-3.196289	28703.753214
HLA A*2902	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.432691	1.236390	-3.196301	27082.647780
HLA A*2403	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.351317	1.154939	-3.196377	22455.188679
HLA A*0101	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.351152	1.154698	-3.196455	22446.686684
HLA B*1501	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.328830	1.132158	-3.196672	21322.090758
HLA B*7301	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-3.988143	0.791452	-3.196691	9730.669338
HLA A*3201	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.604373	1.407681	-3.196692	40213.575551
HLA A*3002	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.516659	1.319849	-3.196810	32859.380100
HLA B*7301	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.575035	1.378166	-3.196869	37586.740923
HLA A*0101	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.340201	1.143250	-3.196951	21887.758841
HLA A*0101	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.365663	1.168679	-3.196984	23209.333230
HLA B*5401	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.282397	1.085412	-3.196985	19160.062240
HLA A*6802	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-3.820394	0.623337	-3.197057	6612.933945
HLA A*2403	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.432536	1.235214	-3.197322	27072.979574
HLA A*2603	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.568844	1.371517	-3.197327	37054.740612
HLA B*5801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.358537	1.161155	-3.197382	22831.617285
HLA A*2301	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.458446	1.261014	-3.197432	28737.314189
HLA B*3801	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.417053	1.219563	-3.197490	26124.798501
HLA B*3901	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.422252	1.224706	-3.197547	26439.446539
HLA B*5801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.352548	1.154927	-3.197621	22518.934552
HLA A*0202	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.091464	0.893801	-3.197663	12344.220402
HLA A*0216	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.179997	0.982334	-3.197663	15135.506579
HLA B*0803	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.434423	1.236758	-3.197664	27190.844239
HLA B*4403	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.614964	1.417212	-3.197753	41206.351997
HLA A*0216	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.393337	1.195398	-3.197939	24736.442876
HLA A*3101	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.353027	1.154939	-3.198088	22543.800559
HLA A*3002	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-3.991460	0.793337	-3.198123	9805.284240
HLA B*1509	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.422889	1.224706	-3.198183	26478.237310
HLA A*0201	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.372852	1.174655	-3.198197	23596.744390
HLA A*0212	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.302873	1.104337	-3.198536	20085.038905
HLA A*6901	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.353286	1.154698	-3.198588	22557.220092
HLA B*1801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.298136	1.099547	-3.198589	19867.174920
HLA B*4501	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.561927	1.363134	-3.198793	36469.255175
HLA B*0801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.348161	1.149326	-3.198835	22292.632171
HLA B*5301	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.511643	1.312789	-3.198854	32482.033927
HLA B*4601	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.367556	1.168679	-3.198877	23310.755484
HLA B*0802	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.378444	1.179436	-3.199008	23902.529475
HLA B*5101	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.435414	1.236390	-3.199024	27252.991122
HLA A*0250	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.394580	1.195398	-3.199182	24807.335798
HLA A*0211	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.469623	1.270418	-3.199205	29486.462713
HLA A*2902	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.423923	1.224706	-3.199217	26541.339888
HLA A*2403	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.342548	1.143250	-3.199298	22006.371010
HLA B*3801	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.498073	1.298743	-3.199330	31482.744892
HLA A*2402	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.343897	1.144551	-3.199346	22074.813084
HLA B*7301	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.607103	1.407681	-3.199422	40467.166033
HLA A*0203	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.303820	1.104337	-3.199482	20128.875781
HLA B*1501	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.302325	1.102823	-3.199503	20059.737579
HLA B*7301	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.609488	1.409864	-3.199624	40689.983950
HLA A*6802	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.354745	1.154927	-3.199818	22633.129440
HLA A*2602	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.449476	1.249564	-3.199912	28149.834280
HLA A*3001	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.281845	1.081848	-3.199997	19135.719071
HLA B*1502	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.381508	1.181170	-3.200338	24071.745926
HLA A*8001	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.332504	1.132158	-3.200346	21503.263766
HLA A*0101	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.299926	1.099547	-3.200379	19949.243122
HLA A*0211	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.329039	1.128536	-3.200503	21332.359393

HLA B*1509	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.349867	1.149326	-3.200541	22380.360423
HLA A*2402	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.313560	1.112976	-3.200585	20585.455661
HLA A*2601	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.355527	1.154927	-3.200600	22673.939615
HLA B*2705	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.194996	0.994371	-3.200625	15667.369048
HLA A*3002	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.437068	1.236390	-3.200678	27356.983732
HLA B*5801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.350029	1.149326	-3.200703	22388.716176
HLA B*4402	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.319467	1.118640	-3.200827	20867.339886
HLA B*2705	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.457443	1.256417	-3.201026	28671.006957
HLA A*8001	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.437430	1.236390	-3.201040	27379.784959
HLA B*5301	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.572666	1.371517	-3.201149	37382.331945
HLA A*0216	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-3.876373	0.675193	-3.201180	7522.687382
HLA B*1517	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.382323	1.181092	-3.201231	24116.976608
HLA A*0212	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.216221	1.014988	-3.201233	16452.099255
HLA A*6901	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.362510	1.161199	-3.201311	23041.442006
HLA A*0212	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.345885	1.144551	-3.201334	22176.075894
HLA A*0201	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.382436	1.181092	-3.201343	24123.239989
HLA B*3801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.462400	1.261014	-3.201386	29000.157694
HLA A*2501	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.471871	1.270418	-3.201453	29639.517773
HLA B*4002	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-3.975963	0.774481	-3.201482	9461.565160
HLA A*3101	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.396979	1.195398	-3.201581	24944.738159
HLA A*0219	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.356580	1.154939	-3.201640	22728.959510
HLA A*0216	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.356732	1.154939	-3.201793	22736.953390
HLA B*5401	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.468201	1.266360	-3.201841	29390.111787
HLA B*0803	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.363083	1.161155	-3.201928	23071.877091
HLA A*3002	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.472386	1.270418	-3.201968	29674.654468
HLA A*1101	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.408252	1.206278	-3.201973	25600.696359
HLA A*0219	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.299825	1.097819	-3.202006	19944.602964
HLA B*1517	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.435701	1.233662	-3.202039	27270.984209
HLA A*2501	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.328522	1.126330	-3.202192	21306.985242
HLA B*4001	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.370902	1.168679	-3.202223	23491.027622
HLA A*3301	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.535180	1.332686	-3.202495	34291.016274
HLA A*2301	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.302057	1.099547	-3.202510	20047.370004
HLA A*0219	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.306914	1.104337	-3.202577	20272.802596
HLA A*6801	1:136-144	9	HRDVKPANI	1.262411	0.208757	-4.673798	1.471168	-3.202629	47184.311467
HLA A*0301	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.363835	1.161155	-3.202680	23111.852898
HLA A*0101	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.252490	1.049687	-3.202803	17885.056684
HLA B*1503	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.347360	1.144551	-3.202810	22251.545252
HLA B*0801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.264597	1.061692	-3.202905	18390.655840
HLA A*0202	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.522916	1.319849	-3.203067	33336.196290
HLA A*0219	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.302614	1.099547	-3.203067	20073.090099
HLA A*2501	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.358069	1.154927	-3.203143	22807.050724
HLA B*0702	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.441875	1.238694	-3.203181	27661.470166
HLA B*3801	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.441302	1.238104	-3.203198	27624.980755
HLA B*4403	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-3.446088	0.242669	-3.203419	2793.111874
HLA A*3001	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.240148	1.036678	-3.203470	17383.950481
HLA A*3001	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.232311	1.028753	-3.203557	17073.029638
HLA A*2301	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.523449	1.319849	-3.203600	33377.159781
HLA A*3101	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.379292	1.175404	-3.203888	23949.256010
HLA A*0250	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.226817	1.022881	-3.203936	16858.444414
HLA A*3002	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.164857	0.960920	-3.203937	14616.953986
HLA B*1503	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.122190	0.918162	-3.204029	13249.217580
HLA A*2501	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.461103	1.257069	-3.204035	28913.684897
HLA B*5101	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.385128	1.181092	-3.204036	24273.262203
HLA A*0219	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.365207	1.161155	-3.204052	23184.987383
HLA A*3301	1:147-155	9	SATNAVKVM	1.243941	0.165923	-4.613949	1.409864	-3.204085	41110.162226
HLA A*8001	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.439305	1.235214	-3.204091	27498.241507
HLA A*0202	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.077512	0.873256	-3.204256	11953.977261
HLA A*2301	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.385605	1.181092	-3.204513	24299.933925
HLA A*0101	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.324901	1.120342	-3.204560	21130.094954
HLA B*5701	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.399561	1.194908	-3.204653	25093.488062
HLA B*1503	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-3.810226	0.605498	-3.204727	6459.897300
HLA A*3201	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.618787	1.413806	-3.204981	41570.646648
HLA B*5401	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.545614	1.340547	-3.205068	35124.845228
HLA B*1503	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.443825	1.238694	-3.205131	27785.955193
HLA A*3002	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.467384	1.262230	-3.205153	29334.832797

HLA A*2902	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.348413	1.143250	-3.205163	22305.540178
HLA B*1801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.359871	1.154698	-3.205173	22901.882569
HLA A*0216	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.240043	1.034768	-3.205274	17379.718960
HLA A*0216	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.331640	1.126330	-3.205310	21460.496811
HLA B*1503	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.045207	0.839877	-3.205330	11097.036298
HLA A*2602	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.201307	0.995952	-3.205355	15896.693110
HLA A*2403	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.328130	1.122659	-3.205471	21287.744108
HLA B*1503	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.386639	1.181092	-3.205547	24357.845199
HLA A*8001	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.413801	1.208137	-3.205664	25929.925095
HLA B*1502	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.305234	1.099547	-3.205687	20194.537427
HLA A*2403	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.303791	1.097819	-3.205972	20127.569084
HLA A*3002	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-3.609913	0.403854	-3.206059	4072.988851
HLA A*2501	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.103427	0.897363	-3.206065	12688.995546
HLA A*2301	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.460225	1.254080	-3.206144	28855.243023
HLA A*2601	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.349423	1.143250	-3.206173	22357.488892
HLA B*1517	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.476906	1.270418	-3.206488	29985.139930
HLA A*3002	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.066771	0.860149	-3.206622	11661.934019
HLA B*5301	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.473053	1.266360	-3.206693	29720.281902
HLA B*4402	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-3.497157	0.290447	-3.206710	3141.642309
HLA A*2402	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.444901	1.238104	-3.206798	27854.886627
HLA B*4801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-3.988237	0.781429	-3.206808	9732.775240
HLA B*1509	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.433239	1.226371	-3.206868	27116.807095
HLA B*4501	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.601760	1.394783	-3.206977	39972.385059
HLA A*3101	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.356366	1.149326	-3.207039	22717.772799
HLA A*0212	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.440748	1.233662	-3.207086	27589.733513
HLA A*0216	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.236321	1.029142	-3.207179	17231.423850
HLA A*3101	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.388507	1.181092	-3.207414	24462.830529
HLA A*2603	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.402829	1.195398	-3.207431	25283.032751
HLA A*2301	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.469688	1.262230	-3.207458	29490.929569
HLA B*3501	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.800865	0.593391	-3.207474	6322.156836
HLA A*0203	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-3.621665	0.414162	-3.207503	4184.709792
HLA A*2501	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.444363	1.236758	-3.207605	27820.399561
HLA A*2501	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.464080	1.256417	-3.207663	29112.549585
HLA B*4402	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.382335	1.174655	-3.207680	24117.628967
HLA A*3101	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.274991	1.067242	-3.207750	18836.115239
HLA B*4402	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.357169	1.149326	-3.207843	22759.843722
HLA B*4001	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.402789	1.194908	-3.207881	25280.707625
HLA A*8001	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.414163	1.206278	-3.207885	25951.536911
HLA A*2601	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.357212	1.149326	-3.207885	22762.060139
HLA A*2603	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.511098	1.303070	-3.208028	32441.291485
HLA B*1517	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.444669	1.236390	-3.208279	27839.972129
HLA A*0203	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.357649	1.149326	-3.208322	22784.975747
HLA B*4402	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.403785	1.195398	-3.208387	25338.762893
HLA A*6901	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.331059	1.122659	-3.208401	21431.839531
HLA B*5401	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.490599	1.282160	-3.208439	30945.597925
HLA B*3501	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.369631	1.161155	-3.208476	23422.375769
HLA A*0216	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.442167	1.233662	-3.208505	27680.032431
HLA A*6901	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.383162	1.174655	-3.208507	24163.599466
HLA B*3501	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.334870	1.126330	-3.208540	21620.728019
HLA A*0250	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.571870	1.363134	-3.208736	37313.837354
HLA B*3901	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.415068	1.206278	-3.208789	26005.645291
HLA B*2705	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.415173	1.206278	-3.208895	26011.977007
HLA A*0301	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.329260	1.120342	-3.208918	21343.210288
HLA A*0301	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.358379	1.149326	-3.209053	22823.343178
HLA A*2602	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.573804	1.364704	-3.209099	37480.341590
HLA B*4801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.383770	1.174655	-3.209115	24197.480297
HLA A*0101	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.125559	0.916314	-3.209245	13352.401832
HLA A*0219	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.276650	1.067242	-3.209408	18908.195116
HLA B*5101	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.512524	1.303070	-3.209454	32547.997390
HLA A*2603	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.617142	1.407681	-3.209462	41413.519537
HLA A*1101	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.124394	0.914880	-3.209514	13316.621292
HLA A*6802	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.448287	1.238694	-3.209593	28072.882186
HLA B*4402	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.429468	1.219563	-3.209904	26882.374575
HLA B*0802	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.399935	1.190001	-3.209933	25115.082073
HLA B*4501	1:265-273	9	TAAEMRADL	1.001324	0.415888	-4.627318	1.417212	-3.210106	42395.304630

HLA B*4403	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-3.500596	0.290447	-3.210149	3166.623155
HLA A*0202	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.179142	0.968816	-3.210326	15105.731071
HLA A*2402	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.492490	1.282160	-3.210330	31080.658668
HLA B*5301	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.573609	1.363134	-3.210475	37463.515915
HLA B*3901	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.286539	1.075727	-3.210812	19343.678150
HLA B*1509	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.342983	1.132158	-3.210825	22028.406660
HLA A*6802	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.446086	1.235214	-3.210872	27930.938954
HLA B*2705	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.379630	1.168679	-3.210951	23967.920325
HLA B*0702	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.379875	1.168679	-3.211196	23981.409154
HLA B*1502	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.228937	1.017549	-3.211388	16940.909943
HLA B*1502	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.468610	1.257069	-3.211541	29417.790333
HLA A*6901	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.360912	1.149326	-3.211586	22956.834605
HLA B*5401	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.281483	1.069720	-3.211763	19119.783304
HLA A*3002	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.238506	1.026649	-3.211858	17318.336992
HLA B*5701	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.366567	1.154698	-3.211869	23257.724176
HLA A*6802	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-3.481669	0.269799	-3.211870	3031.579293
HLA B*3501	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.447241	1.235214	-3.212028	28005.380795
HLA B*1517	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.944889	0.732827	-3.212062	8808.231006
HLA B*5101	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.407589	1.195398	-3.212191	25561.670002
HLA B*5401	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.038788	0.826538	-3.212250	10934.230217
HLA A*2501	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.466385	1.254080	-3.212305	29267.463542
HLA A*2602	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.470722	1.258359	-3.212364	29561.211954
HLA A*2501	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.422010	1.209597	-3.212413	26424.718092
HLA B*5801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.344588	1.132158	-3.212430	22109.951174
HLA A*3001	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.282157	1.069720	-3.212438	19149.492467
HLA A*3002	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.326309	1.113773	-3.212536	21198.678589
HLA A*0301	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.355792	1.143250	-3.212542	22687.804828
HLA B*4403	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.626549	1.413806	-3.212744	42320.372204
HLA B*4402	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.394016	1.181170	-3.212846	24775.147514
HLA A*6802	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.341404	1.128536	-3.212868	21948.468980
HLA A*0219	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.421019	1.208137	-3.212882	26364.459978
HLA B*1503	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.945833	0.732827	-3.213006	8827.407775
HLA A*0250	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.181848	0.968816	-3.213033	15200.166857
HLA A*8001	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.381721	1.168679	-3.213042	24083.599362
HLA A*6802	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.387767	1.174655	-3.213112	24421.178550
HLA A*2902	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.326946	1.113773	-3.213173	21229.780340
HLA B*4501	1:231-239	9	EDPIPPSAR	0.941071	0.472735	-4.626986	1.413806	-3.213181	42362.978062
HLA B*5401	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.525989	1.312789	-3.213200	33572.924287
HLA B*4001	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.282310	1.069099	-3.213211	19156.227432
HLA A*8001	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.394432	1.181092	-3.213340	24798.882327
HLA B*4403	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.608165	1.394783	-3.213382	40566.240258
HLA A*0212	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.311258	1.097819	-3.213439	20476.606725
HLA B*0803	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.408907	1.195398	-3.213509	25639.366178
HLA A*0201	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.382189	1.168679	-3.213510	24109.540955
HLA A*2301	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.356845	1.143250	-3.213595	22742.858368
HLA A*3101	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.327444	1.113773	-3.213671	21254.142669
HLA B*4403	1:162-170	9	AIADSGNSV	1.093291	0.318474	-4.625445	1.411765	-3.213680	42212.903085
HLA A*0301	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.368750	1.154927	-3.213823	23374.906765
HLA A*3002	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.585377	1.371517	-3.213860	38492.587303
HLA B*5101	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.450639	1.236758	-3.213881	28225.317607
HLA B*4801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.408879	1.194908	-3.213971	25637.701759
HLA A*0219	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.447662	1.233662	-3.214000	28032.513505
HLA B*1501	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.118995	0.904921	-3.214074	13152.094860
HLA B*3801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.471171	1.257069	-3.214102	29591.773011
HLA A*0250	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.358842	1.144551	-3.214291	22847.680080
HLA A*0206	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.484915	1.270418	-3.214497	30543.265987
HLA B*1501	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.245714	1.031103	-3.214611	17608.177447
HLA A*1101	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.404859	1.190001	-3.214858	25401.485910
HLA B*1509	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.450113	1.235214	-3.214899	28191.134455
HLA A*6901	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.347978	1.133041	-3.214937	22283.227303
HLA A*3002	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.469047	1.254080	-3.214967	29447.406570
HLA B*1503	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.209525	0.994371	-3.215155	16200.383249
HLA A*2501	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.451687	1.236390	-3.215297	28293.502176
HLA B*0801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.440078	1.224706	-3.215372	27547.227931
HLA B*3901	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.423545	1.208137	-3.215407	26518.232653

HLA B*7301	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.522183	1.306673	-3.215510	33279.976071
HLA B*5301	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.602392	1.386802	-3.215590	40030.597626
HLA A*3301	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.559317	1.343697	-3.215620	36250.718247
HLA A*0250	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.250533	1.034768	-3.215765	17804.640123
HLA B*5101	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.422163	1.206278	-3.215885	26434.011787
HLA B*2705	1:42-50	9	LRADLARDP	0.607027	0.163019	-3.986023	0.770046	-3.215978	9683.302060
HLA A*2403	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.349195	1.133041	-3.216155	22345.759671
HLA B*2705	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.231195	1.014988	-3.216207	17029.213440
HLA A*6801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.451656	1.235214	-3.216442	28291.512405
HLA B*5301	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.397569	1.181092	-3.216476	24978.633182
HLA A*2501	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.474893	1.258359	-3.216534	29846.442344
HLA A*6802	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.441344	1.224706	-3.216639	27627.670952
HLA A*3101	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.177652	0.960920	-3.216732	15054.009132
HLA B*4501	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.285872	1.069099	-3.216773	19313.981178
HLA A*0301	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.330658	1.113773	-3.216885	21412.022296
HLA A*2601	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.378068	1.161155	-3.216913	23881.848821
HLA A*0206	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.114977	0.898050	-3.216927	13030.987051
HLA A*1101	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.473344	1.256417	-3.216927	29740.225736
HLA A*3101	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.131833	0.914880	-3.216953	13546.668977
HLA A*6801	1:475-483	9	NQTSAITNV	1.108161	0.235536	-4.560764	1.343697	-3.217067	36371.724980
HLA B*0801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.132580	0.915512	-3.217068	13569.993976
HLA A*0211	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.425236	1.208137	-3.217099	26621.725785
HLA A*3002	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.478814	1.261650	-3.217164	30117.149286
HLA B*5701	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.412575	1.195398	-3.217177	25856.803263
HLA A*1101	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.133543	0.916314	-3.217229	13600.126368
HLA B*3901	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.412152	1.194908	-3.217244	25831.636680
HLA A*0202	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.146451	0.929186	-3.217265	14010.415474
HLA A*1101	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.471425	1.254080	-3.217344	29609.067589
HLA B*1503	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.244175	1.026649	-3.217527	17545.893684
HLA A*2602	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.539069	1.321448	-3.217621	34599.414854
HLA A*0301	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.362228	1.144551	-3.217677	23026.488663
HLA B*1517	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.456376	1.238694	-3.217682	28600.674800
HLA A*0301	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.134041	0.916314	-3.217727	13615.733253
HLA B*4601	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.244455	1.026649	-3.217806	17557.192960
HLA A*8001	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.442646	1.224706	-3.217940	27710.597459
HLA A*0250	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.537849	1.319849	-3.218000	34502.405206
HLA A*0211	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.162550	0.944464	-3.218086	14539.507156
HLA A*0250	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.315919	1.097819	-3.218100	20697.570355
HLA B*5701	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.373139	1.154939	-3.218199	23612.323535
HLA B*1503	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.224783	1.006578	-3.218205	16779.647932
HLA A*6801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.350372	1.132158	-3.218214	22406.406751
HLA A*3001	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.291818	1.073598	-3.218220	19580.255311
HLA B*0702	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.315844	1.097502	-3.218342	20693.987575
HLA A*3201	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.172770	0.954333	-3.218437	14885.723415
HLA B*3901	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.452128	1.233662	-3.218467	28322.292980
HLA A*1101	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.373430	1.154939	-3.218491	23628.168615
HLA B*7301	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.480938	1.262230	-3.218707	30264.799153
HLA B*1502	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.548509	1.329751	-3.218758	35359.733634
HLA A*0201	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.341454	1.122659	-3.218795	21950.962637
HLA A*2301	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.428439	1.209597	-3.218841	26818.751351
HLA A*3101	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.294612	1.075727	-3.218885	19706.608466
HLA A*2602	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.582046	1.363134	-3.218912	38198.431799
HLA B*0801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.201269	0.982334	-3.218935	15895.317180
HLA B*4403	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.455707	1.236758	-3.218948	28556.611730
HLA B*0802	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.387666	1.168679	-3.218987	24415.498229
HLA A*2601	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.316493	1.097502	-3.218990	20724.909456
HLA B*5401	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.393852	1.174655	-3.219197	24765.767134
HLA B*1502	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.253973	1.034768	-3.219204	17946.214155
HLA A*0216	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.457950	1.238694	-3.219256	28704.529645
HLA A*3001	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.261637	1.042359	-3.219278	18265.722948
HLA A*3101	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.332298	1.112976	-3.219322	21493.029139
HLA A*0301	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.306120	1.086732	-3.219388	20235.766785
HLA B*0803	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.398863	1.179436	-3.219427	25053.201797
HLA A*0203	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.135089	0.915512	-3.219577	13648.625103
HLA A*0201	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.345941	1.126330	-3.219611	22178.955364

HLA B*0803	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.453317	1.233662	-3.219656	28399.928748
HLA A*0250	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.560510	1.340547	-3.219963	36350.480351
HLA A*0201	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.095077	0.875034	-3.220043	12447.357849
HLA A*2403	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.426449	1.206278	-3.220170	26696.144228
HLA B*5401	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.114366	0.894030	-3.220336	13012.670925
HLA A*2602	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.615129	1.394783	-3.220346	41221.959477
HLA B*1503	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.333381	1.112976	-3.220405	21546.698767
HLA B*5701	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.401687	1.181092	-3.220595	25216.645757
HLA A*2601	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.395379	1.174655	-3.220724	24853.007467
HLA B*0803	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.482984	1.262230	-3.220754	30407.743807
HLA A*0301	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.352931	1.132158	-3.220773	22538.800775
HLA A*3002	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.375523	1.154698	-3.220826	23742.336314
HLA A*6802	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.263225	1.042359	-3.220866	18332.644544
HLA A*8001	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.400365	1.179436	-3.220928	25139.958560
HLA A*8001	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.416329	1.195398	-3.220931	26081.304410
HLA A*0201	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.396394	1.175404	-3.220990	24911.158662
HLA A*2603	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.454710	1.233662	-3.221049	28491.183842
HLA B*0802	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.457478	1.236390	-3.221088	28673.333656
HLA A*2403	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.334896	1.113773	-3.221123	21622.014681
HLA A*2403	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.400581	1.179436	-3.221145	25152.474078
HLA B*1509	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.477649	1.256417	-3.221232	30036.444115
HLA A*6901	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.325606	1.104337	-3.221269	21164.416239
HLA A*0101	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.396878	1.175404	-3.221474	24938.936059
HLA B*4501	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.528503	1.306673	-3.221830	33767.827454
HLA B*5301	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.335683	1.113773	-3.221910	21661.236066
HLA A*2601	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.397378	1.175404	-3.221974	24967.689917
HLA B*5301	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.183629	0.961636	-3.221994	15262.626096
HLA B*5301	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.471589	1.249564	-3.222026	29620.282437
HLA A*2403	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.383281	1.161199	-3.222082	24170.267228
HLA B*4601	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.397555	1.175404	-3.222151	24977.822405
HLA A*8001	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.417074	1.194908	-3.222166	26126.070522
HLA B*4001	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.365423	1.143250	-3.222173	23196.529651
HLA B*4601	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.383406	1.161155	-3.222251	24177.198420
HLA B*1501	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.383472	1.161155	-3.222317	24180.860985
HLA A*3101	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.087498	0.865145	-3.222352	12232.007442
HLA B*1502	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.529027	1.306673	-3.222354	33808.589722
HLA B*1502	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.216738	0.994371	-3.222368	16471.691800
HLA B*1517	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.397982	1.175404	-3.222578	25002.427676
HLA A*6901	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.797247	0.574537	-3.222710	6269.704298
HLA B*0801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.391500	1.168679	-3.222821	24632.015578
HLA B*5701	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.391519	1.168679	-3.222840	24633.081653
HLA B*1517	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-3.846224	0.623337	-3.222888	7018.178709
HLA B*4402	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.384050	1.161155	-3.222895	24213.063089
HLA A*0301	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.237963	1.014988	-3.222976	17296.708054
HLA A*0250	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.489434	1.266360	-3.223073	30862.672753
HLA B*0802	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.322834	1.099547	-3.223287	21029.739929
HLA A*2501	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.404415	1.181092	-3.223323	25375.526951
HLA A*2501	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.402820	1.179436	-3.223384	25282.485643
HLA B*0702	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.433083	1.209597	-3.223486	27107.126695
HLA B*1502	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-3.877769	0.654207	-3.223561	7546.900226
HLA A*2902	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.246821	1.022974	-3.223847	17653.101310
HLA B*4002	1:414-422	9	DEITVNVST	1.070685	-0.486156	-3.808473	0.584529	-3.223944	6433.879130
HLA A*6901	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.399382	1.175404	-3.223978	25083.172955
HLA A*3002	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.118182	0.894030	-3.224152	13127.499511
HLA B*1509	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.342849	1.118640	-3.224209	22021.614946
HLA B*0801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.321720	1.097502	-3.224218	20975.882713
HLA A*6901	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.247101	1.022881	-3.224219	17664.469626
HLA B*0702	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.373644	1.149326	-3.224318	23639.803624
HLA A*3001	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-3.956693	0.732333	-3.224359	9050.915465
HLA B*0801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.399068	1.174655	-3.224413	25064.996122
HLA B*3501	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.139299	0.914880	-3.224420	13781.585443
HLA B*4002	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.632261	1.407681	-3.224581	42880.622033
HLA B*0702	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.356885	1.132158	-3.224727	22744.950082
HLA A*0201	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.379560	1.154698	-3.224862	23964.030727
HLA B*3801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.461254	1.236390	-3.224864	28923.697500

HLA A*3201	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.134215	0.909118	-3.225097	13621.185156
HLA B*5401	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.544971	1.319849	-3.225121	35072.817902
HLA B*0801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.380086	1.154939	-3.225147	23993.088306
HLA B*5101	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.463481	1.238104	-3.225377	29072.415879
HLA B*1509	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-3.661442	0.436027	-3.225415	4586.085280
HLA B*0702	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.292704	1.067242	-3.225463	19620.230546
HLA B*1501	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.400167	1.174655	-3.225512	25128.536787
HLA B*1501	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.275311	1.049687	-3.225624	18849.978915
HLA B*5301	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.590471	1.364704	-3.225767	38946.710910
HLA B*5701	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.405237	1.179436	-3.225801	25423.620043
HLA B*1517	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-3.572101	0.346054	-3.226046	3733.366358
HLA A*2403	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.394810	1.168679	-3.226131	24820.491368
HLA B*7301	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.613040	1.386802	-3.226238	41024.182912
HLA A*6901	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.252909	1.026649	-3.226260	17902.287578
HLA A*6901	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-3.901466	0.675193	-3.226273	7970.132000
HLA A*0206	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-3.991620	0.765110	-3.226510	9808.891997
HLA A*3001	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.180852	0.954333	-3.226519	15165.340778
HLA A*2402	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.556333	1.329751	-3.226582	36002.509185
HLA B*1517	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.451431	1.224706	-3.226725	28276.823041
HLA B*1503	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.353065	1.126330	-3.226735	22545.751994
HLA B*5801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.355276	1.128536	-3.226739	22660.818418
HLA B*1517	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.461987	1.235214	-3.226773	28972.558611
HLA A*0101	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.339891	1.112976	-3.226916	21872.134255
HLA A*0202	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.485310	1.258359	-3.226952	30571.038200
HLA A*6802	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.779429	0.552387	-3.227042	6017.672718
HLA B*5801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.347600	1.120342	-3.227258	22263.827237
HLA B*5701	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.360435	1.133041	-3.227394	22931.637076
HLA A*2902	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.221869	0.994371	-3.227499	16667.462354
HLA A*1101	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.408715	1.181170	-3.227545	25627.994798
HLA B*3901	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.388730	1.161155	-3.227575	24475.406174
HLA A*0219	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.466286	1.238694	-3.227592	29260.814281
HLA A*3101	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.372244	1.144551	-3.227693	23563.704697
HLA A*0216	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.382499	1.154698	-3.227801	24126.763856
HLA A*2902	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.407249	1.179436	-3.227812	25541.626423
HLA A*2402	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.277580	1.049687	-3.227893	18948.745868
HLA A*2603	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.245686	1.017549	-3.228137	17607.034384
HLA B*0702	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.403607	1.175404	-3.228203	25328.346962
HLA B*4601	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.402935	1.174655	-3.228280	25289.188528
HLA B*1502	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.146489	0.918162	-3.228327	14011.628243
HLA B*1509	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.251367	1.022881	-3.228486	17838.866980
HLA A*8001	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.403964	1.175404	-3.228560	25349.183107
HLA B*5301	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.513239	1.284672	-3.228567	32601.570073
HLA A*0211	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.354918	1.126330	-3.228589	22642.192015
HLA B*1509	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.467557	1.238694	-3.228864	29346.578814
HLA A*2602	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.495310	1.266360	-3.228949	31283.086526
HLA A*8001	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.189879	0.960920	-3.228959	15483.847849
HLA A*2501	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.404415	1.175404	-3.229011	25375.526951
HLA B*7301	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.499456	1.270418	-3.229038	31583.222285
HLA B*4801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.397733	1.168679	-3.229054	24988.094188
HLA A*0211	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.263906	1.034768	-3.229138	18361.428614
HLA B*0801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.342189	1.112976	-3.229213	21988.163586
HLA B*3801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.467936	1.238694	-3.229242	29372.150589
HLA B*0702	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.343173	1.113773	-3.229401	22038.061645
HLA B*0803	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.485893	1.256417	-3.229476	30612.081437
HLA A*2603	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.592630	1.363134	-3.229496	39140.823945
HLA A*2402	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.145821	0.916286	-3.229536	13990.117187
HLA A*0219	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.961575	0.732039	-3.229536	9153.237653
HLA A*2501	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.419555	1.190001	-3.229554	26275.751805
HLA A*0101	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.378897	1.149326	-3.229571	23927.499345
HLA B*1509	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.439178	1.209597	-3.229581	27490.209509
HLA B*0803	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.490599	1.261014	-3.229584	30945.597925
HLA A*2601	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.384611	1.154939	-3.229672	24244.389944
HLA A*2402	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.456099	1.226371	-3.229728	28582.422901
HLA B*0802	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.425443	1.195398	-3.230045	26634.402614
HLA A*2601	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.398927	1.168679	-3.230248	25056.861511

HLA B*1501	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.358814	1.128536	-3.230278	22846.196888
HLA A*3002	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.184635	0.954333	-3.230301	15298.006622
HLA A*0212	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.405134	1.174655	-3.230479	25417.569049
HLA A*2403	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.334849	1.104337	-3.230512	21619.675353
HLA B*0801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.317263	1.086732	-3.230532	20761.717287
HLA A*2402	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.420575	1.190001	-3.230573	26337.516910
HLA B*3901	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.487039	1.256417	-3.230622	30693.004898
HLA A*6901	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.385551	1.154927	-3.230624	24296.910534
HLA B*5801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.356988	1.126330	-3.230659	22750.364823
HLA A*0250	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.357087	1.126330	-3.230757	22755.534642
HLA A*0206	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.014560	0.783751	-3.230810	10340.947285
HLA A*0201	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.359404	1.128536	-3.230867	22877.240403
HLA B*5801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.349548	1.118640	-3.230907	22363.900243
HLA A*6901	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.124826	0.893801	-3.231026	13329.883517
HLA B*3501	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.455859	1.224706	-3.231154	28566.655223
HLA B*7301	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.602763	1.371517	-3.231246	40064.828907
HLA B*5401	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.345264	1.113773	-3.231492	22144.426391
HLA A*2301	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.329342	1.097819	-3.231523	21347.251924
HLA A*2301	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.469813	1.238104	-3.231709	29499.386542
HLA A*3002	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.153227	0.921444	-3.231783	14230.721815
HLA A*6901	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.187595	0.955683	-3.231912	15402.641090
HLA A*0101	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.360449	1.128536	-3.231913	22932.381434
HLA B*5801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.354641	1.122659	-3.231982	22627.742601
HLA B*4001	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.376611	1.144551	-3.232061	23801.880152
HLA A*2602	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.514322	1.282160	-3.232162	32682.978521
HLA A*3002	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.502396	1.270153	-3.232243	31797.695244
HLA A*2402	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.201081	0.968816	-3.232265	15888.439316
HLA B*4001	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.329993	1.097502	-3.232490	21379.265601
HLA A*2402	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.466214	1.233662	-3.232552	29255.907461
HLA A*0202	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.466249	1.233662	-3.232587	29258.281626
HLA A*2601	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.358971	1.126330	-3.232642	22854.479280
HLA B*1503	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.335796	1.103143	-3.232653	21666.861671
HLA B*0801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.332281	1.099547	-3.232734	21492.215230
HLA A*3301	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.097995	0.865145	-3.232850	12531.274276
HLA A*3002	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.466742	1.233662	-3.233081	29291.540167
HLA A*0202	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.494807	1.261650	-3.233157	31246.890544
HLA A*0201	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.337553	1.104337	-3.233216	21754.716366
HLA A*2402	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.452887	1.219563	-3.233324	28371.826455
HLA B*0802	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.394481	1.161155	-3.233326	24801.699831
HLA A*0201	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.394646	1.161199	-3.233447	24811.093820
HLA B*1501	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.275870	1.042359	-3.233511	18874.264905
HLA A*0206	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.107069	0.873492	-3.233577	12795.844293
HLA B*5701	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.409020	1.175404	-3.233616	25646.024937
HLA A*2402	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.353997	1.120342	-3.233656	22594.226128
HLA A*2501	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.472360	1.238694	-3.233666	29672.888618
HLA B*4501	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.354047	1.120342	-3.233705	22596.793151
HLA B*1501	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.378312	1.144551	-3.233762	23895.289209
HLA A*0212	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.966603	0.732827	-3.233776	9259.821957
HLA B*0801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.303523	1.069720	-3.233804	20115.159688
HLA A*2601	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.395118	1.161199	-3.233919	24838.087773
HLA B*4403	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.488193	1.254080	-3.234113	30774.641739
HLA B*1517	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.442394	1.208137	-3.234257	27694.561596
HLA B*3501	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.443971	1.209597	-3.234374	27795.276530
HLA A*3001	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.257389	1.022974	-3.234415	18087.935353
HLA B*4801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.078584	0.844164	-3.234420	11983.503044
HLA A*1101	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.415827	1.181092	-3.234734	26051.127131
HLA B*2705	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.303897	1.069099	-3.234798	20132.469636
HLA B*1509	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.334438	1.099547	-3.234891	21599.217031
HLA B*4801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.396114	1.161199	-3.234915	24895.126597
HLA B*5101	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.389893	1.154927	-3.234966	24541.036582
HLA A*2501	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.355438	1.120342	-3.235096	22669.278881
HLA B*4001	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.409772	1.174655	-3.235117	25690.460877
HLA B*5701	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.263930	1.028753	-3.235177	18362.421974
HLA B*0702	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.284901	1.049687	-3.235214	19270.876426
HLA B*4001	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.317898	1.082637	-3.235260	20792.065465

HLA B*1501	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.361624	1.126330	-3.235294	22994.496225
HLA B*3501	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.474014	1.238694	-3.235320	29786.115131
HLA B*1501	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.968167	0.732827	-3.235340	9293.245143
HLA B*1503	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.318020	1.082637	-3.235382	20797.915392
HLA A*0201	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.262262	1.026649	-3.235613	18292.026802
HLA A*0202	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.460338	1.224706	-3.235632	28862.736972
HLA B*3901	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.390607	1.154939	-3.235668	24581.430132
HLA A*0250	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.497351	1.261650	-3.235701	31430.500614
HLA B*7301	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.502179	1.266360	-3.235819	31781.873158
HLA A*0101	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.362232	1.126330	-3.235903	23026.737805
HLA B*1501	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.318713	1.082637	-3.236076	20831.133644
HLA B*7301	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.410792	1.174655	-3.236137	25750.850168
HLA B*5101	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.445855	1.209597	-3.236258	27916.134757
HLA A*3001	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.165585	0.929186	-3.236400	14641.488145
HLA B*4002	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.599695	1.363134	-3.236561	39782.755902
HLA B*0803	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.444728	1.208137	-3.236590	27843.737662
HLA B*5101	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.456212	1.219563	-3.236649	28589.845997
HLA B*4601	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.391594	1.154927	-3.236667	24637.346414
HLA B*4001	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.365296	1.128536	-3.236760	23189.754145
HLA B*4403	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.558278	1.321448	-3.236830	36164.140134
HLA B*2705	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.391582	1.154698	-3.236884	24636.679996
HLA B*3801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.341315	1.104337	-3.236978	21943.957370
HLA B*5401	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.470788	1.233662	-3.237126	29565.690134
HLA A*0250	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.446762	1.209597	-3.237165	27974.490618
HLA A*2501	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.472379	1.235214	-3.237165	29674.172862
HLA A*2501	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.461945	1.224706	-3.237239	28969.737458
HLA A*0211	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.461985	1.224706	-3.237279	28972.401873
HLA A*0216	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.144543	0.907250	-3.237293	13949.005082
HLA A*3001	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.129422	0.892112	-3.237310	13471.685856
HLA A*0301	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.365853	1.128536	-3.237317	23219.505812
HLA B*0802	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.443687	1.206278	-3.237408	27777.087791
HLA B*2705	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.351364	1.113773	-3.237591	22457.618412
HLA B*3801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.406384	1.168679	-3.237705	25490.827734
HLA B*0803	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.381005	1.143250	-3.237755	24043.893800
HLA A*2902	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.433224	1.195398	-3.237826	27115.926916
HLA A*6801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-3.640875	0.403047	-3.237828	4373.959270
HLA B*1503	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-3.778273	0.540402	-3.237871	6001.676984
HLA A*1101	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.399119	1.161155	-3.237964	25067.979474
HLA B*1501	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.356671	1.118640	-3.238031	22733.755500
HLA A*2603	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.602822	1.364704	-3.238118	40070.247930
HLA B*1502	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.446349	1.208137	-3.238211	27947.867649
HLA B*5301	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.335742	1.097502	-3.238240	21664.165886
HLA A*2301	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.428401	1.190001	-3.238399	26816.430068
HLA B*4801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.335923	1.097502	-3.238421	21673.192223
HLA A*6901	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.366981	1.128536	-3.238444	23279.879342
HLA A*2601	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.232874	0.994371	-3.238504	17095.211202
HLA B*4801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.192896	0.954333	-3.238562	15591.777687
HLA B*1801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.305819	1.067242	-3.238577	20221.759059
HLA B*2705	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.419684	1.181092	-3.238592	26283.571158
HLA B*0702	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.341747	1.103143	-3.238604	21965.811691
HLA A*8001	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.388077	1.149326	-3.238750	24438.624073
HLA B*1501	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.399951	1.161199	-3.238752	25116.033179
HLA B*4501	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.646475	1.407681	-3.238795	44307.317869
HLA B*5101	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.371031	1.132158	-3.238873	23498.018274
HLA B*5301	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.509071	1.270153	-3.238918	32290.184727
HLA B*5701	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.413576	1.174655	-3.238921	25916.461901
HLA B*4402	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.447086	1.208137	-3.238949	27995.383183
HLA A*3002	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.200250	0.961256	-3.238993	15858.040472
HLA A*2403	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.400224	1.161155	-3.239068	25131.799621
HLA A*0203	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.357766	1.118640	-3.239126	22791.139790
HLA B*1502	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.610658	1.371517	-3.239140	40799.755647
HLA B*4002	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.321889	1.082637	-3.239252	20984.054663
HLA A*0211	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.308354	1.069099	-3.239255	20340.144121
HLA A*0219	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.418813	1.179436	-3.239377	26230.871125
HLA A*0216	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.083673	0.844164	-3.239509	12124.749509

HLA B*4501	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.569276	1.329751	-3.239525	37091.643991
HLA A*2601	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.394279	1.154698	-3.239582	24790.163512
HLA A*3001	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.254600	1.014994	-3.239606	17972.155123
HLA B*4403	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.501853	1.262230	-3.239622	31757.982980
HLA B*5801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.344061	1.104337	-3.239724	22083.174228
HLA B*4403	1:476-484	9	QTSAITNVV	1.187107	0.191059	-4.617941	1.378166	-3.239775	41489.764103
HLA A*0206	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.313694	1.073598	-3.240096	20591.804446
HLA B*1517	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.384879	1.144551	-3.240328	24259.346734
HLA B*1517	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.196096	0.955683	-3.240412	15707.086391
HLA A*0212	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.359110	1.118640	-3.240470	22861.775216
HLA A*2602	1:245-253	9	ADLDAVVLK	1.208601	0.162916	-4.612013	1.371517	-3.240496	40927.311310
HLA B*7301	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.581110	1.340547	-3.240564	38116.273865
HLA A*0301	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.366960	1.126330	-3.240630	23278.745896
HLA A*0201	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.395574	1.154927	-3.240647	24864.169490
HLA A*0201	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.223157	0.982334	-3.240823	16716.948351
HLA B*4002	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.570578	1.329751	-3.240827	37202.977317
HLA B*1801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.385408	1.144551	-3.240857	24288.893798
HLA B*5101	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.338843	1.097819	-3.241024	21819.424553
HLA A*0211	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-3.963046	0.722004	-3.241041	9184.288470
HLA A*3201	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.511225	1.270153	-3.241072	32450.770074
HLA A*8001	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.415735	1.174655	-3.241080	26045.631296
HLA B*5401	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.834482	0.593391	-3.241091	6830.959285
HLA B*5801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.316986	1.075727	-3.241259	20748.467923
HLA A*2902	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.402543	1.161155	-3.241387	25266.351291
HLA B*2705	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.451005	1.209597	-3.241408	28249.148212
HLA B*2705	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.278121	1.036678	-3.241443	18972.337984
HLA A*2403	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.150572	0.909118	-3.241454	14143.992293
HLA A*0216	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.326868	1.085412	-3.241456	21225.990603
HLA A*1101	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.223937	0.982334	-3.241603	16747.000361
HLA B*1502	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.511798	1.270153	-3.241645	32493.633795
HLA B*5701	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.354785	1.112976	-3.241809	22635.211062
HLA B*5701	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.391159	1.149326	-3.241833	24612.700966
HLA A*3301	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.606546	1.364704	-3.241842	40415.314558
HLA A*0101	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.396770	1.154927	-3.241843	24932.730654
HLA B*0801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.196274	0.954333	-3.241941	15713.545712
HLA B*1801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.450148	1.208137	-3.242011	28193.422211
HLA B*5401	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.478814	1.236758	-3.242056	30117.149286
HLA B*3901	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.339910	1.097819	-3.242091	21873.080882
HLA A*2902	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.423343	1.181092	-3.242250	26505.897903
HLA A*0212	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.423432	1.181092	-3.242339	26511.347434
HLA B*4601	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.292105	1.049687	-3.242418	19593.182672
HLA A*3001	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.277235	1.034768	-3.242467	18933.682798
HLA A*0201	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.391803	1.149326	-3.242477	24649.211663
HLA B*0801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.375573	1.133041	-3.242532	23745.033779
HLA B*5801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.340471	1.097819	-3.242653	21901.380268
HLA B*1801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.479418	1.236758	-3.242659	30159.051532
HLA B*4403	1:268-276	9	EMRADLVRV	1.216414	0.187070	-4.646233	1.403484	-3.242750	44282.635885
HLA B*1503	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.403933	1.161155	-3.242778	25347.400398
HLA A*2603	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.116387	0.873492	-3.242895	13073.353490
HLA A*0216	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.417673	1.174655	-3.243018	26162.136876
HLA B*4801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.404220	1.161155	-3.243065	25364.135369
HLA B*5701	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.387644	1.144551	-3.243094	24414.309492
HLA B*3801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.505394	1.262230	-3.243163	32017.954677
HLA A*6802	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.418613	1.175404	-3.243209	26218.811879
HLA A*0206	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.398325	1.154927	-3.243399	25022.183490
HLA A*2403	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.424513	1.181092	-3.243420	26577.404380
HLA A*0212	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.418942	1.175404	-3.243538	26238.677122
HLA B*1801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.376715	1.133041	-3.243674	23807.546510
HLA A*6801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.150934	0.907250	-3.243684	14155.780887
HLA B*4001	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.398438	1.154698	-3.243740	25028.681961
HLA A*3101	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.341597	1.097819	-3.243778	21958.207721
HLA B*1509	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.346975	1.103143	-3.243832	22231.811951
HLA B*4402	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.425076	1.181092	-3.243984	26611.934186
HLA A*0203	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.372864	1.128536	-3.244328	23597.382677
HLA A*0250	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.311570	1.067242	-3.244329	20491.345257

HLA B*3801	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.514749	1.270418	-3.244331	32715.174023
HLA A*0216	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.818994	0.574537	-3.244457	6591.646240
HLA A*6801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.228603	0.984065	-3.244538	16927.900861
HLA A*2403	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.320268	1.075727	-3.244541	20905.870904
HLA A*3101	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.419245	1.174655	-3.244590	26256.994848
HLA A*0216	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.205978	0.961256	-3.244721	16068.582479
HLA A*2301	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.526971	1.282160	-3.244811	33648.929776
HLA A*0203	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.318433	1.073598	-3.244835	20817.727359
HLA A*3301	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.507106	1.262230	-3.244876	32144.476706
HLA B*2705	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.406053	1.161155	-3.244898	25471.390889
HLA B*1503	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.205818	0.960920	-3.244898	16062.672377
HLA B*1801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.481333	1.236390	-3.244943	30292.318163
HLA A*0216	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.426199	1.181092	-3.245107	26680.839760
HLA B*2705	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.330526	1.085412	-3.245115	21405.536425
HLA B*4801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.420695	1.175404	-3.245291	26344.784548
HLA B*0702	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.400233	1.154939	-3.245294	25132.343468
HLA B*5801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.348326	1.102823	-3.245503	22301.075816
HLA B*4801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.400463	1.154939	-3.245524	25145.671393
HLA A*6901	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-3.971513	0.725976	-3.245537	9365.113821
HLA A*3001	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.274782	1.029142	-3.245640	18827.048207
HLA B*3501	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.343559	1.097819	-3.245740	22057.622971
HLA A*3002	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.977833	0.732039	-3.245794	9502.397084
HLA B*7301	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.608966	1.363134	-3.245832	40641.144800
HLA B*0801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.321584	1.075727	-3.245857	20969.302068
HLA B*5401	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.440992	1.194908	-3.246084	27605.260650
HLA A*0301	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.368844	1.122659	-3.246185	23379.965538
HLA A*6802	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.407476	1.161199	-3.246277	25555.033145
HLA A*0211	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.162597	0.916314	-3.246282	14541.080384
HLA A*0206	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.275471	1.029142	-3.246329	18856.914578
HLA A*1101	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.455932	1.209597	-3.246335	28571.446440
HLA B*4002	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.579144	1.332686	-3.246458	37944.070603
HLA B*3501	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.296226	1.049687	-3.246539	19779.986199
HLA A*2602	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.587118	1.340547	-3.246571	38647.203310
HLA A*0212	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.779518	0.532852	-3.246666	6018.909933
HLA B*7301	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.545412	1.298743	-3.246670	35108.507179
HLA A*6901	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.332241	1.085412	-3.246830	21490.238722
HLA B*5801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.346383	1.099547	-3.246836	22201.524148
HLA B*4402	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.391514	1.144551	-3.246963	24632.815130
HLA B*1503	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.308789	1.061692	-3.247097	20360.511328
HLA B*1517	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.262158	1.014994	-3.247165	18287.673175
HLA A*0201	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.135131	0.887960	-3.247171	13649.954244
HLA A*3201	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.501261	1.254080	-3.247180	31714.717073
HLA B*1501	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.201946	0.954621	-3.247325	15920.102152
HLA B*3901	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.428619	1.181170	-3.247449	26829.925337
HLA A*0301	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.366090	1.118640	-3.247450	23232.196389
HLA B*2705	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.351892	1.104337	-3.247555	22484.971032
HLA B*3801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.262753	1.014994	-3.247759	18312.720686
HLA A*2603	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.457370	1.209597	-3.247773	28666.199044
HLA A*2301	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.506160	1.258359	-3.247801	32074.472129
HLA B*5801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.262793	1.014988	-3.247805	18314.404950
HLA A*0301	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.297518	1.049687	-3.247831	19838.927987
HLA A*0211	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.481504	1.233662	-3.247842	30304.283626
HLA B*0702	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.381021	1.133041	-3.247981	24044.804341
HLA A*2403	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.376555	1.128536	-3.248019	23798.789980
HLA A*2601	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.350913	1.102823	-3.248090	22434.303823
HLA B*5701	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.409333	1.161199	-3.248133	25664.484283
HLA A*6801	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.502229	1.254080	-3.248148	31785.484027
HLA A*0219	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.274815	1.026649	-3.248167	18828.474192
HLA B*4601	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.351082	1.102823	-3.248259	22443.043957
HLA A*0219	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.370961	1.122659	-3.248302	23494.204934
HLA B*5701	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.362315	1.113773	-3.248542	23031.098242
HLA B*0801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.424003	1.175404	-3.248599	26546.222251
HLA B*4601	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.393168	1.144551	-3.248617	24726.809611
HLA A*2902	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.403647	1.154939	-3.248707	25330.676470
HLA B*4801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.398046	1.149326	-3.248719	25006.079973

HLA B*4601	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.410023	1.161199	-3.248824	25705.336315
HLA B*4002	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.635797	1.386802	-3.248995	43231.176196
HLA A*2602	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.119009	0.869990	-3.249019	13152.521775
HLA A*6801	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.589630	1.340547	-3.249083	38871.354241
HLA B*1517	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.266719	1.017549	-3.249170	18480.716382
HLA A*2402	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.458883	1.209597	-3.249286	28766.245360
HLA B*1503	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.112243	0.862842	-3.249401	12949.187301
HLA A*6802	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.334849	1.085412	-3.249438	21619.675353
HLA B*4001	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.398797	1.149326	-3.249471	25049.407104
HLA B*4001	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.404462	1.154927	-3.249535	25378.272675
HLA B*0802	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.410792	1.161199	-3.249592	25750.850168
HLA A*0203	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.425018	1.175404	-3.249614	26608.335239
HLA B*4001	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.410909	1.161199	-3.249710	25757.816572
HLA B*4801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.404446	1.154698	-3.249748	25377.311638
HLA B*5101	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.483412	1.233662	-3.249750	30437.698010
HLA B*5701	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.393011	1.143250	-3.249760	24717.848692
HLA B*4601	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.362881	1.112976	-3.249905	23061.145386
HLA B*4402	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.393185	1.143250	-3.249934	24727.746014
HLA A*0206	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.483677	1.233662	-3.250016	30456.310796
HLA B*5301	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.512423	1.262230	-3.250193	32540.426786
HLA A*0211	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.429641	1.179436	-3.250205	26893.138599
HLA B*3501	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.405174	1.154939	-3.250234	25419.906762
HLA B*0801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.354585	1.104337	-3.250248	22624.804866
HLA A*0219	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.424997	1.174655	-3.250342	26607.039737
HLA A*0219	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.405099	1.154698	-3.250401	25415.506539
HLA B*4501	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.333073	1.082637	-3.250436	21531.434129
HLA B*0803	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.486873	1.236390	-3.250483	30681.217913
HLA B*0801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.014908	0.764421	-3.250487	10349.230221
HLA B*1501	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.405691	1.154927	-3.250764	25450.178926
HLA B*4001	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.364612	1.113773	-3.250840	23153.275753
HLA A*3002	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.533066	1.282160	-3.250906	34124.462533
HLA A*2601	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.326840	1.075727	-3.251113	21224.612685
HLA B*4801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.395710	1.144551	-3.251160	24871.972433
HLA B*4001	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.383347	1.132158	-3.251189	24173.928742
HLA B*4601	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.379729	1.128536	-3.251193	23973.366823
HLA A*0201	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.350814	1.099547	-3.251267	22429.206984
HLA B*0801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.377673	1.126330	-3.251343	23860.153391
HLA A*3002	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.406335	1.154939	-3.251395	25487.931945
HLA A*0301	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.336896	1.085412	-3.251484	21721.787943
HLA A*0206	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.206283	0.954621	-3.251662	16079.887256
HLA B*4601	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.406617	1.154939	-3.251677	25504.483744
HLA A*6802	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.401044	1.149326	-3.251717	25179.294570
HLA B*1801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.349287	1.097502	-3.251784	22350.474803
HLA A*2902	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.427315	1.175404	-3.251911	26749.489609
HLA B*5801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.319298	1.067242	-3.252056	20859.213390
HLA A*0301	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.365040	1.112976	-3.252064	23176.083690
HLA B*4402	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-3.832076	0.579907	-3.252169	6793.222261
HLA B*5701	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.413416	1.161155	-3.252261	25906.929702
HLA B*4402	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.258937	1.006578	-3.252359	18152.536044
HLA A*0250	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.534548	1.282160	-3.252389	34241.150216
HLA A*0211	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.275304	1.022881	-3.252423	18849.672988
HLA B*0803	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.433739	1.181170	-3.252569	27148.071975
HLA A*2601	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.381132	1.128536	-3.252595	24050.918865
HLA B*1503	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.375343	1.122659	-3.252684	23732.448231
HLA B*5101	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.157611	0.904921	-3.252690	14375.106406
HLA B*1502	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.397244	1.144551	-3.252694	24959.991976
HLA B*4403	1:306-314	9	GPRTDPLPR	0.929420	0.478261	-4.660394	1.407681	-3.252713	45750.285658
HLA A*2601	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.373061	1.120342	-3.252719	23608.108489
HLA B*5801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.355962	1.103143	-3.252819	22696.643722
HLA A*3201	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.514472	1.261650	-3.252822	32694.296403
HLA A*2902	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.350666	1.097819	-3.252847	22421.563897
HLA A*2301	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.489767	1.236758	-3.253009	30886.390699
HLA B*3901	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.491774	1.238694	-3.253080	31029.417364
HLA A*0206	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.371788	1.118640	-3.253147	23538.987127
HLA B*1517	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.141122	0.887960	-3.253162	13839.563170

HLA A*2501	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.356140	1.102823	-3.253318	22705.977401
HLA A*2402	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.514545	1.261014	-3.253530	32699.779911
HLA B*1509	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.408637	1.154927	-3.253710	25623.419934
HLA A*6801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.403038	1.149326	-3.253712	25295.208960
HLA B*4001	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.374156	1.120342	-3.253814	23667.699811
HLA A*0219	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.434982	1.181092	-3.253890	27225.876457
HLA B*1501	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.351808	1.097819	-3.253989	22480.592375
HLA A*0101	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.398586	1.144551	-3.254035	25037.213766
HLA B*3801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.478743	1.224706	-3.254038	30112.261770
HLA A*0212	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.408752	1.154698	-3.254054	25630.213208
HLA B*7301	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-3.520205	0.266144	-3.254061	3312.876032
HLA B*1517	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.386251	1.132158	-3.254093	24336.112316
HLA A*2501	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.387182	1.133041	-3.254141	24388.303846
HLA A*2402	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.368007	1.113773	-3.254235	23334.980915
HLA A*8001	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.397585	1.143250	-3.254335	24979.579121
HLA A*3002	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.358767	1.104337	-3.254430	22843.725113
HLA B*1801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.196744	0.942253	-3.254491	15730.556621
HLA B*4403	1:300-308	9	AAGNLSGPR	0.680995	0.682139	-4.617715	1.363134	-3.254582	41468.222015
HLA B*1801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.328268	1.073598	-3.254670	21294.539888
HLA A*6802	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.423472	1.168679	-3.254793	26513.785745
HLA B*3801	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.488569	1.233662	-3.254907	30801.291255
HLA A*8001	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.368719	1.113773	-3.254947	23373.262899
HLA B*5101	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.284100	1.029142	-3.254959	19235.358820
HLA A*0216	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.322225	1.067242	-3.254984	21000.294506
HLA B*0802	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.430431	1.175404	-3.255027	26942.067325
HLA B*5301	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.511836	1.256417	-3.255419	32496.446508
HLA B*5301	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.575321	1.319849	-3.255472	37611.556604
HLA B*0801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.171797	0.916314	-3.255483	14852.421256
HLA B*7301	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.325385	1.069720	-3.255666	21153.656244
HLA B*1517	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.416870	1.161199	-3.255671	26113.776910
HLA A*2601	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.378399	1.122659	-3.255740	23900.072710
HLA A*3101	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.410676	1.154927	-3.255750	25744.024920
HLA A*3101	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.388016	1.132158	-3.255858	24435.186849
HLA B*4001	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.382219	1.126330	-3.255890	24111.236603
HLA A*0206	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-3.931262	0.675193	-3.256069	8536.143021
HLA A*0212	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.282721	1.026649	-3.256073	19174.371807
HLA A*0219	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.374755	1.118640	-3.256115	23700.372448
HLA B*0702	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.417518	1.161199	-3.256319	26152.797282
HLA A*6901	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-3.989209	0.732827	-3.256382	9754.598108
HLA B*3801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.514893	1.258359	-3.256534	32725.971918
HLA A*8001	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.389663	1.133041	-3.256622	24528.029130
HLA A*3001	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.217706	0.960920	-3.256786	16508.446076
HLA A*6901	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.225615	0.968816	-3.256799	16811.813439
HLA B*5101	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.383152	1.126330	-3.256822	24163.076582
HLA B*1801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.389005	1.132158	-3.256847	24490.902959
HLA B*5101	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.359679	1.102823	-3.256856	22891.725297
HLA A*3301	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.418056	1.161199	-3.256857	26185.217135
HLA B*4002	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.515229	1.258359	-3.256870	32751.298988
HLA B*3901	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.356455	1.099547	-3.256908	22722.443503
HLA A*3101	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.342389	1.085412	-3.256977	21998.276961
HLA A*3201	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.361436	1.104337	-3.257099	22984.546564
HLA A*2403	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.431787	1.174655	-3.257132	27026.298546
HLA B*4601	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.383547	1.126330	-3.257217	24185.047452
HLA B*2705	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.377990	1.120342	-3.257649	23877.585662
HLA A*3001	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.056358	0.798696	-3.257662	11385.645626
HLA B*0802	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.412641	1.154939	-3.257701	25860.720268
HLA A*0301	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.362129	1.104337	-3.257792	23021.257285
HLA B*0702	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.438920	1.181092	-3.257827	27473.855287
HLA B*3501	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.386446	1.128536	-3.257910	24347.042190
HLA A*0206	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.466181	1.208137	-3.258043	29253.691748
HLA B*1801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.372100	1.113773	-3.258328	23555.929882
HLA B*3901	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.174090	0.915512	-3.258579	14931.050209
HLA A*3201	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-3.971541	0.712902	-3.258639	9365.721811
HLA A*3001	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.163353	0.904590	-3.258764	14566.432793
HLA A*2501	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.465208	1.206278	-3.258930	29188.245744

HLA A*0206	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.362103	1.103143	-3.258960	23019.887359
HLA B*4601	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.153091	0.894030	-3.259060	14226.257291
HLA B*1502	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.379410	1.120342	-3.259068	23955.735027
HLA A*3301	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.494288	1.235214	-3.259074	31209.554538
HLA A*0201	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.392181	1.133041	-3.259141	24670.690285
HLA A*6901	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.320860	1.061692	-3.259168	20934.391149
HLA B*7301	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.572128	1.312789	-3.259339	37336.048972
HLA B*1503	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-3.877299	0.617889	-3.259410	7538.739063
HLA A*0203	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.420720	1.161199	-3.259521	26346.352341
HLA B*5401	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.562622	1.303070	-3.259552	36527.701168
HLA A*3101	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.385955	1.126330	-3.259625	24319.529354
HLA A*3001	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.266221	1.006578	-3.259643	18459.533063
HLA B*4801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.382370	1.122659	-3.259711	24119.586152
HLA B*4002	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.558513	1.298743	-3.259771	36183.709826
HLA B*1517	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.286626	1.026649	-3.259977	19347.550483
HLA A*0203	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-3.942929	0.682948	-3.259981	8768.579129
HLA A*0250	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.792882	0.532852	-3.260030	6206.999570
HLA B*4001	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.378672	1.118640	-3.260031	23915.075840
HLA A*3101	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.378695	1.118640	-3.260055	23916.369654
HLA B*0803	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.380399	1.120342	-3.260057	24010.357911
HLA A*0216	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.164721	0.904590	-3.260131	14612.368292
HLA A*6901	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.089838	0.829510	-3.260328	12298.094438
HLA A*2601	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.378977	1.118640	-3.260337	23931.900883
HLA A*1101	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.404911	1.144551	-3.260360	25404.509313
HLA A*8001	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.373357	1.112976	-3.260382	23624.206348
HLA A*2403	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.297093	1.036678	-3.260415	19819.511416
HLA A*8001	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.329542	1.069099	-3.260442	21357.070514
HLA B*4501	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.573266	1.312789	-3.260476	37433.937272
HLA A*0301	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.363689	1.103143	-3.260546	23104.102179
HLA B*0702	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.415530	1.154927	-3.260604	26033.375534
HLA B*4801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.415561	1.154927	-3.260634	26035.206488
HLA B*1502	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.580749	1.319849	-3.260899	38084.531548
HLA A*0202	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.383580	1.122659	-3.260921	24186.879259
HLA B*4403	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.625741	1.364704	-3.261037	42241.687152
HLA A*2902	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.435785	1.174655	-3.261131	27276.295915
HLA A*2601	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.358957	1.097819	-3.261138	22853.737451
HLA B*1517	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.346554	1.085412	-3.261143	22210.293748
HLA A*0212	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.410498	1.149326	-3.261172	25733.442399
HLA A*2501	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.456287	1.194908	-3.261379	28594.795798
HLA B*2705	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.380058	1.118640	-3.261418	23991.530757
HLA A*2602	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.495136	1.233662	-3.261474	31270.565418
HLA B*1503	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.279296	1.017549	-3.261747	19023.726577
HLA B*4501	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.288499	1.026649	-3.261850	19431.151061
HLA A*3301	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.394096	1.132158	-3.261938	24779.704980
HLA B*4601	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.394124	1.132158	-3.261966	24781.313698
HLA B*1501	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.331896	1.069720	-3.262176	21473.155324
HLA A*2902	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.329483	1.067242	-3.262241	21354.182225
HLA A*6802	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.178615	0.916286	-3.262330	15087.436804
HLA A*3101	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.204587	0.942253	-3.262334	16017.202683
HLA B*4601	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.380993	1.118640	-3.262353	24043.243435
HLA A*0216	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.331487	1.069099	-3.262388	21452.951709
HLA B*4601	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.405670	1.143250	-3.262419	25448.939813
HLA B*1801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.338317	1.075727	-3.262590	21792.999458
HLA A*0212	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.365486	1.102823	-3.262664	23199.918146
HLA A*0203	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.160914	0.898050	-3.262864	14484.864736
HLA B*1502	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.496569	1.233662	-3.262907	31373.929756
HLA A*8001	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.360489	1.097502	-3.262987	22934.490578
HLA B*3501	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.179330	0.916314	-3.263015	15112.270112
HLA B*1801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.237444	0.974301	-3.263143	17276.040718
HLA B*0803	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.472799	1.209597	-3.263202	29702.922363
HLA A*0101	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.339062	1.075727	-3.263335	21830.405097
HLA A*0202	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.305779	1.042359	-3.263420	20219.899388
HLA A*2603	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.604074	1.340547	-3.263527	40185.956065
HLA A*3001	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.078838	0.815296	-3.263541	11990.506668
HLA B*5401	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.525193	1.261650	-3.263543	33511.409566

HLA B*1503	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-3.995891	0.732039	-3.263853	9905.840170
HLA B*1501	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.047759	0.783751	-3.264008	11162.424831
HLA A*3101	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.345918	1.081848	-3.264070	22177.755539
HLA B*5101	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.418780	1.154698	-3.264082	26228.884514
HLA B*3801	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.443619	1.179436	-3.264182	27772.730274
HLA A*2501	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.361716	1.097502	-3.264213	22999.348246
HLA A*0203	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.397371	1.133041	-3.264331	24967.284703
HLA B*1502	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.454363	1.190001	-3.264361	28468.381118
HLA A*0202	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.219045	0.954621	-3.264424	16559.430696
HLA A*3001	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.287345	1.022881	-3.264464	19379.605447
HLA A*6802	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.419421	1.154939	-3.264482	26267.650567
HLA B*4002	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.137669	0.873123	-3.264546	13729.940000
HLA A*3001	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-3.760271	0.495678	-3.264593	5757.989432
HLA A*0301	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.367474	1.102823	-3.264652	23306.342100
HLA A*0250	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.521069	1.256417	-3.264652	33194.745970
HLA B*5401	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.484535	1.219563	-3.264972	30516.509532
HLA A*0301	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.346926	1.081848	-3.265078	22229.286390
HLA A*0201	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.109268	0.844164	-3.265104	12860.802374
HLA B*0801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.393643	1.128536	-3.265106	24753.845779
HLA A*2402	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.519190	1.254080	-3.265109	33051.392487
HLA A*0301	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.362766	1.097502	-3.265263	23055.033042
HLA B*5101	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.439993	1.174655	-3.265339	27541.863465
HLA A*6901	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.194564	0.929186	-3.265378	15651.781201
HLA B*1501	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.226324	0.960920	-3.265404	16839.302803
HLA B*0702	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.440221	1.174655	-3.265567	27556.320105
HLA A*2501	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.370005	1.104337	-3.265667	23442.531717
HLA B*0802	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.398715	1.133041	-3.265675	25044.664545
HLA A*0203	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.420608	1.154927	-3.265681	26339.511748
HLA B*0803	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.460735	1.194908	-3.265827	28889.137410
HLA B*1502	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.532215	1.266360	-3.265855	34057.699268
HLA A*2902	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.370200	1.104337	-3.265862	23453.060265
HLA A*8001	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.427064	1.161199	-3.265865	26734.009930
HLA B*1502	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.490662	1.224706	-3.265957	30950.118386
HLA B*4402	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.399070	1.133041	-3.266029	25065.131721
HLA A*0201	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.384729	1.118640	-3.266088	24250.948804
HLA A*0206	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.441509	1.175404	-3.266105	27638.135318
HLA A*8001	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.427325	1.161155	-3.266170	26750.068463
HLA A*0101	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.339776	1.073598	-3.266178	21866.337058
HLA B*4001	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.369032	1.102823	-3.266209	23390.086370
HLA A*3101	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.394801	1.128536	-3.266265	24819.954270
HLA A*2501	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.415615	1.149326	-3.266289	26038.446184
HLA B*4402	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.386665	1.120342	-3.266323	24359.294748
HLA B*7301	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.599115	1.332686	-3.266429	39729.631989
HLA B*5801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.348276	1.081848	-3.266429	22298.542387
HLA A*1101	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.415977	1.149326	-3.266651	26060.148450
HLA B*4402	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.435405	1.168679	-3.266726	27252.401385
HLA B*0702	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.195964	0.929186	-3.266778	15702.328590
HLA A*0219	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.074745	0.807959	-3.266786	11878.038594
HLA B*1801	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.435675	1.168679	-3.266996	27269.361395
HLA B*4801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.366699	1.099547	-3.267152	23264.771259
HLA B*5101	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.462353	1.194908	-3.267446	28997.020111
HLA B*5801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.354204	1.086732	-3.267473	22604.985127
HLA A*0216	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.442923	1.175404	-3.267519	27728.292636
HLA B*0802	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.317216	1.049687	-3.267529	20759.471037
HLA A*0206	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.186016	0.918327	-3.267689	15346.747289
HLA B*4403	1:480-488	9	ITNVVIIIV	1.144626	0.162047	-4.574391	1.306673	-3.267717	37531.067008
HLA B*3501	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.176858	0.909118	-3.267740	15026.507388
HLA B*4403	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.654614	1.386802	-3.267812	45145.459423
HLA A*6802	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-3.982758	0.714935	-3.267822	9610.759183
HLA A*2403	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.302598	1.034768	-3.267829	20072.329961
HLA A*2403	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.417173	1.149326	-3.267846	26132.007441
HLA A*0301	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.182826	0.914880	-3.267946	15234.413565
HLA A*0216	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.184395	0.916286	-3.268110	15289.567377
HLA B*5701	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.423063	1.154927	-3.268136	26488.839512
HLA A*0101	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.386801	1.118640	-3.268161	24366.939250

HLA A*3002	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.186449	0.918162	-3.268287	15362.031348
HLA A*0212	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.184602	0.916314	-3.268288	15296.848018
HLA B*1503	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.186618	0.918327	-3.268291	15368.016209
HLA A*2403	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-3.959178	0.690866	-3.268312	9102.868391
HLA B*5301	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.538815	1.270418	-3.268397	34579.205427
HLA B*4501	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.588288	1.319849	-3.268439	38751.464081
HLA A*3002	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.338160	1.069720	-3.268440	21785.101743
HLA A*0219	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.417845	1.149326	-3.268518	26172.470917
HLA B*4801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.401593	1.133041	-3.268553	25211.189577
HLA A*3002	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.413237	1.144551	-3.268687	25896.280216
HLA B*3501	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.411959	1.143250	-3.268709	25820.180025
HLA B*4402	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.423707	1.154939	-3.268767	26528.133289
HLA A*2902	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.429975	1.161199	-3.268776	26913.805960
HLA A*8001	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.413362	1.144551	-3.268811	25903.706369
HLA A*0301	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.366635	1.097819	-3.268816	23261.373292
HLA B*4501	1:2-10	9	TTPSHLSDR	0.752148	0.634654	-4.655690	1.386802	-3.268888	45257.456339
HLA B*2705	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.430128	1.161199	-3.268929	26923.271670
HLA B*1501	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.330639	1.061692	-3.268947	21411.095623
HLA A*2902	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.318649	1.049687	-3.268962	20828.091125
HLA A*0201	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.371811	1.102823	-3.268989	23540.260594
HLA B*1501	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.224684	0.955683	-3.269001	16775.835772
HLA A*3001	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.163001	0.893801	-3.269200	14554.617170
HLA A*2403	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.423967	1.154698	-3.269270	26544.068156
HLA B*1501	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.392191	1.122659	-3.269532	24671.224154
HLA A*6901	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.338738	1.069099	-3.269638	21814.113369
HLA A*8001	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.424360	1.154698	-3.269662	26568.060270
HLA A*0212	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.424646	1.154927	-3.269720	26585.601150
HLA B*4002	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.610336	1.340547	-3.269789	40769.527915
HLA A*0101	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.373019	1.103143	-3.269876	23605.809691
HLA A*6802	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.161991	0.892112	-3.269878	14520.798808
HLA A*0201	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.186171	0.916286	-3.269886	15352.227864
HLA A*6801	1:31-39	9	LRLHRDVAV	1.220351	0.174432	-4.664808	1.394783	-3.270026	46217.717364
HLA A*2403	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.396535	1.126330	-3.270205	24919.245971
HLA B*7301	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.600033	1.329751	-3.270282	39813.759700
HLA B*4001	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.346101	1.075727	-3.270374	22187.115892
HLA A*6901	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.231697	0.961256	-3.270441	17048.939854
HLA B*5301	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.508601	1.238104	-3.270497	32255.266357
HLA B*1502	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.162648	0.892112	-3.270536	14542.811131
HLA B*5801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.288085	1.017549	-3.270536	19412.658680
HLA A*0219	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.399242	1.128536	-3.270705	25075.032445
HLA B*1801	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.506009	1.235214	-3.270795	32063.368814
HLA A*3001	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.281495	1.010656	-3.270838	19120.300490
HLA B*5101	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.509611	1.238694	-3.270917	32330.387587
HLA B*3901	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.439747	1.168679	-3.271068	27526.223073
HLA B*5801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.353798	1.082637	-3.271160	22583.838774
HLA B*5801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.356706	1.085412	-3.271295	22735.600382
HLA A*6802	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.404558	1.133041	-3.271518	25383.902338
HLA A*2501	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.022097	0.750403	-3.271694	10521.980004
HLA A*2402	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.180815	0.909118	-3.271696	15164.028150
HLA B*4002	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.556392	1.284672	-3.271720	36007.378754
HLA B*4403	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.601480	1.329751	-3.271730	39946.660046
HLA A*0301	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.354390	1.082637	-3.271753	22614.648139
HLA A*2602	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.200945	0.929186	-3.271759	15883.454726
HLA A*0250	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.004641	0.732827	-3.271814	10107.431310
HLA A*3002	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.055977	0.783751	-3.272226	11375.671594
HLA B*3501	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.233257	0.960920	-3.272338	17110.292612
HLA B*1801	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.511103	1.238694	-3.272409	32441.642494
HLA B*4801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.386286	1.113773	-3.272514	24338.087231
HLA A*3002	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.404674	1.132158	-3.272515	25390.632111
HLA A*3002	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.372194	1.099547	-3.272647	23561.027832
HLA A*2602	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.023145	0.750403	-3.272742	10547.398201
HLA B*2705	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.238076	0.965301	-3.272775	17301.200154
HLA B*1509	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.215037	0.942253	-3.272784	16407.302322
HLA B*4402	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.434023	1.161199	-3.272824	27165.848828
HLA A*0301	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.255279	0.982334	-3.272945	18000.275809

HLA A*3001	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.180232	0.907250	-3.272982	15143.696935
HLA A*3201	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.508312	1.235214	-3.273098	32233.810314
HLA B*3901	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.393664	1.120342	-3.273322	24755.051048
HLA A*2501	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.416670	1.143250	-3.273420	26101.771496
HLA A*2301	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.498138	1.224706	-3.273433	31487.514162
HLA B*3901	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.454577	1.181092	-3.273484	28482.399550
HLA A*6901	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.376661	1.103143	-3.273518	23804.584382
HLA A*0301	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.349345	1.075727	-3.273618	22353.497848
HLA A*3101	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.376764	1.103143	-3.273621	23810.251384
HLA A*2301	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.418202	1.144551	-3.273651	26194.001473
HLA B*5401	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.511834	1.238104	-3.273730	32496.270706
HLA A*2403	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.359281	1.085412	-3.273870	22870.805615
HLA B*4801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.417130	1.143250	-3.273880	26129.462882
HLA B*4601	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.396728	1.122659	-3.274069	24930.302873
HLA B*3801	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.500525	1.226371	-3.274154	31661.060132
HLA A*2403	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.360928	1.086732	-3.274197	22957.703979
HLA B*0802	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.469150	1.194908	-3.274243	29454.416921
HLA B*0702	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.229073	0.954621	-3.274452	16946.226387
HLA A*0219	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.166652	0.892112	-3.274540	14677.493150
HLA A*0219	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.429501	1.154927	-3.274574	26884.410681
HLA A*3301	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.596032	1.321448	-3.274584	39448.638413
HLA A*0201	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.343707	1.069099	-3.274607	22065.141998
HLA A*8001	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.374285	1.099547	-3.274738	23674.743039
HLA A*2402	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.455949	1.181092	-3.274856	28572.528439
HLA B*0801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.356850	1.081848	-3.275002	22743.104442
HLA A*2402	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.536679	1.261650	-3.275029	34409.576523
HLA A*6802	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.393701	1.118640	-3.275061	24757.193894
HLA A*0211	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.191383	0.916286	-3.275097	15537.550940
HLA B*2705	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.290188	1.014994	-3.275194	19506.879795
HLA B*3501	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-3.817749	0.542449	-3.275299	6572.773469
HLA B*1517	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.449974	1.174655	-3.275319	28182.137747
HLA A*2501	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.430412	1.154939	-3.275473	26940.901321
HLA B*4402	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.290540	1.014994	-3.275546	19522.715728
HLA B*3501	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.358208	1.082637	-3.275570	22814.331520
HLA B*1509	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.419261	1.143250	-3.276011	26257.989199
HLA B*5801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.349646	1.073598	-3.276048	22368.982241
HLA A*3301	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.244869	0.968816	-3.276053	17573.917835
HLA A*0211	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.305243	1.029142	-3.276102	20194.974432
HLA A*2601	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.375716	1.099547	-3.276169	23752.871010
HLA A*0101	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.379043	1.102823	-3.276220	23935.526288
HLA B*5701	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.379511	1.102823	-3.276688	23961.308384
HLA B*4402	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.221024	0.944277	-3.276746	16635.033059
HLA B*1517	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.456200	1.179436	-3.276764	28589.072667
HLA A*2402	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.484965	1.208137	-3.276828	30546.736133
HLA A*3101	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.381463	1.104337	-3.277126	24069.271769
HLA A*0201	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.206330	0.929186	-3.277144	16081.627159
HLA A*1101	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.472581	1.195398	-3.277183	29687.981997
HLA A*0101	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.399855	1.122659	-3.277196	25110.462924
HLA B*5401	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-3.848433	0.571232	-3.277201	7053.959124
HLA B*4002	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.467207	1.190001	-3.277206	29322.932846
HLA B*4402	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.409380	1.132158	-3.277221	25667.261274
HLA B*1501	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.390238	1.112976	-3.277263	24560.560694
HLA B*3901	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.486955	1.209597	-3.277357	30687.027833
HLA B*4403	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.618141	1.340547	-3.277594	41508.847167
HLA B*3901	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.452636	1.174655	-3.277981	28355.407945
HLA A*0219	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.453435	1.175404	-3.278031	28407.611810
HLA A*3101	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.347175	1.069099	-3.278075	22242.037391
HLA B*0801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.811034	0.532852	-3.278182	6471.930374
HLA B*1509	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.484556	1.206278	-3.278278	30517.995387
HLA B*0801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.352069	1.073598	-3.278470	22494.095973
HLA A*0250	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.244110	0.965301	-3.278809	17543.236087
HLA B*3901	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.293844	1.014988	-3.278856	19671.777628
HLA A*6901	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.365663	1.086732	-3.278931	23209.333230
HLA A*0206	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.447686	1.168679	-3.279006	28034.030074
HLA B*1501	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.186322	0.907250	-3.279072	15357.544231

HLA B*5401	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.540107	1.261014	-3.279093	34682.246965
HLA A*0212	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.440360	1.161199	-3.279161	27565.117031
HLA A*0250	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.533263	1.254080	-3.279183	34139.973260
HLA A*2403	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.454734	1.175404	-3.279330	28492.725225
HLA A*3002	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.377156	1.097819	-3.279337	23831.772511
HLA B*4801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.366128	1.086732	-3.279396	23234.207414
HLA A*2603	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.434387	1.154927	-3.279461	27188.637837
HLA B*1801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.535967	1.256417	-3.279551	34353.218672
HLA B*0702	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.382419	1.102823	-3.279597	24122.326478
HLA A*0201	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.066503	0.786863	-3.279639	11654.744003
HLA B*4801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.355398	1.075727	-3.279671	22667.194126
HLA A*2402	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.516584	1.236758	-3.279826	32853.692093
HLA A*0201	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.365350	1.085412	-3.279939	23192.639767
HLA B*5701	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.400334	1.120342	-3.279992	25138.190565
HLA B*1801	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.504987	1.224706	-3.280281	31988.002745
HLA A*0219	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.406614	1.126330	-3.280284	25504.345768
HLA B*1502	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.486565	1.206278	-3.280286	30659.481976
HLA B*1502	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.536851	1.256417	-3.280434	34423.168302
HLA B*4801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.274810	0.994371	-3.280440	18828.270473
HLA B*5101	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.505177	1.224706	-3.280472	32002.022992
HLA A*1101	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.435222	1.154698	-3.280524	27240.904078
HLA A*3002	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.538890	1.258359	-3.280532	34585.192174
HLA A*0212	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.407061	1.126330	-3.280731	25530.574625
HLA B*4402	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.309905	1.029142	-3.280763	20412.898961
HLA A*0101	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.385239	1.104337	-3.280902	24279.434824
HLA A*0101	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.367664	1.086732	-3.280933	23316.557201
HLA A*0212	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.414076	1.133041	-3.281036	25946.342818
HLA B*1517	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.235445	0.954333	-3.281111	17196.687814
HLA B*0801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.317942	1.036678	-3.281264	20794.202747
HLA B*0802	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.430600	1.149326	-3.281274	26952.563628
HLA B*5801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.350548	1.069099	-3.281449	22415.499808
HLA B*5101	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.197007	0.915512	-3.281495	15740.090773
HLA A*0250	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.874893	0.593391	-3.281502	7497.091974
HLA B*4501	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.129370	0.847787	-3.281583	13470.082584
HLA B*5801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.014419	0.732827	-3.281592	10337.591227
HLA A*0201	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.384750	1.103143	-3.281607	24252.129587
HLA B*0802	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.462783	1.181092	-3.281691	29025.741658
HLA B*3901	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.144604	0.862842	-3.281763	13950.967247
HLA A*3101	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.384729	1.102823	-3.281906	24250.948804
HLA A*6801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.349294	1.067242	-3.282052	22350.837547
HLA B*3901	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.384940	1.102823	-3.282118	24262.759224
HLA B*5801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.198487	0.916314	-3.282173	15793.828147
HLA B*1501	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.278215	0.995952	-3.282263	18976.443958
HLA B*3501	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.456968	1.174655	-3.282314	28639.692463
HLA A*0201	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.155623	0.873256	-3.282367	14309.465232
HLA A*2301	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.544144	1.261650	-3.282494	35006.092954
HLA B*0802	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.427052	1.144551	-3.282502	26733.286800
HLA B*4402	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.396634	1.113773	-3.282861	24924.908650
HLA B*1501	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.369718	1.086732	-3.282986	23427.064599
HLA A*6901	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.056776	0.773768	-3.283008	11396.614831
HLA B*2705	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.415237	1.132158	-3.283079	26015.776776
HLA A*2501	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.332815	1.049687	-3.283127	21518.624846
HLA A*2902	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.319850	1.036678	-3.283172	20885.749071
HLA A*0301	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.311958	1.028753	-3.283205	20509.644648
HLA A*6901	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.325592	1.042359	-3.283233	21163.729268
HLA A*2602	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.277696	0.994371	-3.283325	18953.769554
HLA B*3501	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.403687	1.120342	-3.283345	25333.006191
HLA A*0216	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.386676	1.103143	-3.283534	24359.953663
HLA A*0202	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.438234	1.154698	-3.283536	27430.489439
HLA A*2902	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.228105	0.944464	-3.283641	16908.497440
HLA B*0702	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.298669	1.014988	-3.283682	19891.587689
HLA B*0802	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.415843	1.132158	-3.283685	26052.113685
HLA A*0201	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.188399	0.904590	-3.283809	15431.165160
HLA B*5701	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.410145	1.126330	-3.283816	25712.568609
HLA A*2602	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.310527	1.026649	-3.283879	20442.184301

HLA B*4801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.175993	0.892112	-3.283881	14996.621786
HLA A*2602	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-3.777995	0.494046	-3.283950	5997.846934
HLA B*1509	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.351242	1.067242	-3.284000	22451.301653
HLA A*3001	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-3.547436	0.263371	-3.284064	3527.245728
HLA A*1101	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.312818	1.028753	-3.284065	20550.294373
HLA A*2301	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.517811	1.233662	-3.284149	32946.600799
HLA B*0803	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.474169	1.190001	-3.284167	29796.752242
HLA A*2602	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.081084	0.796898	-3.284185	12052.680456
HLA A*0203	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.294884	1.010656	-3.284228	19718.979173
HLA A*3201	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.178066	0.893801	-3.284265	15068.349489
HLA B*0801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.249568	0.965301	-3.284266	17765.096118
HLA B*0803	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.453007	1.168679	-3.284328	28379.655446
HLA A*2902	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.366212	1.081848	-3.284365	23238.732856
HLA A*0216	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.445571	1.161199	-3.284372	27897.866930
HLA B*5101	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.313154	1.028753	-3.284401	20566.198523
HLA B*5701	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.403045	1.118640	-3.284405	25295.619496
HLA A*2301	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.510793	1.226371	-3.284422	32418.484013
HLA A*2501	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.445865	1.161199	-3.284666	27916.738856
HLA A*0250	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.543049	1.258359	-3.284690	34917.953448
HLA B*7301	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.604704	1.319849	-3.284855	40244.261942
HLA B*0801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.387882	1.102823	-3.285059	24427.653086
HLA A*3001	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.279437	0.994371	-3.285066	19029.902554
HLA B*4801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.352513	1.067242	-3.285271	22517.107252
HLA B*4601	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.383162	1.097819	-3.285343	24163.599466
HLA B*3501	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.372258	1.086732	-3.285526	23564.469572
HLA B*5801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.312198	1.026649	-3.285549	20520.965171
HLA B*0702	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.361302	1.075727	-3.285575	22977.460057
HLA B*4001	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.398687	1.112976	-3.285711	25043.038731
HLA B*3501	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.447002	1.161199	-3.285803	27989.931445
HLA A*3002	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.316965	1.031103	-3.285862	20747.457725
HLA A*0250	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.371292	1.085412	-3.285880	23512.133018
HLA A*2603	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.542654	1.256417	-3.286237	34886.232287
HLA B*0702	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.429625	1.143250	-3.286375	26892.120196
HLA B*0803	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.492666	1.206278	-3.286388	31093.271946
HLA B*1517	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.481795	1.195398	-3.286397	30324.619355
HLA A*8001	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.389571	1.103143	-3.286428	24522.854613
HLA B*4402	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.384040	1.097502	-3.286538	24212.539135
HLA B*0801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.247829	0.961256	-3.286573	17694.118956
HLA B*2705	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.247500	0.960920	-3.286580	17680.722779
HLA A*6801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-3.812636	0.525884	-3.286752	6495.852953
HLA A*6802	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.195875	0.909118	-3.286756	15699.100903
HLA B*5701	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.415368	1.128536	-3.286832	26023.659548
HLA A*0201	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.360480	1.073598	-3.286881	22933.994292
HLA A*0212	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.323675	1.036678	-3.286997	21070.508541
HLA B*4402	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.348728	1.061692	-3.287036	22321.715887
HLA B*4501	1:127-135	9	NFSHQNGII	1.000888	0.339659	-4.627651	1.340547	-3.287105	42427.885397
HLA B*5401	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.545473	1.258359	-3.287115	35113.445788
HLA B*5801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.356878	1.069720	-3.287158	22744.580942
HLA A*2301	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.523548	1.236390	-3.287158	33384.744446
HLA B*4402	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.269536	0.982334	-3.287202	18600.980377
HLA B*4001	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.386810	1.099547	-3.287263	24367.466546
HLA A*2601	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.013254	0.725976	-3.287278	10309.889499
HLA A*2601	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.400292	1.112976	-3.287316	25135.742777
HLA B*0802	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.401093	1.113773	-3.287320	25182.155294
HLA A*2602	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.302370	1.014994	-3.287376	20061.799584
HLA B*7301	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.372838	1.085412	-3.287426	23595.978468
HLA A*2402	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.544524	1.257069	-3.287455	35036.785813
HLA B*1801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.390306	1.102823	-3.287484	24564.414224
HLA A*8001	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.442434	1.154927	-3.287508	27697.108730
HLA A*0203	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.248482	0.960920	-3.287562	17720.750033
HLA B*5801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.337290	1.049687	-3.287603	21741.539011
HLA A*0219	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.242268	0.954621	-3.287646	17468.986599
HLA B*1801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.482641	1.194908	-3.287733	30383.735921
HLA B*0803	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.387283	1.099547	-3.287735	24393.977841
HLA A*0216	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.442679	1.154927	-3.287752	27712.696297

HLA B*4402	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.442575	1.154698	-3.287878	27706.100487
HLA B*1503	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-3.787370	0.499448	-3.287921	6128.720608
HLA A*2402	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.387525	1.099547	-3.287977	24407.574407
HLA B*4001	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.385802	1.097819	-3.287984	24310.979070
HLA A*3001	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.193304	0.905205	-3.288099	15606.461461
HLA A*3001	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.203684	0.915512	-3.288173	15983.963125
HLA A*0212	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.391444	1.103143	-3.288301	24628.817630
HLA A*3101	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.314982	1.026649	-3.288333	20652.941886
HLA A*0211	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.407192	1.118640	-3.288552	25538.310381
HLA A*2402	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.391603	1.102823	-3.288781	24637.879561
HLA A*2601	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.392219	1.103143	-3.289076	24672.825829
HLA B*2705	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.433715	1.144551	-3.289165	27146.603334
HLA B*0801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.243896	0.954621	-3.289275	17534.601679
HLA B*0803	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.463970	1.174655	-3.289315	29105.148230
HLA B*5301	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.450474	1.161155	-3.289319	28214.630922
HLA A*2403	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.386829	1.097502	-3.289327	24368.521171
HLA B*0801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.450573	1.161199	-3.289374	28221.042447
HLA A*0219	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.149543	0.860149	-3.289394	14110.517334
HLA A*2601	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.371261	1.081848	-3.289414	23510.479502
HLA B*5401	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-3.935359	0.645932	-3.289427	8617.061347
HLA B*5701	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.421632	1.132158	-3.289474	26401.712390
HLA A*2301	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.495765	1.206278	-3.289487	31315.935939
HLA A*6802	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.318668	1.029142	-3.289526	20828.992566
HLA A*0212	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.231824	0.942253	-3.289571	17053.921157
HLA A*0219	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.450869	1.161199	-3.289670	28240.285767
HLA B*7301	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.574478	1.284672	-3.289806	37538.580200
HLA B*1501	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.324620	1.034768	-3.289851	21116.382029
HLA B*5101	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.525216	1.235214	-3.290002	33513.222545
HLA A*0301	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.357263	1.067242	-3.290022	22764.769385
HLA A*3101	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.285980	0.995952	-3.290028	19318.788155
HLA A*2902	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.258855	0.968816	-3.290039	18149.099257
HLA B*4001	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.357301	1.067242	-3.290059	22766.739948
HLA A*0216	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.418639	1.128536	-3.290103	26220.372175
HLA A*6901	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.300822	1.010656	-3.290165	19990.404264
HLA B*1509	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.365900	1.075727	-3.290173	23222.018247
HLA A*3002	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.525390	1.235214	-3.290176	33526.641640
HLA A*0250	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.418766	1.128536	-3.290229	26228.033156
HLA B*5101	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.459071	1.168679	-3.290392	28778.697830
HLA A*0212	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.163809	0.873256	-3.290553	14581.728559
HLA B*1503	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.198135	0.907250	-3.290885	15781.016917
HLA A*2602	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.620659	1.329751	-3.290908	41750.273010
HLA B*5301	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.594112	1.303070	-3.291042	39274.664941
HLA B*0702	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.086906	0.795837	-3.291069	12215.343005
HLA B*0801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.388970	1.097819	-3.291151	24488.915643
HLA B*3901	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.301909	1.010656	-3.291253	20040.538564
HLA B*1509	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.388786	1.097502	-3.291284	24478.584202
HLA A*2403	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.410019	1.118640	-3.291378	25705.058190
HLA B*3801	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.499602	1.208137	-3.291465	31593.817489
HLA A*3101	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.322601	1.031103	-3.291498	21018.479857
HLA B*5401	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.517949	1.226371	-3.291578	32957.118487
HLA B*1517	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.038285	0.746693	-3.291593	10921.578805
HLA B*0702	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.395940	1.104337	-3.291603	24885.162281
HLA A*6801	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.552637	1.261014	-3.291623	35697.436518
HLA A*3301	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.541244	1.249564	-3.291681	34773.177480
HLA B*3901	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.374382	1.082637	-3.291744	23679.994808
HLA A*3201	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.274240	0.982334	-3.291906	18803.535034
HLA A*6801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.274258	0.982334	-3.291925	18804.348851
HLA A*3002	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.453364	1.161155	-3.292209	28403.001723
HLA B*1509	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.473328	1.181092	-3.292235	29739.099518
HLA B*7301	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.595395	1.303070	-3.292325	39390.845929
HLA B*4001	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.362138	1.069720	-3.292419	23021.755461
HLA B*1801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.498862	1.206278	-3.292584	31540.023837
HLA B*0802	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.447575	1.154927	-3.292648	28026.902913
HLA B*1509	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.467330	1.174655	-3.292675	29331.182965
HLA B*0803	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.447794	1.154927	-3.292867	28041.007348

HLA A*3101	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.366480	1.073598	-3.292882	23253.069239
HLA B*4801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.419330	1.126330	-3.293000	26262.109053
HLA B*1801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.310591	1.017549	-3.293042	20445.170448
HLA B*4801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.362153	1.069099	-3.293053	23022.502744
HLA A*0212	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.362366	1.069099	-3.293267	23033.839510
HLA A*0301	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.330188	1.036678	-3.293510	21388.867492
HLA A*1101	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.378998	1.085412	-3.293587	23933.066132
HLA A*0301	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.367300	1.073598	-3.293702	23297.013698
HLA A*0101	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.320360	1.026649	-3.293711	20910.282209
HLA B*1517	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.443132	1.149326	-3.293806	27741.646472
HLA A*3002	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.092601	0.798791	-3.293810	12376.584693
HLA A*3301	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.555574	1.261650	-3.293924	35939.653542
HLA B*5401	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.500279	1.206278	-3.294000	31643.080543
HLA A*2602	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.391530	1.097502	-3.294028	24633.747973
HLA A*2602	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.473469	1.179436	-3.294033	29748.754199
HLA A*0211	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.102027	0.807959	-3.294068	12648.148382
HLA A*2602	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.530857	1.236758	-3.294099	33951.370033
HLA B*2705	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.391716	1.097502	-3.294214	24644.278225
HLA B*1801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.475405	1.181170	-3.294235	29881.662684
HLA B*4501	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.455613	1.161155	-3.294458	28550.432875
HLA A*2902	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.449387	1.154927	-3.294460	28144.047950
HLA B*1502	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.223655	0.929186	-3.294469	16736.131960
HLA B*4403	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.627290	1.332686	-3.294604	42392.552473
HLA B*1509	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.398950	1.104337	-3.294613	25058.217096
HLA B*5301	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.551709	1.257069	-3.294640	35621.235890
HLA B*5101	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.502779	1.208137	-3.294641	31825.747198
HLA A*3201	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.076230	0.781429	-3.294801	11918.719707
HLA A*3101	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.309982	1.014988	-3.294994	20416.543526
HLA B*5701	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.417814	1.122659	-3.295155	26170.630310
HLA A*2902	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.210164	0.914880	-3.295285	16224.239497
HLA B*1503	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.324549	1.029142	-3.295407	21112.955189
HLA A*3002	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.520144	1.224706	-3.295438	33124.066844
HLA B*4601	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.357162	1.061692	-3.295470	22759.474341
HLA B*5401	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.428537	1.133041	-3.295497	26824.845676
HLA A*0219	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.200090	0.904590	-3.295500	15852.207808
HLA A*0212	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.269846	0.974301	-3.295545	18614.268181
HLA A*0301	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.365021	1.069099	-3.295922	23175.080672
HLA A*0101	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.381348	1.085412	-3.295936	24062.892223
HLA B*4601	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.400282	1.104337	-3.295945	25135.198857
HLA B*3801	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.445341	1.149326	-3.296014	27883.080262
HLA B*0803	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.428187	1.132158	-3.296029	26803.231591
HLA A*1101	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.422384	1.126330	-3.296054	26447.457683
HLA A*0211	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.534769	1.238694	-3.296075	34258.567282
HLA B*0801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.302654	1.006578	-3.296076	20074.936268
HLA B*4801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.399025	1.102823	-3.296203	25062.555461
HLA B*4403	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.553382	1.257069	-3.296313	35758.707819
HLA B*5701	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.400651	1.104337	-3.296314	25156.556572
HLA A*2403	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.395893	1.099547	-3.296346	24882.469907
HLA B*4402	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.409337	1.112976	-3.296362	25664.761969
HLA A*0212	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.225549	0.929186	-3.296363	16809.267030
HLA B*5701	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.395964	1.099547	-3.296417	24886.508577
HLA B*5801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.201514	0.904921	-3.296592	15904.262854
HLA A*2501	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.396265	1.099547	-3.296717	24903.747602
HLA B*4801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.409704	1.112976	-3.296728	25686.430700
HLA B*1801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.423084	1.126330	-3.296754	26490.129259
HLA B*4601	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.382313	1.085412	-3.296902	24116.454733
HLA A*0301	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.366703	1.069720	-3.296984	23265.022980
HLA A*6901	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.047387	0.750403	-3.296984	11152.887685
HLA A*1101	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.346735	1.049687	-3.297048	22219.547628
HLA A*6901	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.379842	1.082637	-3.297204	23979.592908
HLA A*3301	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.627069	1.329751	-3.297318	42371.000087
HLA B*5801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.359063	1.061692	-3.297371	22859.301756
HLA B*1501	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.191406	0.894030	-3.297376	15538.391527
HLA B*1509	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.492305	1.194908	-3.297397	31067.378216
HLA B*1801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.417741	1.120342	-3.297400	26166.241691

HLA A*8001	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.423747	1.126330	-3.297417	26530.573144
HLA A*0216	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.112759	0.815296	-3.297463	12964.608283
HLA A*2301	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.458669	1.161199	-3.297470	28752.087225
HLA B*4001	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.371144	1.073598	-3.297546	23504.120907
HLA A*0211	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.532763	1.235214	-3.297549	34100.656208
HLA A*0203	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.379398	1.081848	-3.297550	23955.087047
HLA B*2705	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.395419	1.097819	-3.297600	24855.293256
HLA B*4402	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.400426	1.102823	-3.297603	25143.494923
HLA A*6801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.473093	1.175404	-3.297689	29723.015346
HLA B*3501	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-3.808224	0.510481	-3.297743	6430.190691
HLA B*1509	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.487822	1.190001	-3.297820	30748.347969
HLA A*3002	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.410829	1.112976	-3.297854	25753.079212
HLA B*4801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.426547	1.128536	-3.298011	26702.210691
HLA A*2403	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.411036	1.112976	-3.298060	25765.342406
HLA B*0802	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.441361	1.143250	-3.298111	27628.717210
HLA A*0203	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.367382	1.069099	-3.298283	23301.425315
HLA B*4501	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.142584	0.844164	-3.298420	13886.211063
HLA A*6802	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.398095	1.099547	-3.298548	25008.921017
HLA A*1101	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.473210	1.174655	-3.298556	29731.056344
HLA B*1501	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.106519	0.807959	-3.298561	12779.656103
HLA A*0219	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.431615	1.133041	-3.298574	27015.627376
HLA B*4501	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.494003	1.195398	-3.298605	31189.131556
HLA B*1503	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.146606	0.847787	-3.298819	14015.418823
HLA B*4801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.327688	1.028753	-3.298935	21266.104219
HLA B*5101	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.421714	1.122659	-3.299055	26406.711925
HLA A*0202	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.193102	0.894030	-3.299072	15599.202236
HLA A*8001	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.417718	1.118640	-3.299078	26164.826165
HLA B*0702	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.425434	1.126330	-3.299104	26633.826263
HLA B*2705	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-3.904647	0.605498	-3.299148	8028.727480
HLA A*2902	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.453940	1.154698	-3.299242	28440.672670
HLA B*3901	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-3.904835	0.605498	-3.299336	8032.202994
HLA B*3501	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.293733	0.994371	-3.299362	19666.776423
HLA A*2602	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.164622	0.865145	-3.299476	14609.048515
HLA B*1509	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.460659	1.161155	-3.299504	28884.136658
HLA B*5401	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.553598	1.254080	-3.299518	35776.509708
HLA A*0202	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-3.982495	0.682948	-3.299547	9604.937715
HLA A*2902	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.428187	1.128536	-3.299651	26803.231591
HLA B*4403	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.556077	1.256417	-3.299660	35981.285558
HLA B*3901	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.294156	0.994371	-3.299785	19685.936865
HLA B*0801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.317414	1.017549	-3.299865	20768.906921
HLA A*0216	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.032825	0.732827	-3.299998	10785.125936
HLA B*4402	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.428556	1.128536	-3.300020	26826.006656
HLA B*1501	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.022257	0.722004	-3.300253	10525.851463
HLA B*4601	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.399824	1.099547	-3.300277	25108.697004
HLA B*4801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.432437	1.132158	-3.300279	27066.828877
HLA B*1503	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.315297	1.014988	-3.300309	20667.919151
HLA B*4601	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.403473	1.103143	-3.300330	25320.537824
HLA B*4801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.420751	1.120342	-3.300409	26348.205307
HLA A*2402	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.525122	1.224706	-3.300417	33505.971217
HLA B*3801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.403285	1.102823	-3.300462	25309.581691
HLA B*4001	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.385950	1.085412	-3.300539	24319.266223
HLA A*1101	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.398048	1.097502	-3.300546	25006.215253
HLA A*0201	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.370326	1.069720	-3.300607	23459.912703
HLA B*2705	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.403929	1.103143	-3.300786	25347.126147
HLA B*1502	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.165933	0.865145	-3.300787	14653.215745
HLA B*0802	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.419461	1.118640	-3.300821	26270.066464
HLA B*7301	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.561880	1.261014	-3.300865	36465.309496
HLA A*3101	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.423540	1.122659	-3.300881	26517.945733
HLA A*2601	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.405334	1.104337	-3.300997	25429.259766
HLA A*0101	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.074806	0.773768	-3.301038	11879.709442
HLA A*0206	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.323924	1.022881	-3.301043	21082.594852
HLA A*2602	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.311737	1.010656	-3.301081	20499.217539
HLA B*4002	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.527498	1.226371	-3.301126	33689.730776
HLA A*0216	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.088043	0.786863	-3.301179	12247.369403
HLA A*2403	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.456266	1.154927	-3.301339	28593.403579

HLA A*0211	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.176454	0.875034	-3.301420	15012.531712
HLA B*1509	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.319108	1.017549	-3.301559	20850.074863
HLA B*3801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.507858	1.206278	-3.301580	32200.172279
HLA A*2602	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.509782	1.208137	-3.301645	32343.158087
HLA A*3001	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.247939	0.946270	-3.301670	17698.618520
HLA A*0201	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.195532	0.893801	-3.301731	15686.705961
HLA B*5401	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.558203	1.256417	-3.301786	36157.880068
HLA B*4501	1:126-134	9	LNFSHQNGI	1.038583	0.282865	-4.623312	1.321448	-3.301864	42006.054190
HLA A*3002	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.497473	1.195398	-3.302075	31439.343705
HLA A*3001	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.135244	0.833148	-3.302096	13653.499252
HLA B*4002	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.605273	1.303070	-3.302202	40296.983959
HLA A*6801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.223989	0.921765	-3.302224	16748.993667
HLA B*4402	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.400085	1.097819	-3.302266	25123.779246
HLA A*8001	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.430821	1.128536	-3.302285	26966.273289
HLA A*0201	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.086079	0.783751	-3.302328	12192.103694
HLA A*2902	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.384975	1.082637	-3.302338	24264.728186
HLA B*5301	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.536031	1.233662	-3.302369	34358.236910
HLA A*3001	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.162564	0.860149	-3.302415	14539.979107
HLA A*3002	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.477844	1.175404	-3.302439	30049.934132
HLA B*4001	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.389202	1.086732	-3.302470	24502.034906
HLA B*2705	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.271493	0.968816	-3.302677	18684.993694
HLA A*0101	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.331839	1.029142	-3.302698	21470.367487
HLA A*3101	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.257055	0.954333	-3.302722	18074.045460
HLA A*3001	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.288170	0.985326	-3.302843	19416.439780
HLA B*4402	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.339576	1.036678	-3.302898	21856.284340
HLA B*1502	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.285254	0.982334	-3.302920	19286.520769
HLA B*0803	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.478370	1.175404	-3.302966	30086.371171
HLA A*0301	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.268382	0.965301	-3.303081	18551.636983
HLA B*5401	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.552764	1.249564	-3.303200	35707.866477
HLA B*5301	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.522876	1.219563	-3.303313	33333.130564
HLA A*0250	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.573745	1.270418	-3.303327	37475.272821
HLA B*5801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.318438	1.014994	-3.303444	20817.952604
HLA A*0101	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.385295	1.081848	-3.303447	24282.587406
HLA A*3002	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.540354	1.236758	-3.303596	34701.953408
HLA A*0212	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.385450	1.081848	-3.303602	24291.259117
HLA B*5301	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.530138	1.226371	-3.303767	33895.212545
HLA A*3001	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.677155	0.373369	-3.303786	4755.054315
HLA A*8001	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.426521	1.122659	-3.303862	26700.621722
HLA B*1502	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.472635	1.168679	-3.303956	29691.676227
HLA A*0202	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.202919	0.898882	-3.304036	15955.798270
HLA A*0212	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.286431	0.982334	-3.304097	19338.864980
HLA B*0802	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.371351	1.067242	-3.304109	23515.313184
HLA A*2902	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.426810	1.122659	-3.304151	26718.394665
HLA B*5701	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.402070	1.097819	-3.304251	25238.891903
HLA B*3801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.541197	1.236758	-3.304439	34769.415303
HLA A*3001	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.104438	0.799991	-3.304446	12718.547712
HLA A*2301	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.539684	1.235214	-3.304471	34648.490523
HLA B*1502	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.542619	1.238104	-3.304515	34883.401442
HLA B*4403	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.530916	1.226371	-3.304545	33955.962173
HLA B*5401	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-3.825629	0.521039	-3.304590	6693.123480
HLA B*7301	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.484088	1.179436	-3.304652	30485.158370
HLA B*4402	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.404298	1.099547	-3.304750	25368.663939
HLA A*3301	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.305845	1.001026	-3.304818	20222.962467
HLA A*0219	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.407643	1.102823	-3.304821	25564.850773
HLA A*6801	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.554394	1.249564	-3.304831	35842.182327
HLA B*4501	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.603574	1.298743	-3.304831	40139.676201
HLA B*5801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.300887	0.995952	-3.304935	19993.432578
HLA A*2601	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.378639	1.073598	-3.305041	23913.264617
HLA B*4601	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.259532	0.954333	-3.305198	18177.398466
HLA A*8001	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.409650	1.104337	-3.305313	25683.234801
HLA A*2403	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.437508	1.132158	-3.305349	27384.673408
HLA B*0702	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.387280	1.081848	-3.305433	24393.845873
HLA B*5301	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.563802	1.258359	-3.305443	36627.036621
HLA A*2602	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.515052	1.209597	-3.305455	32738.013117
HLA B*5801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.193478	0.887960	-3.305518	15612.710474

HLA A*0301	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.367321	1.061692	-3.305630	23298.148034
HLA A*2601	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.392456	1.086732	-3.305725	24686.310715
HLA A*0101	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.375455	1.069720	-3.305736	23738.611747
HLA B*5401	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.542163	1.236390	-3.305773	34846.809872
HLA A*0101	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.388443	1.082637	-3.305806	24459.257577
HLA A*0219	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.328827	1.022881	-3.305946	21321.975408
HLA A*2501	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.381733	1.075727	-3.306006	24084.250819
HLA B*0801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.321015	1.014988	-3.306027	20941.867164
HLA B*5701	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.409196	1.103143	-3.306053	25656.432710
HLA B*0702	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.434634	1.128536	-3.306098	27204.086414
HLA A*2301	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.419294	1.112976	-3.306319	26259.978013
HLA B*4501	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.609410	1.303070	-3.306340	40682.720364
HLA B*0802	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.403879	1.097502	-3.306377	25344.246682
HLA B*0702	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.337502	1.031103	-3.306398	21752.127327
HLA A*0202	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.410754	1.104337	-3.306417	25748.621317
HLA A*2501	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.429089	1.122659	-3.306430	26858.970432
HLA A*0250	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.335662	1.029142	-3.306520	21660.181428
HLA B*4002	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.619355	1.312789	-3.306566	41625.106296
HLA A*3001	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.181637	0.875034	-3.306603	15192.767849
HLA A*2601	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.389296	1.082637	-3.306659	24507.337611
HLA A*6802	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.429334	1.122659	-3.306675	26874.086305
HLA A*2501	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.481429	1.174655	-3.306774	30299.037910
HLA A*2602	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.526386	1.219563	-3.306823	33603.633083
HLA B*3901	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.435370	1.128536	-3.306833	27250.189988
HLA B*4002	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.626773	1.319849	-3.306923	42342.127904
HLA A*0219	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.236472	0.929186	-3.307286	17237.390969
HLA A*8001	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.374539	1.067242	-3.307297	23688.579476
HLA B*5701	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.383063	1.075727	-3.307336	24158.109749
HLA A*0201	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.394329	1.086732	-3.307597	24792.980025
HLA A*6901	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.226037	0.918327	-3.307710	16828.192421
HLA B*3501	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.342581	1.034768	-3.307813	22008.037801
HLA A*0206	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.139633	0.831818	-3.307815	13792.176583
HLA A*6802	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.094758	0.786863	-3.307894	12438.203137
HLA A*2602	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.564415	1.256417	-3.307998	36678.789832
HLA A*2501	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.469223	1.161155	-3.308068	29459.357035
HLA A*0201	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.390201	1.081848	-3.308353	24558.434868
HLA B*4002	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.578667	1.270153	-3.308514	37902.423013
HLA B*3901	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.463232	1.154698	-3.308534	29055.749133
HLA B*3901	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.483952	1.175404	-3.308548	30475.594434
HLA B*0801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.331536	1.022974	-3.308563	21455.389067
HLA B*4403	1:249-257	9	AVVLKALAK	1.021065	0.298784	-4.628690	1.319849	-3.308840	42529.459118
HLA B*7301	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.171684	0.862842	-3.308843	14848.564959
HLA B*4402	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.376350	1.067242	-3.309109	23787.591469
HLA B*5101	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.484533	1.175404	-3.309128	30516.344442
HLA A*2602	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.477888	1.168679	-3.309209	30053.023060
HLA A*3101	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.392031	1.082637	-3.309394	24662.149959
HLA A*6802	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.182812	0.873256	-3.309555	15233.919075
HLA B*4001	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.359258	1.049687	-3.309571	22869.568363
HLA B*2705	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.412394	1.102823	-3.309571	25846.034559
HLA B*1509	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.490817	1.181170	-3.309647	30961.171182
HLA A*3301	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.534360	1.224706	-3.309655	34226.334157
HLA A*6801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.346355	1.036678	-3.309677	22200.082902
HLA B*1501	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.316316	1.006578	-3.309738	20716.502202
HLA B*1501	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.208651	0.898882	-3.309769	16167.813106
HLA A*0212	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.926356	0.616515	-3.309840	8440.262587
HLA B*1502	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.442004	1.132158	-3.309846	27669.701892
HLA B*2705	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.464813	1.154927	-3.309887	29161.729727
HLA A*2602	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.580314	1.270418	-3.309896	38046.434493
HLA A*0203	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.226263	0.916286	-3.309977	16836.934401
HLA B*4501	1:304-312	9	LSGPRTDPL	0.906188	0.426498	-4.642686	1.332686	-3.310000	43922.367525
HLA A*0211	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.491217	1.181092	-3.310124	30989.658685
HLA A*0216	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.336832	1.026649	-3.310184	21718.615338
HLA B*4403	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.042557	0.732333	-3.310224	11029.524444
HLA A*0101	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.379431	1.069099	-3.310331	23956.901436
HLA B*3801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.505849	1.195398	-3.310451	32051.575753

HLA B*4002	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.505361	1.194908	-3.310453	32015.529779
HLA A*3001	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.215399	0.904921	-3.310478	16420.977317
HLA A*0216	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.392329	1.081848	-3.310482	24679.100057
HLA B*5801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.352900	1.042359	-3.310541	22537.215709
HLA A*2501	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.408661	1.097819	-3.310842	25624.806170
HLA A*0201	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.227217	0.916314	-3.310902	16873.955939
HLA B*5101	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.431312	1.120342	-3.310970	26996.780403
HLA A*3301	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.581404	1.270153	-3.311251	38142.058184
HLA B*4801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.409095	1.097819	-3.311276	25650.465070
HLA B*4501	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.501324	1.190001	-3.311323	31719.349885
HLA A*0219	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.904788	0.593391	-3.311397	8031.333975
HLA B*3801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.521135	1.209597	-3.311538	33199.774587
HLA B*3501	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.415970	1.104337	-3.311633	26059.725506
HLA A*2601	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.267821	0.956046	-3.311775	18527.665894
HLA B*5701	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.380993	1.069099	-3.311894	24043.243435
HLA A*0201	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.394735	1.082637	-3.312098	24816.194905
HLA B*1517	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.394895	1.082637	-3.312258	24825.325779
HLA B*1517	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.455542	1.143250	-3.312292	28545.799610
HLA B*4601	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.308248	0.995952	-3.312296	20335.193017
HLA A*6801	1:55-63	9	RFRREAQNA	1.374976	-0.010272	-4.677021	1.364704	-3.312317	47535.833736
HLA A*2902	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.397775	1.085412	-3.312364	24990.527597
HLA B*0702	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.327397	1.014994	-3.312403	21251.843142
HLA B*5701	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.397954	1.085412	-3.312542	25000.804604
HLA B*0702	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.412105	1.099547	-3.312558	25828.841905
HLA A*3101	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.330122	1.017549	-3.312573	21385.627818
HLA B*5801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.349306	1.036678	-3.312628	22351.442133
HLA A*0202	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.493872	1.181092	-3.312779	31179.684121
HLA B*4601	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.395454	1.082637	-3.312817	24857.310303
HLA A*0203	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.281638	0.968816	-3.312822	19126.611293
HLA B*0803	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.494031	1.181092	-3.312939	31191.156378
HLA B*1501	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.382071	1.069099	-3.312972	24103.020339
HLA A*3001	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.287380	0.974301	-3.313079	19381.178134
HLA B*5801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.347868	1.034768	-3.313099	22277.562183
HLA B*1502	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.551982	1.238694	-3.313288	35643.596910
HLA A*0301	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.330839	1.017549	-3.313290	21420.943578
HLA B*4403	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.492805	1.179436	-3.313369	31103.197988
HLA A*3001	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.234839	0.921444	-3.313394	17172.702256
HLA A*6802	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.011407	0.697848	-3.313559	10266.143141
HLA B*2705	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.426641	1.112976	-3.313666	26707.989556
HLA A*2603	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.440007	1.126330	-3.313678	27542.757470
HLA B*3801	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.494849	1.181170	-3.313679	31249.933452
HLA A*0216	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.201664	0.887960	-3.313704	15909.770387
HLA A*0201	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.336592	1.022881	-3.313711	21706.634124
HLA B*2705	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.489161	1.175404	-3.313757	30843.311047
HLA B*1517	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.432517	1.118640	-3.313877	27071.807905
HLA A*3002	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.463312	1.149326	-3.313986	29061.094029
HLA B*1509	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.399448	1.085412	-3.314037	25086.972764
HLA B*5101	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.463364	1.149326	-3.314037	29064.553016
HLA A*3001	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.230363	0.916286	-3.314077	16996.631989
HLA B*5801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.343345	1.029142	-3.314203	22046.766677
HLA A*8001	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.412056	1.097819	-3.314237	25825.907717
HLA B*4501	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.596547	1.282160	-3.314387	39495.403505
HLA B*4402	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.399808	1.085412	-3.314396	25107.746175
HLA A*0211	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.489081	1.174655	-3.314426	30837.638366
HLA B*4501	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.400094	1.085412	-3.314683	25124.322919
HLA A*0219	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.189771	0.875034	-3.314737	15479.995097
HLA B*0802	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.435264	1.120342	-3.314922	27243.556873
HLA B*2705	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.458298	1.143250	-3.315048	28727.521520
HLA B*4601	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.224210	0.909118	-3.315091	16757.513192
HLA A*0212	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.338174	1.022881	-3.315292	21785.808884
HLA B*4001	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-3.632760	0.317460	-3.315299	4292.987396
HLA A*6901	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.330416	1.014994	-3.315422	21400.094443
HLA A*3101	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.028422	0.712902	-3.315520	10676.337291
HLA B*1509	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.398398	1.082637	-3.315761	25026.380226
HLA A*1101	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.434451	1.118640	-3.315811	27192.609490

HLA B*0702	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.402634	1.086732	-3.315902	25271.682692
HLA A*2601	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.350797	1.034768	-3.316029	22428.357624
HLA B*1502	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.290437	0.974301	-3.316136	19518.069189
HLA A*0219	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.419301	1.103143	-3.316158	26260.404208
HLA A*8001	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.365884	1.049687	-3.316196	23221.138864
HLA B*4001	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.189376	0.873123	-3.316254	15465.932319
HLA A*6801	1:412-420	9	AGDEITVNV	1.300588	0.029163	-4.646060	1.329751	-3.316309	44264.911686
HLA B*3901	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.353114	1.036678	-3.316436	22548.313510
HLA A*1101	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.281791	0.965301	-3.316490	19133.338210
HLA A*6901	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-3.591658	0.275124	-3.316534	3905.329867
HLA A*2902	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.419370	1.102823	-3.316547	26264.524441
HLA A*2902	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-3.531351	0.214737	-3.316614	3398.999822
HLA B*5101	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.383885	1.067242	-3.316644	24203.895526
HLA A*2601	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.378343	1.061692	-3.316651	23896.969790
HLA A*0202	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.107746	0.790996	-3.316750	12815.796373
HLA B*1503	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.448914	1.132158	-3.316756	28113.461091
HLA A*6901	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.386780	1.069720	-3.317060	24365.752877
HLA A*0202	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.485766	1.168679	-3.317087	30603.139913
HLA A*6801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.261834	0.944464	-3.317370	18274.025339
HLA A*0202	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.232924	0.915512	-3.317412	17097.153459
HLA B*4403	1:216-224	9	FTGDSPVSV	1.347532	-0.048789	-4.616223	1.298743	-3.317481	41326.011484
HLA A*0219	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.402989	1.085412	-3.317577	25292.335393
HLA A*0212	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.391187	1.073598	-3.317589	24614.298842
HLA B*4501	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-3.797496	0.479739	-3.317757	6273.300681
HLA B*3501	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.440477	1.122659	-3.317818	27572.574251
HLA B*4402	1:414-422	9	DEITVNVST	1.070685	-0.486156	-3.902405	0.584529	-3.317877	7987.397687
HLA B*1501	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.157794	0.839877	-3.317917	14381.173569
HLA B*5701	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.367648	1.049687	-3.317961	23315.674238
HLA A*0219	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.347165	1.029142	-3.318023	22241.556088
HLA A*3001	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.216113	0.898050	-3.318063	16448.005579
HLA A*3001	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.274115	0.956046	-3.318069	18798.144379
HLA B*5701	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.400740	1.082637	-3.318103	25161.728683
HLA A*0203	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.303617	0.985326	-3.318291	20119.512990
HLA B*0802	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.421550	1.103143	-3.318407	26396.713801
HLA B*1509	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.300789	0.982334	-3.318455	19988.890279
HLA B*1509	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.431465	1.112976	-3.318489	27006.275296
HLA A*2902	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.347666	1.029142	-3.318524	22267.199948
HLA A*2601	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.403987	1.085412	-3.318576	25350.554507
HLA A*3002	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.557338	1.238694	-3.318644	36085.967150
HLA B*0702	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.380340	1.061692	-3.318648	24007.110796
HLA A*2403	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.421987	1.103143	-3.318844	26423.288582
HLA A*0101	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.355560	1.036678	-3.318882	22675.656969
HLA B*2705	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.394611	1.075727	-3.318883	24809.080523
HLA A*0250	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.423223	1.104337	-3.318886	26498.585819
HLA B*4601	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.400736	1.081848	-3.318888	25161.456440
HLA A*0101	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.347663	1.028753	-3.318910	22267.079485
HLA B*4001	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.347715	1.028753	-3.318962	22269.729816
HLA B*1501	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-3.843109	0.524138	-3.318971	6968.013857
HLA A*2902	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.437764	1.118640	-3.319123	27400.826308
HLA A*0201	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.355828	1.036678	-3.319150	22689.645980
HLA A*0250	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.134450	0.815296	-3.319154	13628.556059
HLA B*4801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.368900	1.049687	-3.319213	23383.001328
HLA A*0206	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.381071	1.061692	-3.319379	24047.536170
HLA B*7301	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.514449	1.194908	-3.319541	32692.527725
HLA A*0301	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.342523	1.022974	-3.319549	22005.061476
HLA B*4501	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.604243	1.284672	-3.319572	40201.612027
HLA B*0801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.442270	1.122659	-3.319611	27686.622036
HLA B*7301	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.395344	1.075727	-3.319616	24850.990768
HLA A*3201	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.499193	1.179436	-3.319757	31564.091568
HLA B*2705	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.446125	1.126330	-3.319796	27933.507828
HLA B*1502	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.446177	1.126330	-3.319847	27936.832603
HLA A*3301	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.501063	1.181170	-3.319893	31700.308206
HLA A*6901	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.401868	1.081848	-3.320020	25227.152228
HLA A*6801	1:327-335	9	GSVGRWVAV	1.149893	0.112337	-4.582264	1.262230	-3.320034	38217.655017
HLA B*0802	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.494807	1.174655	-3.320152	31246.890544

HLA B*0803	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.464703	1.144551	-3.320152	29154.315868
HLA A*6901	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.349334	1.029142	-3.320192	22352.893206
HLA B*4601	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.389914	1.069720	-3.320194	24542.231489
HLA A*0101	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.382100	1.061692	-3.320408	24104.585126
HLA B*1517	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.242279	0.921765	-3.320515	17469.459132
HLA B*0702	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.440900	1.120342	-3.320558	27599.436950
HLA A*6802	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.407361	1.086732	-3.320630	25548.259798
HLA A*8001	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.423556	1.102823	-3.320734	26518.949967
HLA B*1503	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.351859	1.031103	-3.320756	22483.268120
HLA B*1801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.464170	1.143250	-3.320919	29118.535036
HLA B*4001	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.402806	1.081848	-3.320958	25281.665004
HLA B*1517	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.441372	1.120342	-3.321031	27629.464562
HLA B*4801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.406633	1.085412	-3.321221	25505.449597
HLA A*0203	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.403926	1.082637	-3.321289	25346.989022
HLA A*6901	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.315680	0.994371	-3.321309	20686.152407
HLA A*2603	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.540995	1.219563	-3.321432	34753.242579
HLA B*1517	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.295768	0.974301	-3.321467	19759.130732
HLA A*2402	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.500927	1.179436	-3.321491	31690.363047
HLA B*4801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.404199	1.082637	-3.321562	25362.900444
HLA A*0206	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.560275	1.238694	-3.321581	36330.820462
HLA B*4403	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.603799	1.282160	-3.321640	40160.528130
HLA A*1101	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.397383	1.075727	-3.321656	24967.960064
HLA B*1801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.531254	1.209597	-3.321657	33982.424990
HLA A*3002	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.317667	0.995952	-3.321715	20781.045075
HLA A*6801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-3.707022	0.385288	-3.321734	5093.568316
HLA B*1801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.502858	1.181092	-3.321766	31831.601644
HLA A*0201	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.290681	0.968816	-3.321865	19529.053700
HLA B*5301	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.754200	0.432298	-3.321902	5678.057605
HLA A*2902	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.243684	0.921765	-3.321920	17526.066335
HLA A*3201	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.419814	1.097819	-3.321995	26291.392838
HLA B*5101	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.455089	1.133041	-3.322048	28516.010250
HLA A*6802	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.425196	1.103143	-3.322053	26619.277547
HLA A*2603	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.592372	1.270153	-3.322219	39117.538647
HLA B*5101	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.501688	1.179436	-3.322252	31745.958755
HLA A*0203	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.409011	1.086732	-3.322279	25645.469974
HLA A*2403	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.389576	1.067242	-3.322334	24523.119946
HLA A*2403	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.349028	1.026649	-3.322380	22337.178265
HLA A*1101	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.349068	1.026649	-3.322420	22339.232668
HLA B*0702	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.405176	1.082637	-3.322539	25420.044281
HLA B*1503	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-3.865189	0.542619	-3.322570	7331.443056
HLA B*1801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.445249	1.122659	-3.322590	27877.197952
HLA B*4601	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.409387	1.086732	-3.322655	25667.677848
HLA A*2501	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.349317	1.026649	-3.322669	22352.046735
HLA A*6802	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.427041	1.104337	-3.322704	26732.563689
HLA B*5801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.353831	1.031103	-3.322727	22585.549304
HLA B*3801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.512792	1.190001	-3.322791	32568.076822
HLA A*0201	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.357595	1.034768	-3.322826	22782.140847
HLA B*0803	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.477599	1.154698	-3.322901	30033.031939
HLA B*4801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.288278	0.965301	-3.322977	19421.272258
HLA B*4002	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.577126	1.254080	-3.323045	37768.149987
HLA A*6802	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.392896	1.069720	-3.323176	24711.297240
HLA B*4601	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.392299	1.069099	-3.323200	24677.364473
HLA A*3301	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.605409	1.282160	-3.323249	40309.630072
HLA B*5401	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.562162	1.238694	-3.323468	36488.989975
HLA A*2402	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.559873	1.236390	-3.323484	36297.226687
HLA B*1517	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-3.830069	0.506563	-3.323506	6761.909655
HLA B*1801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.442174	1.118640	-3.323533	27680.481673
HLA A*2501	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.358335	1.034768	-3.323566	22820.997335
HLA B*5401	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.484772	1.161155	-3.323617	30533.188273
HLA B*1517	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.426834	1.103143	-3.323691	26719.840140
HLA A*0216	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.330275	1.006578	-3.323697	21393.149242
HLA A*0301	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.366163	1.042359	-3.323804	23236.092907
HLA B*4403	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.393029	1.069099	-3.323930	24718.918482
HLA A*3001	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.217974	0.894030	-3.323944	16518.630426
HLA B*4002	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.478915	1.154927	-3.323988	30124.156110

HLA B*3901	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.456343	1.132158	-3.324185	28598.508711
HLA B*0802	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.411045	1.086732	-3.324314	25765.899963
HLA B*0802	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.437317	1.112976	-3.324342	27372.676045
HLA B*1502	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.559556	1.235214	-3.324342	36270.727229
HLA B*0702	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.409774	1.085412	-3.324363	25690.599860
HLA A*0201	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.353535	1.029142	-3.324393	22570.159200
HLA A*2602	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-3.828866	0.504447	-3.324419	6743.206005
HLA A*1101	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.499903	1.175404	-3.324499	31615.702704
HLA B*4601	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.398123	1.073598	-3.324525	25010.544615
HLA A*3001	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.168748	0.844164	-3.324584	14748.492341
HLA A*3002	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.530940	1.206278	-3.324661	33957.799202
HLA A*2403	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.386395	1.061692	-3.324703	24344.144637
HLA A*2902	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.280524	0.955683	-3.324841	19077.627994
HLA B*3901	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.437860	1.112976	-3.324884	27406.904635
HLA B*4801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.428063	1.103143	-3.324920	26795.547560
HLA A*0202	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.398558	1.073598	-3.324959	25035.588436
HLA A*2403	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.407624	1.082637	-3.324987	25563.744373
HLA B*5701	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.406938	1.081848	-3.325091	25523.393521
HLA B*4501	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.479845	1.154698	-3.325148	30188.760752
HLA A*6801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.918607	0.593391	-3.325216	8291.008430
HLA A*6901	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.241690	0.916286	-3.325404	17445.753763
HLA A*0212	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.408151	1.082637	-3.325513	25594.741684
HLA A*3001	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.240395	0.914880	-3.325516	17393.828037
HLA B*0802	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.454071	1.128536	-3.325535	28449.290185
HLA A*8001	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.326772	1.001026	-3.325745	21221.283085
HLA B*3801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.520719	1.194908	-3.325811	33167.999346
HLA A*0216	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.444464	1.118640	-3.325824	27826.872041
HLA A*2601	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.362550	1.036678	-3.325872	23043.561181
HLA B*1509	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.487110	1.161199	-3.325911	30697.986675
HLA B*4801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.395673	1.069720	-3.325953	24869.819652
HLA B*0803	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.459019	1.133041	-3.325979	28775.272864
HLA B*3901	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.375702	1.049687	-3.326015	23752.100020
HLA A*8001	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.401826	1.075727	-3.326099	25224.695778
HLA A*0212	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.332850	1.006578	-3.326272	21520.371118
HLA A*0301	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.357444	1.031103	-3.326341	22774.254286
HLA B*4403	1:554-562	9	QVSKGNQFV	1.092740	0.220049	-4.639199	1.312789	-3.326410	43571.158347
HLA A*0201	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.388192	1.061692	-3.326500	24445.103234
HLA A*0216	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.459626	1.133041	-3.326585	28815.464033
HLA B*0801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.369067	1.042359	-3.326708	23391.984514
HLA B*0802	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.355485	1.028753	-3.326732	22671.731779
HLA A*0250	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.551542	1.224706	-3.326837	35607.556325
HLA B*0802	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.481668	1.154698	-3.326971	30315.761796
HLA A*0203	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.288235	0.961256	-3.326979	19419.381145
HLA A*0212	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.361760	1.034768	-3.326992	23001.712422
HLA A*3301	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.553457	1.226371	-3.327086	35764.898776
HLA B*4403	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.597247	1.270153	-3.327094	39559.127252
HLA B*2705	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.396859	1.069720	-3.327139	24937.856747
HLA B*1502	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.394387	1.067242	-3.327146	24796.333433
HLA A*0250	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.560886	1.233662	-3.327225	36381.958303
HLA B*5701	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.394519	1.067242	-3.327277	24803.846715
HLA B*5801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.350255	1.022974	-3.327281	22400.346761
HLA A*3101	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.167300	0.839877	-3.327423	14699.424916
HLA B*0802	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.431881	1.104337	-3.327543	27032.147550
HLA A*0216	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.476873	1.149326	-3.327547	29982.868988
HLA A*0216	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.401203	1.073598	-3.327605	25188.559043
HLA B*2705	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.456174	1.128536	-3.327638	28587.371417
HLA A*3002	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.202787	0.875034	-3.327753	15950.965132
HLA A*0216	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.311843	0.984065	-3.327778	20504.208578
HLA A*3001	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.289476	0.961636	-3.327840	19474.930381
HLA B*5301	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.534156	1.206278	-3.327878	34210.228968
HLA A*1101	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.482902	1.154927	-3.327975	30401.986764
HLA A*2601	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.397780	1.069720	-3.328060	24990.797991
HLA A*0202	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.563398	1.235214	-3.328184	36592.970981
HLA A*0202	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.236269	0.908065	-3.328205	17229.373130
HLA A*3201	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.536411	1.208137	-3.328274	34388.361738

HLA B*1517	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.343343	1.014988	-3.328355	22046.647407
HLA B*7301	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.577955	1.249564	-3.328391	37840.344391
HLA B*4402	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.339097	1.010656	-3.328441	21832.176670
HLA A*0101	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.351429	1.022974	-3.328456	22461.020480
HLA A*3201	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.586853	1.258359	-3.328494	38623.584819
HLA B*7301	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.553274	1.224706	-3.328568	35749.810197
HLA B*0801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.246920	0.918327	-3.328593	17657.112821
HLA A*6802	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.365287	1.036678	-3.328609	23189.252335
HLA A*3101	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.284462	0.955683	-3.328779	19251.390916
HLA A*3101	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.390485	1.061692	-3.328793	24574.515998
HLA A*2602	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.585913	1.257069	-3.328844	38540.095461
HLA A*3001	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.273175	0.944277	-3.328898	18757.510010
HLA B*4501	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.583004	1.254080	-3.328924	38282.837823
HLA B*4001	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.390661	1.061692	-3.328969	24584.488927
HLA B*0803	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.442878	1.113773	-3.329106	27725.442649
HLA B*0802	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.455462	1.126330	-3.329133	28540.549486
HLA B*4403	1:144-152	9	IMISATNAV	0.995514	0.289158	-4.613883	1.284672	-3.329212	41103.935458
HLA A*2902	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.432414	1.103143	-3.329271	27065.364631
HLA B*4501	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.590292	1.261014	-3.329278	38930.701200
HLA A*2902	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.223148	0.893801	-3.329347	16716.586608
HLA B*0803	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.479025	1.149326	-3.329699	30131.816596
HLA A*2902	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.456068	1.126330	-3.329739	28580.412811
HLA A*0206	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.291222	0.961256	-3.329965	19553.368328
HLA A*3301	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.591025	1.261014	-3.330011	38996.467249
HLA A*0206	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.250131	0.920120	-3.330011	17788.176826
HLA A*3301	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.443790	1.113773	-3.330017	27783.700500
HLA A*6901	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.192877	0.862842	-3.330035	15591.102904
HLA A*2601	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.399399	1.069099	-3.330300	25084.122853
HLA B*0702	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.399439	1.069099	-3.330340	25086.429899
HLA B*0803	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.491572	1.161199	-3.330372	31014.984271
HLA A*6802	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.299252	0.968816	-3.330436	19918.293198
HLA A*3001	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.272745	0.942253	-3.330492	18738.949082
HLA A*6801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.541900	0.211378	-3.330522	3482.573808
HLA B*0802	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.239824	0.909118	-3.330706	17370.977080
HLA B*1503	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.485764	1.154927	-3.330837	30602.974354
HLA B*1502	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.063199	0.732333	-3.330866	11566.430770
HLA A*0101	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.361995	1.031103	-3.330892	23014.159460
HLA B*3801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.453597	1.122659	-3.330938	28418.217849
HLA B*4001	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.367721	1.036678	-3.331043	23319.584758
HLA A*8001	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.359937	1.028753	-3.331184	22905.351938
HLA B*4501	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.601375	1.270153	-3.331222	39936.936414
HLA B*1509	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.457626	1.126330	-3.331296	28683.107854
HLA A*0301	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.358020	1.026649	-3.331371	22804.459816
HLA B*1503	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.275654	0.944277	-3.331376	18864.873335
HLA B*2705	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.285884	0.954333	-3.331550	19314.503617
HLA A*3201	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.613724	1.282160	-3.331564	41088.817233
HLA A*6901	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.293263	0.961636	-3.331628	19645.508915
HLA B*1801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.346651	1.014988	-3.331663	22215.220659
HLA A*3001	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.113272	0.781429	-3.331843	12979.907189
HLA A*0301	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.366619	1.034768	-3.331850	23260.492418
HLA B*5301	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.541583	1.209597	-3.331985	34800.277176
HLA B*1501	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.405698	1.073598	-3.332100	25450.591978
HLA B*0801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.306446	0.974301	-3.332145	20250.989291
HLA B*5101	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.405822	1.073598	-3.332224	25457.890323
HLA B*5401	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.556969	1.224706	-3.332264	36055.330453
HLA A*2603	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.288315	0.956046	-3.332269	19422.953402
HLA B*1517	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.436791	1.104337	-3.332454	27339.525512
HLA B*1801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.415155	1.082637	-3.332517	26010.851256
HLA B*3901	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.250909	0.918162	-3.332747	17820.058176
HLA B*2705	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.414617	1.081848	-3.332769	25978.647285
HLA A*1101	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.464971	1.132158	-3.332813	29172.301678
HLA B*1503	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.119775	0.786863	-3.332912	13175.738343
HLA A*2402	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.568184	1.235214	-3.332970	36998.453573
HLA B*4801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.414882	1.081848	-3.333034	25994.533341
HLA A*0101	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.949621	0.616515	-3.333105	8904.725961

HLA A*0216	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.327488	0.994371	-3.333118	21256.327449
HLA A*0250	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.571839	1.238694	-3.333145	37311.213218
HLA B*3801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.494506	1.161199	-3.333307	31225.260630
HLA B*0702	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.446332	1.112976	-3.333357	27946.809305
HLA B*0702	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.327742	0.994371	-3.333371	21268.750471
HLA A*0250	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.488158	1.154698	-3.333460	30772.144529
HLA B*4001	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.177633	0.844164	-3.333469	15053.357622
HLA A*0206	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.908086	0.574537	-3.333549	8092.568103
HLA A*2601	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.376061	1.042359	-3.333702	23771.768081
HLA B*1509	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.456390	1.122659	-3.333731	28601.603174
HLA A*2501	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.488524	1.154698	-3.333827	30798.125418
HLA B*4801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.407730	1.073598	-3.334132	25569.968496
HLA B*4001	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.368912	1.034768	-3.334144	23383.633834
HLA B*4601	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.363405	1.029142	-3.334263	23088.983262
HLA B*4402	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.410096	1.075727	-3.334369	25709.647630
HLA B*5701	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.421115	1.086732	-3.334384	26370.308408
HLA A*0219	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.408017	1.073598	-3.334418	25586.850412
HLA B*5401	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.569701	1.235214	-3.334488	37127.981543
HLA A*6802	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.396229	1.061692	-3.334538	24901.726786
HLA B*0801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.417246	1.082637	-3.334608	26136.390317
HLA B*0803	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.453331	1.118640	-3.334691	28400.850605
HLA A*2403	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.349689	1.014988	-3.334701	22371.160594
HLA A*0301	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.363849	1.029142	-3.334707	23112.603106
HLA B*1509	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.421491	1.086732	-3.334759	26393.143960
HLA A*6802	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.416799	1.081848	-3.334951	26109.539075
HLA A*0202	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.484319	1.149326	-3.334992	30501.324946
HLA B*5801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.357874	1.022881	-3.334993	22796.812183
HLA A*8001	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.067344	0.732333	-3.335011	11677.338088
HLA B*1517	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.490009	1.154927	-3.335083	30903.605966
HLA B*4501	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.596866	1.261650	-3.335216	39524.472740
HLA A*0202	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.490174	1.154939	-3.335234	30915.311138
HLA A*2603	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.525522	1.190001	-3.335520	33536.800202
HLA B*1801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.510264	1.174655	-3.335609	32379.047429
HLA A*0212	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.421282	1.085412	-3.335870	26380.439245
HLA B*1509	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.449737	1.113773	-3.335964	28166.743267
HLA B*1517	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.462342	1.126330	-3.336012	28996.235768
HLA B*2705	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.252495	0.916314	-3.336181	17885.250197
HLA A*2403	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.405287	1.069099	-3.336187	25426.508525
HLA B*2705	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.353807	1.017549	-3.336258	22584.327484
HLA B*5101	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.497579	1.161199	-3.336380	31446.998388
HLA B*3801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.480985	1.144551	-3.336434	30268.073914
HLA B*7301	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.439655	1.103143	-3.336512	27520.416046
HLA B*5701	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.351566	1.014988	-3.336578	22468.069261
HLA B*4002	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.593060	1.256417	-3.336643	39179.592928
HLA A*3002	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.101801	0.765110	-3.336691	12641.581280
HLA B*3801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.517811	1.181092	-3.336718	32946.600799
HLA B*1509	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.311049	0.974301	-3.336748	20466.750019
HLA A*2402	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.373477	1.036678	-3.336799	23630.725269
HLA B*1503	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-3.960170	0.623337	-3.336833	9123.673736
HLA A*0202	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.575559	1.238694	-3.336865	37632.113129
HLA B*5801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.302259	0.965301	-3.336958	20056.699223
HLA A*3201	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.418820	1.081848	-3.336972	26231.296846
HLA A*0206	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.293054	0.956046	-3.337008	19636.052269
HLA A*8001	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.373703	1.036678	-3.337025	23643.001058
HLA B*4501	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.607533	1.270418	-3.337115	40507.248759
HLA B*3801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.492079	1.154927	-3.337152	31051.247582
HLA B*1517	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.436798	1.099547	-3.337251	27339.969227
HLA A*8001	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.366398	1.029142	-3.337256	23248.666777
HLA B*5301	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.574036	1.236758	-3.337278	37500.420652
HLA B*3501	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-3.911550	0.574191	-3.337358	8157.357649
HLA A*0219	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.406492	1.069099	-3.337393	25497.172041
HLA B*3801	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.470464	1.133041	-3.337423	29543.625671
HLA A*8001	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.407157	1.069720	-3.337437	25536.238074
HLA A*0203	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.379835	1.042359	-3.337475	23979.203730
HLA A*1101	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.440313	1.102823	-3.337490	27562.134707

HLA A*1101	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.460182	1.122659	-3.337524	28852.433294
HLA A*2601	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.225911	0.888375	-3.337535	16823.277051
HLA A*1101	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.440698	1.103143	-3.337555	27586.599286
HLA B*1501	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.360553	1.022974	-3.337579	22937.840796
HLA B*5401	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.387283	1.049687	-3.337595	24393.977841
HLA A*2402	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.469806	1.132158	-3.337648	29498.907781
HLA B*0702	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.460481	1.122659	-3.337822	28872.263341
HLA B*5301	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.598880	1.261014	-3.337865	39708.144512
HLA B*4402	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.387623	1.049687	-3.337936	24413.120812
HLA A*0101	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.380312	1.042359	-3.337952	24005.552337
HLA B*4002	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.573174	1.235214	-3.337960	37426.040080
HLA B*0801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.367180	1.029142	-3.338039	23290.586837
HLA A*0101	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.372822	1.034768	-3.338053	23595.084923
HLA B*0802	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.440957	1.102823	-3.338134	27603.020620
HLA A*2501	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.451177	1.112976	-3.338201	28260.306623
HLA B*0801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.364890	1.026649	-3.338241	23168.060756
HLA A*0101	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.361161	1.022881	-3.338280	22970.002937
HLA A*6802	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.421002	1.082637	-3.338365	26363.461595
HLA A*0101	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.203529	0.865145	-3.338384	15978.257027
HLA B*3801	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.513819	1.175404	-3.338415	32645.162799
HLA B*2705	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.461110	1.122659	-3.338452	28914.154160
HLA B*4002	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.282763	0.944277	-3.338486	19176.239060
HLA A*0206	1:452-460	9	FKQANSPST	0.861933	-0.283110	-3.917320	0.578823	-3.338497	8266.465146
HLA A*8001	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.412427	1.073598	-3.338828	25847.992171
HLA A*2301	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.518553	1.179436	-3.339117	33002.972006
HLA A*2402	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.500337	1.161199	-3.339138	31647.360471
HLA B*3801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.374032	1.034768	-3.339263	23660.914683
HLA A*3001	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.288423	0.949124	-3.339299	19427.787500
HLA B*4001	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.357160	1.017549	-3.339611	22759.351215
HLA B*1503	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.133073	0.793337	-3.339736	13585.419291
HLA B*0803	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.444173	1.104337	-3.339836	27808.211304
HLA A*3301	1:261-269	9	NRYQTAAEM	1.007560	0.246520	-4.593990	1.254080	-3.339910	39263.617973
HLA A*2403	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.232092	0.892112	-3.339980	17064.442021
HLA A*0206	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.355012	1.014994	-3.340019	22647.092215
HLA B*1502	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.549691	1.209597	-3.340093	35456.084665
HLA B*7301	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.578319	1.238104	-3.340216	37872.088069
HLA A*2301	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.535660	1.195398	-3.340262	34328.881326
HLA A*6901	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.377074	1.036678	-3.340396	23827.260485
HLA B*3901	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.463143	1.122659	-3.340484	29049.776588
HLA A*2602	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.483823	1.143250	-3.340573	30466.527955
HLA B*4801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.377286	1.036678	-3.340608	23838.864565
HLA A*0101	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.358170	1.017549	-3.340621	22812.356837
HLA B*1801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.369579	1.028753	-3.340826	23419.588261
HLA A*0216	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.309670	0.968816	-3.340854	20401.858795
HLA A*2602	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.611031	1.270153	-3.340878	40834.865568
HLA A*0202	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.714291	0.373369	-3.340922	5179.542989
HLA A*0301	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.342457	1.001026	-3.341430	22001.728470
HLA B*1503	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.428192	1.086732	-3.341460	26803.521598
HLA B*1517	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.470027	1.128536	-3.341490	29513.912663
HLA B*4001	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.348314	1.006578	-3.341736	22300.472593
HLA B*1503	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.174936	0.833148	-3.341789	14960.157662
HLA A*6802	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.173832	0.831818	-3.342014	14922.167566
HLA B*4601	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.376809	1.034768	-3.342040	23812.698915
HLA B*1509	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.376813	1.034768	-3.342045	23812.956565
HLA B*2705	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.391791	1.049687	-3.342104	24648.544924
HLA B*0702	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.365195	1.022974	-3.342222	23184.360251
HLA A*3001	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.230704	0.888375	-3.342328	17009.969954
HLA B*1503	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.384719	1.042359	-3.342360	24250.424030
HLA B*7301	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.577673	1.235214	-3.342459	37815.786915
HLA A*2403	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.384846	1.042359	-3.342487	24257.509438
HLA A*1101	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.455559	1.112976	-3.342583	28546.880638
HLA B*0702	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.412429	1.069720	-3.342709	25848.132006
HLA B*0802	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.440656	1.097819	-3.342837	27583.913089
HLA B*4501	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.601234	1.258359	-3.342875	39923.975254
HLA A*0206	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.504141	1.161199	-3.342942	31925.764813

HLA A*2403	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.337354	0.994371	-3.342983	21744.714965
HLA A*0206	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.425053	1.081848	-3.343205	26610.494549
HLA A*0250	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.317576	0.974301	-3.343275	20776.661035
HLA B*3901	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.325618	0.982334	-3.343284	21164.988733
HLA B*0803	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.498249	1.154939	-3.343309	31495.521346
HLA A*2501	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.471928	1.128536	-3.343391	29643.366339
HLA A*3101	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.413146	1.069720	-3.343426	25890.817048
HLA A*3201	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.504590	1.161155	-3.343435	31958.770399
HLA B*5401	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.551599	1.208137	-3.343461	35612.179815
HLA A*0206	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.238241	0.894591	-3.343650	17307.753225
HLA B*3901	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.486938	1.143250	-3.343688	30685.865761
HLA A*2403	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.361267	1.017549	-3.343718	22975.595550
HLA A*2301	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.519131	1.175404	-3.343727	33046.922680
HLA B*4501	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.577478	1.233662	-3.343817	37798.810652
HLA A*6901	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.159213	0.815296	-3.343917	14428.241962
HLA A*0203	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.299971	0.956046	-3.343925	19951.293768
HLA B*7301	1:433-441	9	STLTYAEAV	1.049463	0.176908	-4.570303	1.226371	-3.343932	37179.436882
HLA A*2602	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.237733	0.893801	-3.343933	17287.540304
HLA B*1517	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.134995	0.790996	-3.343999	13645.671921
HLA B*4501	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.413829	1.069720	-3.344110	25931.608486
HLA A*0206	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.260410	0.916286	-3.344125	18214.214002
HLA B*3501	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.188356	0.844164	-3.344192	15429.662577
HLA B*4402	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.430934	1.086732	-3.344202	26973.276657
HLA A*3201	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.580629	1.236390	-3.344239	38074.025309
HLA A*0212	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.414095	1.069720	-3.344375	25947.465777
HLA B*1517	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.442315	1.097819	-3.344496	27689.468031
HLA A*0301	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.367382	1.022881	-3.344501	23301.425315
HLA B*0802	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.427207	1.082637	-3.344570	26742.833696
HLA B*1801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.306225	0.961636	-3.344590	20240.693682
HLA B*5301	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.581117	1.236390	-3.344728	38116.892484
HLA B*0802	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.420483	1.075727	-3.344756	26331.960658
HLA A*0212	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.339130	0.994371	-3.344759	21833.830268
HLA A*3201	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.444504	1.099547	-3.344957	27829.431343
HLA B*7301	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.601504	1.256417	-3.345087	39948.821174
HLA A*2403	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.261508	0.916314	-3.345193	18260.288902
HLA B*3901	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.506413	1.161199	-3.345214	32093.217693
HLA B*4001	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.319704	0.974301	-3.345403	20878.744892
HLA B*4402	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.415171	1.069720	-3.345451	26011.836285
HLA B*4601	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.376635	1.031103	-3.345531	23803.167843
HLA B*4403	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.616120	1.270418	-3.345702	41316.175612
HLA A*8001	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.407425	1.061692	-3.345733	25551.991828
HLA B*4002	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.582187	1.236390	-3.345797	38210.832768
HLA A*6901	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.265932	0.920120	-3.345811	18447.253873
HLA A*0212	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.432628	1.086732	-3.345896	27078.692188
HLA B*3901	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.500826	1.154927	-3.345900	31682.991927
HLA B*1801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.382647	1.036678	-3.345969	24134.988214
HLA A*2603	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.603113	1.257069	-3.346045	40097.137123
HLA B*1509	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.382746	1.036678	-3.346068	24140.472676
HLA A*2902	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.275276	0.929186	-3.346090	18848.449332
HLA B*4501	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.356760	1.010656	-3.346104	22738.429491
HLA B*5801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.352750	1.006578	-3.346172	22529.413934
HLA A*0219	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.428838	1.082637	-3.346201	26843.427397
HLA A*0201	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.388608	1.042359	-3.346248	24468.521863
HLA B*3901	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.419884	1.073598	-3.346286	26295.660190
HLA B*4001	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.375434	1.029142	-3.346292	23737.455966
HLA A*2402	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.375164	1.028753	-3.346411	23722.692603
HLA B*5401	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.556048	1.209597	-3.346451	35978.949777
HLA A*0211	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.495808	1.149326	-3.346481	31318.985571
HLA B*1801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.433269	1.086732	-3.346537	27118.714248
HLA A*0219	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.262847	0.916286	-3.346561	18316.683907
HLA B*5101	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.501531	1.154939	-3.346592	31734.454118
HLA B*4501	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.526102	1.179436	-3.346666	33581.643458
HLA A*1101	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.475318	1.128536	-3.346782	29875.681993
HLA A*0203	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.145502	0.798696	-3.346806	13979.827815
HLA A*3201	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.262328	0.915512	-3.346816	18294.797831

HLA B*0801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.361948	1.014994	-3.346954	23011.669514
HLA B*5401	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.496576	1.149326	-3.347250	31374.438948
HLA A*1101	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.451703	1.104337	-3.347366	28294.573650
HLA A*2501	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.030433	0.682948	-3.347486	10725.892623
HLA B*4801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.409382	1.061692	-3.347690	25667.400131
HLA A*2403	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.421343	1.073598	-3.347745	26384.150102
HLA A*2602	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.354333	1.006578	-3.347755	22611.712104
HLA A*0201	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.354348	1.006578	-3.347770	22612.446077
HLA B*4501	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.330134	0.982334	-3.347800	21386.206295
HLA A*8001	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.370954	1.022974	-3.347980	23493.823634
HLA B*5301	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.516793	1.168679	-3.348114	32869.514302
HLA B*3501	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.268246	0.920120	-3.348126	18545.816883
HLA B*7301	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.606675	1.258359	-3.348317	40427.341678
HLA B*5101	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-3.900756	0.552387	-3.348369	7957.121137
HLA B*0803	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.377138	1.028753	-3.348384	23830.741115
HLA A*3101	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.253397	0.904921	-3.348476	17922.443590
HLA B*1517	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.451332	1.102823	-3.348509	28270.398843
HLA A*2403	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.209196	0.860149	-3.349048	16188.117976
HLA B*4801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.364079	1.014988	-3.349091	23124.859943
HLA B*1501	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.202773	0.853416	-3.349357	15950.447383
HLA B*5701	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.423096	1.073598	-3.349497	26490.845812
HLA B*4402	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.376186	1.026649	-3.349537	23778.584998
HLA A*3101	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.378695	1.029142	-3.349553	23916.369654
HLA A*0301	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.364674	1.014994	-3.349680	23156.532655
HLA A*2902	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.418857	1.069099	-3.349758	26233.567479
HLA B*4402	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.254971	0.905205	-3.349766	17987.523614
HLA A*2301	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.544856	1.194908	-3.349948	35063.521872
HLA A*6801	1:578-586	9	LRALGWTGM	0.993924	0.288236	-4.632151	1.282160	-3.349991	42869.720386
HLA B*4501	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.574706	1.224706	-3.350000	37558.284086
HLA B*1509	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.504740	1.154698	-3.350043	31969.837492
HLA B*5701	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.419774	1.069720	-3.350054	26288.974979
HLA A*3002	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.478680	1.128536	-3.350144	30107.863683
HLA B*3501	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.453343	1.103143	-3.350200	28401.618843
HLA A*0201	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.311519	0.961256	-3.350263	20488.906573
HLA B*1517	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.463260	1.112976	-3.350285	29057.635454
HLA B*1517	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.472999	1.122659	-3.350340	29716.584113
HLA B*4403	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.433008	1.082637	-3.350371	27102.434411
HLA A*2902	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.315703	0.965301	-3.350402	20687.271535
HLA A*3001	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.268664	0.918162	-3.350503	18563.684369
HLA B*5701	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.412283	1.061692	-3.350592	25839.463657
HLA B*4601	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.365592	1.014994	-3.350598	23205.566738
HLA A*2603	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.448515	1.097819	-3.350696	28087.617556
HLA B*4002	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.530174	1.179436	-3.350737	33897.963197
HLA A*1101	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.448719	1.097819	-3.350900	28100.840396
HLA B*0802	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.473621	1.122659	-3.350963	29759.216973
HLA A*0206	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-3.875109	0.524138	-3.350971	7500.824279
HLA B*4402	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.373900	1.022881	-3.351019	23653.747605
HLA B*4801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.267588	0.916314	-3.351274	18517.745521
HLA A*2501	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.470029	1.118640	-3.351389	29514.072330
HLA A*2602	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.546907	1.195398	-3.351509	35229.512702
HLA B*5801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.362352	1.010656	-3.351696	23033.091859
HLA B*4801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.135451	0.783751	-3.351700	13660.000824
HLA A*2301	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.438473	1.086732	-3.351742	27445.629998
HLA B*5301	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.576529	1.224706	-3.351823	37716.287965
HLA A*3201	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.145192	0.793337	-3.351855	13969.848308
HLA B*1509	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.472231	1.120342	-3.351889	29664.060944
HLA A*6802	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.337253	0.985326	-3.351926	21739.657184
HLA A*0202	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.884963	0.532852	-3.352111	7672.956419
HLA B*7301	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.527526	1.175404	-3.352122	33691.917939
HLA B*0801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.246732	0.894591	-3.352141	17649.472633
HLA A*0206	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.501496	1.149326	-3.352169	31731.879025
HLA B*1503	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.122289	0.770046	-3.352243	13252.228348
HLA B*4002	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.622725	1.270418	-3.352306	41949.280567
HLA B*5101	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.367397	1.014988	-3.352409	23302.181676
HLA B*7301	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.475111	1.122659	-3.352452	29861.462455

HLA A*6801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.450453	1.097819	-3.352634	28213.257213
HLA B*1509	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.367648	1.014994	-3.352654	23315.674238
HLA A*2501	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.439530	1.086732	-3.352799	27512.526410
HLA B*0803	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.481361	1.128536	-3.352824	30294.284764
HLA B*1501	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.267708	0.914880	-3.352828	18522.855353
HLA A*8001	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.347215	0.994371	-3.352844	22244.083043
HLA A*3201	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.559176	1.206278	-3.352897	36238.953415
HLA A*0216	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.160882	0.807959	-3.352923	14483.767716
HLA B*5401	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.534100	1.181092	-3.353007	34205.787492
HLA B*3801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.514387	1.161155	-3.353232	32687.929612
HLA B*0801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.376376	1.022881	-3.353495	23789.007082
HLA A*3201	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.592193	1.238694	-3.353499	39101.458715
HLA A*1101	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.496750	1.143250	-3.353500	31387.001648
HLA A*0219	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.327871	0.974301	-3.353570	21275.079799
HLA A*3201	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.587257	1.233662	-3.353595	38659.540827
HLA A*2402	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.559888	1.206278	-3.353609	36298.404890
HLA A*3001	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.100302	0.746693	-3.353610	12598.023957
HLA A*0101	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.337737	0.984065	-3.353672	21763.898171
HLA A*0101	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-3.485903	0.132177	-3.353726	3061.277531
HLA B*3501	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.439145	1.085412	-3.353734	27488.127522
HLA A*3301	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.610907	1.257069	-3.353838	40823.158905
HLA B*5801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.348274	0.994371	-3.353903	22298.421754
HLA B*1801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.508854	1.154939	-3.353915	32274.117584
HLA A*0216	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.436594	1.082637	-3.353956	27327.104415
HLA A*0250	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.314954	0.960920	-3.354034	20651.601168
HLA A*0216	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.423822	1.069720	-3.354102	26535.166420
HLA B*1509	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.529614	1.175404	-3.354210	33854.345838
HLA A*8001	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.439676	1.085412	-3.354265	27521.756021
HLA B*1801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.482810	1.128536	-3.354274	30395.573057
HLA A*0101	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.365254	1.010656	-3.354597	23187.496083
HLA B*3501	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.248510	0.893801	-3.354710	17721.900478
HLA A*0202	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.087761	0.733042	-3.354719	12239.421154
HLA A*0203	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.259323	0.904590	-3.354733	18168.648516
HLA B*3501	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.246938	0.892112	-3.354826	17657.877022
HLA B*3901	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.271204	0.916314	-3.354890	18672.564529
HLA B*0801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.389782	1.034768	-3.355014	24534.797453
HLA A*2402	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.516175	1.161155	-3.355020	32822.780783
HLA B*1501	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.316394	0.961256	-3.355138	20720.200974
HLA B*1502	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.504520	1.149326	-3.355193	31953.584017
HLA B*0702	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.391874	1.036678	-3.355196	24653.212473
HLA A*6901	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.259882	0.904590	-3.355292	18192.056692
HLA A*3101	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.390189	1.034768	-3.355420	24557.770585
HLA A*2602	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.475823	1.120342	-3.355481	29910.451397
HLA A*0211	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.458641	1.103143	-3.355498	28750.220738
HLA A*3201	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.474160	1.118640	-3.355519	29796.107461
HLA B*4501	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.592172	1.236390	-3.355782	39099.554950
HLA B*3901	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.458949	1.103143	-3.355806	28770.603111
HLA B*5701	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.370843	1.014994	-3.355849	23487.850741
HLA B*1503	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.429517	1.073598	-3.355919	26885.428792
HLA A*3002	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.405627	1.049687	-3.355940	25446.461766
HLA A*0219	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.185485	0.829510	-3.355976	15327.995285
HLA A*6802	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.378883	1.022881	-3.356002	23926.722686
HLA B*4601	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.371095	1.014988	-3.356107	23501.450810
HLA B*1501	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.129995	0.773768	-3.356227	13489.480397
HLA A*2603	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.253653	0.897363	-3.356291	17933.015175
HLA B*4402	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.429966	1.073598	-3.356367	26913.223563
HLA A*2403	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.438332	1.081848	-3.356485	27436.722775
HLA A*2601	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.342055	0.985326	-3.356729	21981.384280
HLA B*3501	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.340817	0.984065	-3.356752	21918.804349
HLA A*0101	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.363341	1.006578	-3.356763	23085.610969
HLA B*1509	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.425866	1.069099	-3.356767	26660.351295
HLA B*1503	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.312499	0.955683	-3.356815	20535.180159
HLA A*0211	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.532366	1.175404	-3.356962	34069.493205
HLA A*2501	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.438854	1.081848	-3.357006	27469.693948
HLA B*3901	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.443748	1.086732	-3.357016	27780.995111

HLA B*4801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.391787	1.034768	-3.357018	24648.278234
HLA A*0219	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.322376	0.965301	-3.357075	21007.566757
HLA A*2601	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.388218	1.031103	-3.357114	24446.557976
HLA B*4001	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.353105	0.995952	-3.357153	22547.825580
HLA B*5401	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.424412	1.067242	-3.357170	26571.222524
HLA A*2501	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.460399	1.103143	-3.357256	28866.797007
HLA B*0801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.388396	1.031103	-3.357293	24456.611283
HLA A*0301	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.368057	1.010656	-3.357400	23337.632098
HLA B*3501	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.427142	1.069720	-3.357422	26738.783081
HLA B*4501	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.532126	1.174655	-3.357471	34050.698549
HLA A*2902	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.222640	0.865145	-3.357495	16697.064082
HLA A*3101	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.364154	1.006578	-3.357576	23128.863584
HLA B*2705	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.444309	1.086732	-3.357578	27816.938155
HLA A*8001	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.444321	1.086732	-3.357589	27817.690598
HLA B*7301	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.619252	1.261650	-3.357602	41615.199238
HLA B*0803	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.190772	0.833148	-3.357624	15515.711632
HLA B*4501	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.144524	0.786863	-3.357661	13948.401394
HLA A*2603	1:569-577	9	MFWVDAEPR	0.471442	0.798976	-4.628084	1.270418	-3.357666	42470.139973
HLA A*0203	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.372721	1.014994	-3.357727	23589.596749
HLA B*4001	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.368513	1.010656	-3.357856	23362.138232
HLA A*1101	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.439965	1.081848	-3.358117	27540.075542
HLA A*2403	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.354091	0.995952	-3.358140	22599.115947
HLA B*5301	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.513314	1.154927	-3.358387	32607.214430
HLA A*6801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.319338	0.960920	-3.358418	20861.131860
HLA B*4001	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.400968	1.042359	-3.358609	25174.935998
HLA B*4403	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.619626	1.261014	-3.358611	41651.010883
HLA B*1801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.519779	1.161155	-3.358624	33096.302869
HLA A*0301	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.265896	0.907250	-3.358646	18445.756970
HLA B*5101	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.420523	1.061692	-3.358831	26334.382470
HLA A*2603	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.155971	0.796898	-3.359073	14320.926887
HLA B*5101	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.428800	1.069720	-3.359081	26841.103978
HLA A*0212	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.420777	1.061692	-3.359085	26349.773303
HLA A*2602	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.508424	1.149326	-3.359098	32242.181705
HLA A*0250	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.594364	1.235214	-3.359150	39297.405982
HLA A*2602	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.520513	1.161199	-3.359313	33152.212807
HLA A*2301	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.435128	1.075727	-3.359400	27235.009905
HLA A*6901	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.264339	0.904921	-3.359418	18379.715040
HLA A*2603	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.479852	1.120342	-3.359511	30189.250709
HLA A*3002	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.288893	0.929186	-3.359708	19448.819311
HLA B*4402	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.390835	1.031103	-3.359732	24594.332850
HLA B*1509	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.320745	0.960920	-3.359825	20928.842500
HLA A*6801	1:33-41	9	LHRDVAVKV	1.051447	0.218706	-4.629989	1.270153	-3.359836	42656.883680
HLA A*0216	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.234895	0.875034	-3.359861	17174.932059
HLA B*4601	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.377600	1.017549	-3.360052	23856.152222
HLA A*3101	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.143909	0.783751	-3.360158	13928.645061
HLA A*3001	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.208026	0.847787	-3.360239	16144.563862
HLA A*0211	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.259149	0.898882	-3.360267	18161.376484
HLA A*0301	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.366983	1.006578	-3.360405	23280.005284
HLA B*5801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.361483	1.001026	-3.360457	22987.033576
HLA B*4601	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.403083	1.042359	-3.360724	25297.809135
HLA B*1501	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.389968	1.029142	-3.360826	24545.285407
HLA A*2601	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.356901	0.995952	-3.360950	22745.811432
HLA B*5101	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.489591	1.128536	-3.361055	30873.861345
HLA B*3901	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.147936	0.786863	-3.361072	14058.399767
HLA A*2602	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.586007	1.224706	-3.361301	38548.436269
HLA B*4001	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.376296	1.014988	-3.361309	23784.631824
HLA A*3002	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.343700	0.982334	-3.361366	22064.783891
HLA A*6801	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.551378	1.190001	-3.361376	35594.074572
HLA A*0202	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.431133	1.069720	-3.361414	26985.682916
HLA A*0101	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.249535	0.887960	-3.361575	17763.750668
HLA B*5701	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.390720	1.029142	-3.361578	24587.814135
HLA B*0803	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.487991	1.126330	-3.361661	30760.327153
HLA A*0203	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.384607	1.022881	-3.361725	24244.127626
HLA A*0216	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.255573	0.893801	-3.361772	18012.452362
HLA B*4801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.379348	1.017549	-3.361800	23952.365720

HLA A*2601	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.376795	1.014994	-3.361801	23811.925983
HLA B*4402	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.357785	0.995952	-3.361833	22792.126192
HLA A*6802	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.306409	0.944464	-3.361945	20249.236477
HLA A*3101	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.404368	1.042359	-3.362009	25372.781523
HLA A*0211	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.270090	0.908065	-3.362025	18624.744045
HLA B*0802	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.431157	1.069099	-3.362058	26987.142851
HLA B*3801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.480766	1.118640	-3.362126	30252.849280
HLA B*1501	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.259600	0.897363	-3.362237	18180.250483
HLA A*0301	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.358196	0.995952	-3.362244	22813.714413
HLA B*7301	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.572018	1.209597	-3.362421	37326.556936
HLA A*3002	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.505701	1.143250	-3.362451	32040.653699
HLA B*5301	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.601175	1.238694	-3.362481	39918.576012
HLA A*8001	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.445235	1.082637	-3.362598	27876.293091
HLA A*6901	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.393744	1.031103	-3.362640	24759.604818
HLA A*3002	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.318699	0.956046	-3.362653	20830.457491
HLA A*6802	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.257286	0.894591	-3.362695	18083.630301
HLA A*0206	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.053317	0.690572	-3.362746	11306.219922
HLA A*1101	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.358703	0.995952	-3.362752	22840.388643
HLA A*0101	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.358793	0.995952	-3.362841	22845.084556
HLA A*0216	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.399528	1.036678	-3.362850	25091.587592
HLA A*2601	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-3.937474	0.574537	-3.362936	8659.119264
HLA A*0206	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.495989	1.133041	-3.362948	31332.034571
HLA A*6901	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.347111	0.984065	-3.363046	22238.788801
HLA A*0216	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.424743	1.061692	-3.363051	26591.498635
HLA A*2601	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.305335	0.942253	-3.363082	20199.235732
HLA A*0250	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.345553	0.982334	-3.363220	22159.166558
HLA B*1801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.386214	1.022974	-3.363240	24334.005916
HLA B*4001	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.386247	1.022974	-3.363273	24335.849006
HLA A*2902	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.433053	1.069720	-3.363333	27105.220357
HLA B*0803	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.466620	1.103143	-3.363477	29283.301199
HLA B*4601	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.386524	1.022974	-3.363550	24351.389166
HLA B*1517	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.425419	1.061692	-3.363728	26632.961761
HLA B*5301	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.439479	1.075727	-3.363752	27509.252131
HLA B*5401	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.539266	1.175404	-3.363862	34615.141463
HLA A*2601	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.393051	1.029142	-3.363909	24720.122050
HLA A*0212	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.313119	0.949124	-3.363995	20564.529678
HLA A*0211	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.518924	1.154927	-3.363998	33031.193768
HLA A*0211	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.320078	0.956046	-3.364032	20896.711937
HLA B*3901	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.256170	0.892112	-3.364057	18037.220500
HLA B*5301	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.599335	1.235214	-3.364122	39749.840820
HLA B*4403	1:32-40	9	RLHRDVAVK	0.951924	0.351146	-4.667245	1.303070	-3.364174	46477.729963
HLA B*4402	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.446083	1.081848	-3.364235	27930.787851
HLA A*0101	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.325543	0.961256	-3.364287	21161.325042
HLA B*3501	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.054882	0.690572	-3.364310	11347.029550
HLA A*0202	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.539776	1.175404	-3.364372	34655.801630
HLA A*0202	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-3.744778	0.380356	-3.364422	5556.206259
HLA B*7301	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.600823	1.236390	-3.364433	39886.195891
HLA B*0803	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.461977	1.097502	-3.364475	28971.931664
HLA B*5801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.348551	0.984065	-3.364486	22312.660874
HLA A*2601	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.391162	1.026649	-3.364513	24612.834118
HLA B*0802	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.426225	1.061692	-3.364533	26682.427551
HLA A*3002	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.282864	0.918327	-3.364537	19180.700456
HLA B*5701	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.382187	1.017549	-3.364638	24109.410525
HLA A*2403	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.434430	1.069720	-3.364710	27191.285541
HLA A*6901	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.365757	1.001026	-3.364730	23214.356170
HLA A*0211	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.258604	0.893801	-3.364803	18138.596543
HLA A*6802	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.263693	0.898882	-3.364811	18352.391509
HLA B*2705	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-3.773696	0.408739	-3.364957	5938.760630
HLA B*4002	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.257114	0.892112	-3.365002	18076.490089
HLA A*0211	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.498148	1.133041	-3.365107	31488.195545
HLA A*3001	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.264062	0.898882	-3.365179	18367.985782
HLA A*3301	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.485637	1.120342	-3.365295	30594.035490
HLA A*1101	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.432578	1.067242	-3.365337	27075.616016
HLA B*4002	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.590107	1.224706	-3.365401	38914.066503
HLA A*0212	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.407772	1.042359	-3.365413	25572.458570

HLA B*1517	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.097507	0.732039	-3.365468	12517.181303
HLA A*0201	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.396575	1.031103	-3.365472	24921.537853
HLA A*0219	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.400383	1.034768	-3.365615	25141.046619
HLA B*1509	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.360106	0.994371	-3.365735	22914.275585
HLA A*2501	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.326692	0.960920	-3.365772	21217.380081
HLA B*3901	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.327580	0.961636	-3.365944	21260.812703
HLA A*0211	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.041199	0.675193	-3.366006	10995.089913
HLA B*0803	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.427809	1.061692	-3.366117	26779.896351
HLA B*2705	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.401018	1.034768	-3.366249	25177.796226
HLA B*1503	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.494828	1.128536	-3.366292	31248.411961
HLA A*2601	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.377001	1.010656	-3.366345	23823.264832
HLA A*6801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.120889	0.754459	-3.366430	13209.568080
HLA B*5701	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.393084	1.026649	-3.366435	24721.994385
HLA A*0101	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.381501	1.014994	-3.366507	24071.355253
HLA A*2602	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.541977	1.175404	-3.366573	34831.920181
HLA B*1502	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.381738	1.014994	-3.366744	24084.511407
HLA A*3101	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.381740	1.014994	-3.366746	24084.641702
HLA B*4403	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.601967	1.235214	-3.366753	39991.419252
HLA A*3101	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.389813	1.022881	-3.366932	24536.523011
HLA B*5401	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.546376	1.179436	-3.366939	35186.466190
HLA A*3201	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.398203	1.031103	-3.367100	25015.145384
HLA B*1517	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.062697	0.695361	-3.367335	11553.047873
HLA B*4001	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.398607	1.031103	-3.367504	25038.432832
HLA B*1501	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.289112	0.921444	-3.367667	19458.606857
HLA A*2902	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.454473	1.086732	-3.367742	28475.620545
HLA A*2301	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.542483	1.174655	-3.367828	34872.457669
HLA A*2602	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.562937	1.194908	-3.368029	36554.190617
HLA B*7301	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.260192	0.892112	-3.368080	18205.052377
HLA A*2601	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.374739	1.006578	-3.368161	23699.474951
HLA A*2403	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.353509	0.985326	-3.368182	22568.816117
HLA B*4002	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.634549	1.266360	-3.368189	43107.166312
HLA B*3801	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.467825	1.099547	-3.368278	29364.683234
HLA B*5401	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.537008	1.168679	-3.368329	34435.647674
HLA B*1801	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.529567	1.161199	-3.368368	33850.683071
HLA A*0301	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.312867	0.944464	-3.368403	20552.629177
HLA A*8001	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.450289	1.081848	-3.368441	28202.575094
HLA A*0219	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.450298	1.081848	-3.368450	28203.185392
HLA B*1517	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.437590	1.069099	-3.368491	27389.859081
HLA B*7301	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.386115	1.017549	-3.368566	24328.477485
HLA B*1501	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.263286	0.894591	-3.368696	18335.223343
HLA B*1503	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.263300	0.894591	-3.368710	18335.818502
HLA B*5101	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.437825	1.069099	-3.368725	27404.680700
HLA B*2705	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.435969	1.067242	-3.368727	27287.808159
HLA A*2902	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.395419	1.026649	-3.368770	24855.293256
HLA A*0211	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.051795	0.682948	-3.368847	11266.654136
HLA B*5801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.354373	0.985326	-3.369047	22613.791756
HLA A*3201	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.593849	1.224706	-3.369144	39250.875332
HLA A*2501	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.379832	1.010656	-3.369176	23979.074006
HLA A*3001	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.209098	0.839877	-3.369221	16184.440205
HLA A*6801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.266658	0.897363	-3.369295	18478.117120
HLA B*4001	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.392287	1.022881	-3.369406	24676.696973
HLA B*4601	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.376010	1.006578	-3.369432	23768.938992
HLA A*3101	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.380119	1.010656	-3.369463	23994.905574
HLA A*2301	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.483424	1.113773	-3.369651	30438.521344
HLA B*4403	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.631326	1.261650	-3.369676	42788.393553
HLA A*0216	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.242968	0.873256	-3.369712	17497.171886
HLA B*3801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.419520	1.049687	-3.369833	26273.619658
HLA B*0702	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.467701	1.097819	-3.369882	29356.264878
HLA A*2602	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.605101	1.235214	-3.369887	40281.072940
HLA B*1502	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.355226	0.985326	-3.369900	22658.244122
HLA B*3501	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.451919	1.081848	-3.370072	28308.659641
HLA A*0301	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.364479	0.994371	-3.370108	23146.137224
HLA A*2601	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.393029	1.022881	-3.370148	24718.918482
HLA B*1517	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.399439	1.029142	-3.370297	25086.429899
HLA A*6802	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.439408	1.069099	-3.370309	27504.787833

HLA B*5701	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.412671	1.042359	-3.370312	25862.539079
HLA A*2501	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.432043	1.061692	-3.370351	27042.240057
HLA A*0212	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.339250	0.968816	-3.370434	21839.855148
HLA B*3901	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.393410	1.022974	-3.370437	24740.591688
HLA B*0803	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.457250	1.086732	-3.370519	28658.291006
HLA B*4501	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.626963	1.256417	-3.370546	42360.686333
HLA B*3501	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.154416	0.783751	-3.370665	14269.730415
HLA B*4002	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.620248	1.249564	-3.370685	41710.765453
HLA B*4002	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.608942	1.238104	-3.370839	40638.946219
HLA A*6901	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.317120	0.946270	-3.370850	20754.866983
HLA B*4403	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.595560	1.224706	-3.370854	39405.765762
HLA B*5401	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.491299	1.120342	-3.370957	30995.527012
HLA A*0101	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.259370	0.888375	-3.370994	18170.614430
HLA B*1509	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.444662	1.073598	-3.371063	27839.520299
HLA A*6802	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.326976	0.955683	-3.371293	21231.273452
HLA A*0216	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.315785	0.944464	-3.371321	20691.188960
HLA B*4801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.400510	1.029142	-3.371368	25148.392246
HLA A*6802	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.300671	0.929186	-3.371486	19983.484126
HLA A*0202	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.454133	1.082637	-3.371495	28453.292061
HLA B*1502	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-3.945753	0.574191	-3.371562	8825.784245
HLA A*0203	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.345967	0.974301	-3.371666	22180.275246
HLA B*2705	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.158551	0.786863	-3.371687	14406.247181
HLA B*5101	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.474994	1.103143	-3.371851	29853.386187
HLA A*0201	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.366281	0.994371	-3.371910	23242.378992
HLA A*3001	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-3.860251	0.488312	-3.371939	7248.545148
HLA B*4403	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.561950	1.190001	-3.371949	36471.228174
HLA B*4801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.165294	0.793337	-3.371957	14631.669544
HLA A*0211	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.201523	0.829510	-3.372013	15904.607019
HLA A*3101	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.400809	1.028753	-3.372055	25165.676535
HLA B*4001	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.398779	1.026649	-3.372130	25048.323011
HLA B*0803	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.441253	1.069099	-3.372153	27621.842524
HLA B*1801	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.421919	1.049687	-3.372231	26419.143443
HLA B*0803	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.422010	1.049687	-3.372323	26424.718092
HLA B*1517	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.454189	1.081848	-3.372341	28456.986601
HLA B*4501	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.610463	1.238104	-3.372359	40781.439821
HLA B*4601	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.225803	0.853416	-3.372387	16819.091017
HLA A*0211	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.533700	1.161199	-3.372501	34174.343535
HLA B*3801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.527305	1.154698	-3.372607	33674.788958
HLA A*2301	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.527366	1.154698	-3.372668	33679.525890
HLA A*0212	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.402047	1.029142	-3.372905	25237.526544
HLA B*1503	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.334182	0.961256	-3.372926	21586.484204
HLA B*1517	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.246539	0.873492	-3.373047	17641.644871
HLA B*4002	1:79-87	9	EAETPAGPL	0.986891	0.274759	-4.634857	1.261650	-3.373207	43137.726994
HLA A*3002	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.217373	0.844164	-3.373208	16495.769087
HLA A*2603	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.608426	1.235214	-3.373212	40590.607508
HLA B*3801	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.402117	1.028753	-3.373364	25241.622843
HLA B*4601	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.410068	1.036678	-3.373390	25707.978648
HLA B*5801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.355745	0.982334	-3.373412	22685.350190
HLA B*5701	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.410106	1.036678	-3.373428	25710.203981
HLA B*1501	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.384228	1.010656	-3.373572	24223.020375
HLA A*0101	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.367972	0.994371	-3.373602	23333.087397
HLA A*2602	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.262116	0.888375	-3.373741	18285.892445
HLA A*2402	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.568665	1.194908	-3.373757	37039.508628
HLA A*3101	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-3.985779	0.612002	-3.373778	9677.855491
HLA B*3801	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.506091	1.132158	-3.373933	32069.440463
HLA B*1501	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.221771	0.847787	-3.373984	16663.675681
HLA A*0201	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.389134	1.014994	-3.374140	24498.191162
HLA B*4501	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.640508	1.266360	-3.374148	43702.649690
HLA A*3301	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.632534	1.258359	-3.374175	42907.540090
HLA B*1503	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.282286	0.908065	-3.374222	19155.191130
HLA B*5801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.348627	0.974301	-3.374326	22316.523897
HLA B*5701	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.397320	1.022974	-3.374346	24964.313335
HLA B*7301	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.580695	1.206278	-3.374416	38079.793081
HLA B*5701	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.409286	1.034768	-3.374517	25661.707593
HLA B*1503	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.456466	1.081848	-3.374618	28606.555010

HLA B*5101	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.370587	0.995952	-3.374635	23474.004557
HLA B*3901	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.443767	1.069099	-3.374667	27782.197473
HLA B*0702	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.401488	1.026649	-3.374839	25205.052786
HLA B*0801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.214859	0.839877	-3.374982	16400.557820
HLA B*4402	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.409894	1.034768	-3.375126	25697.688986
HLA B*5401	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-3.295895	-0.079239	-3.375134	1976.492419
HLA B*1801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.488285	1.112976	-3.375309	30781.135433
HLA A*2501	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.369737	0.994371	-3.375366	23428.078524
HLA A*0219	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.412051	1.036678	-3.375373	25825.628288
HLA A*0211	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.324655	0.949124	-3.375531	21118.095658
HLA A*0219	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.264080	0.888375	-3.375705	18368.780750
HLA A*1101	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.458481	1.082637	-3.375844	28739.646269
HLA A*0250	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.058872	0.682948	-3.375924	11451.743484
HLA B*4403	1:435-443	9	LTYAEAVKK	0.985875	0.280485	-4.642352	1.266360	-3.375992	43888.639132
HLA A*2603	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.614870	1.238694	-3.376176	41197.436090
HLA A*2902	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.449824	1.073598	-3.376225	28172.381853
HLA A*0219	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.249483	0.873256	-3.376227	17761.636595
HLA A*2301	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.508427	1.132158	-3.376269	32242.356132
HLA B*7301	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.480651	1.104337	-3.376314	30244.830780
HLA A*2602	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.612723	1.236390	-3.376333	40994.232452
HLA A*0203	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.208186	0.831818	-3.376368	16150.504095
HLA A*0216	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.331045	0.954621	-3.376424	21431.143879
HLA A*0219	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.270330	0.893801	-3.376529	18635.024177
HLA A*0212	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.251612	0.875034	-3.376578	17848.906459
HLA B*5101	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.399606	1.022974	-3.376632	25096.067501
HLA B*4801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.407808	1.031103	-3.376704	25574.533817
HLA A*2501	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.462226	1.085412	-3.376815	28988.550332
HLA B*4001	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.268956	0.892112	-3.376843	18576.141554
HLA A*3002	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.499562	1.122659	-3.376903	31590.911999
HLA B*4402	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.405693	1.028753	-3.376940	25450.316609
HLA A*8001	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.391960	1.014988	-3.376973	24658.147699
HLA B*1501	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.285066	0.908065	-3.377001	19278.175540
HLA A*0203	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.000393	0.623337	-3.377056	10009.051634
HLA B*4601	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.399982	1.022881	-3.377100	25117.799616
HLA A*0212	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.293472	0.916286	-3.377187	19654.970115
HLA A*0211	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.331879	0.954621	-3.377258	21472.342167
HLA B*1509	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-3.772385	0.395099	-3.377286	5920.860217
HLA B*1801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.462889	1.085412	-3.377477	29032.808690
HLA B*5101	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.481838	1.104337	-3.377501	30327.572450
HLA B*1801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.251224	0.873492	-3.377732	17832.981068
HLA A*0219	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.447514	1.069720	-3.377794	28022.961007
HLA A*0201	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.293385	0.915512	-3.377874	19651.036254
HLA B*4403	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.611539	1.233662	-3.377877	40882.610471
HLA B*7301	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.392874	1.014988	-3.377886	24710.094101
HLA A*0202	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.164843	0.786863	-3.377979	14616.479538
HLA A*6802	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.409083	1.031103	-3.377980	25649.771249
HLA B*3801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.533007	1.154939	-3.378068	34119.847606
HLA A*2603	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.586300	1.208137	-3.378163	38574.512931
HLA B*5101	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.412977	1.034768	-3.378208	25880.734228
HLA A*2501	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.363553	0.985326	-3.378227	23096.853860
HLA A*3301	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.614988	1.236758	-3.378229	41208.581275
HLA A*2902	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.401192	1.022881	-3.378310	25187.877716
HLA B*1503	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.231869	0.853416	-3.378453	17055.674184
HLA A*3001	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.275908	0.897363	-3.378545	18875.898698
HLA A*2301	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.539795	1.161155	-3.378640	34657.301534
HLA A*0206	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.251832	0.873123	-3.378710	17857.985464
HLA A*8001	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.413482	1.034768	-3.378713	25910.854300
HLA A*2603	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.413517	1.034768	-3.378749	25912.957008
HLA B*0702	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.413557	1.034768	-3.378788	25915.340284
HLA A*6901	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.169875	0.790996	-3.378880	14786.840209
HLA B*5701	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.375032	0.995952	-3.379081	23715.506812
HLA B*4002	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.588716	1.209597	-3.379118	38789.637556
HLA A*0301	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.272943	0.893801	-3.379142	18747.466571
HLA A*0206	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.421543	1.042359	-3.379184	26396.285395
HLA B*1501	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.364615	0.985326	-3.379289	23153.401010

HLA A*3301	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.635720	1.256417	-3.379303	43223.458981
HLA A*0211	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.386056	1.006578	-3.379478	24325.187348
HLA B*5101	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.465074	1.085412	-3.379662	29179.246537
HLA A*2601	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.345018	0.965301	-3.379717	22131.851079
HLA A*2403	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.341101	0.961256	-3.379845	21933.157021
HLA A*2403	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.410996	1.031103	-3.379893	25762.972925
HLA B*4501	1:314-322	9	RQDLDDTDR	0.591891	0.643323	-4.615258	1.235214	-3.380044	41234.226645
HLA A*0201	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.274136	0.894030	-3.380106	18799.059664
HLA B*5301	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.447389	1.067242	-3.380148	28014.927300
HLA A*2301	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.482972	1.102823	-3.380150	30406.921306
HLA A*2301	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.416919	1.036678	-3.380241	26116.743804
HLA A*3301	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.408999	1.028753	-3.380246	25644.776288
HLA A*0219	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.391000	1.010656	-3.380343	24603.648296
HLA B*1503	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.162052	0.781690	-3.380361	14522.841405
HLA B*5401	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.541566	1.161199	-3.380367	34798.959341
HLA B*0802	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.465798	1.085412	-3.380386	29227.906864
HLA A*0212	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.268434	0.887960	-3.380474	18553.845085
HLA B*1502	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.403473	1.022974	-3.380499	25320.537824
HLA A*2902	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.442202	1.061692	-3.380510	27682.278711
HLA B*1509	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.403581	1.022974	-3.380607	25326.839748
HLA A*0203	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.411760	1.031103	-3.380656	25808.309588
HLA B*5701	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.411771	1.031103	-3.380668	25809.007698
HLA A*0206	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-3.997202	0.616515	-3.380687	9935.788289
HLA B*3801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.555478	1.174655	-3.380823	35931.682815
HLA A*0203	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.254417	0.873492	-3.380925	17964.572988
HLA B*0802	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.404009	1.022974	-3.381035	25351.788830
HLA A*2902	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.154951	0.773768	-3.381183	14287.342341
HLA A*0203	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.162940	0.781690	-3.381250	14552.570103
HLA B*0702	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.391925	1.010656	-3.381269	24656.146812
HLA B*5401	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.524540	1.143250	-3.381289	33461.047989
HLA A*3002	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.542520	1.161199	-3.381321	34875.476298
HLA B*5401	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.310640	0.929186	-3.381454	20447.493308
HLA A*2902	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.323715	0.942253	-3.381462	21072.446445
HLA A*3002	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.365536	0.984065	-3.381471	23202.553984
HLA A*0301	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.366863	0.985326	-3.381537	23273.583116
HLA B*4601	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.365613	0.984065	-3.381548	23206.696621
HLA A*2301	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.536503	1.154927	-3.381577	34395.617955
HLA A*2402	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.556399	1.174655	-3.381744	36007.963146
HLA A*0201	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.392545	1.010656	-3.381889	24691.386145
HLA A*3101	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.235757	0.853416	-3.382341	17209.065546
HLA B*5801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.351166	0.968816	-3.382351	22447.415300
HLA A*3301	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.572791	1.190001	-3.382789	37393.051898
HLA B*4002	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.621536	1.238694	-3.382842	41834.605470
HLA A*2403	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.397855	1.014994	-3.382861	24995.124683
HLA B*4402	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.425271	1.042359	-3.382912	26623.886181
HLA B*2705	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.465708	1.082637	-3.383071	29221.898932
HLA B*0803	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.409772	1.026649	-3.383123	25690.460877
HLA A*0301	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.223007	0.839877	-3.383130	16711.161396
HLA A*0216	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.299461	0.916314	-3.383147	19927.885770
HLA B*0802	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.377633	0.994371	-3.383263	23857.959119
HLA A*2601	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.365616	0.982334	-3.383282	23206.822167
HLA B*1503	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.280651	0.897363	-3.383289	19083.202032
HLA B*0802	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.325550	0.942253	-3.383297	21161.668486
HLA B*3501	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.412514	1.029142	-3.383372	25853.166576
HLA A*0201	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.198774	0.815296	-3.383478	15804.255617
HLA B*5301	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.591676	1.208137	-3.383539	39054.948795
HLA B*4601	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.394235	1.010656	-3.383578	24787.615514
HLA B*0801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.288595	0.904921	-3.383674	19435.461474
HLA A*2402	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.481293	1.097502	-3.383790	30289.532364
HLA B*4002	1:325-333	9	SIGSVGRWV	1.060463	0.200551	-4.644814	1.261014	-3.383800	44138.175284
HLA B*5101	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.483508	1.099547	-3.383961	30444.450007
HLA B*4001	1:414-422	9	DEITVNVST	1.070685	-0.486156	-3.968562	0.584529	-3.384033	9301.695254
HLA A*0212	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.415155	1.031103	-3.384051	26010.851256
HLA A*3201	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.302250	0.918162	-3.384088	20056.265209
HLA A*2501	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.453855	1.069720	-3.384136	28435.134217

HLA B*0801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.385330	1.001026	-3.384304	24284.557977
HLA B*4601	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.378712	0.994371	-3.384341	23917.275365
HLA A*0212	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.288950	0.904590	-3.384360	19451.344658
HLA B*3501	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.421047	1.036678	-3.384369	26366.171579
HLA B*5801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.345349	0.960920	-3.384429	22148.739571
HLA A*0250	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.565651	1.181092	-3.384558	36783.311701
HLA A*3301	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.471314	1.086732	-3.384583	29601.540003
HLA B*4501	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.634221	1.249564	-3.384657	43074.529974
HLA A*1101	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.149792	0.765110	-3.384682	14118.611306
HLA B*5701	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.407704	1.022881	-3.384823	25568.446904
HLA A*0219	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.446701	1.061692	-3.385009	27970.556084
HLA A*3001	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.258604	0.873492	-3.385112	18138.596543
HLA B*0801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.346249	0.960920	-3.385329	22194.679060
HLA A*3002	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.284232	0.898882	-3.385350	19241.187128
HLA B*2705	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.369443	0.984065	-3.385378	23412.240966
HLA B*2705	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.412051	1.026649	-3.385402	25825.628288
HLA B*1509	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.412126	1.026649	-3.385477	25830.099516
HLA B*1502	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.482989	1.097502	-3.385487	30408.072814
HLA B*5801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.327775	0.942253	-3.385522	21270.361394
HLA B*1503	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.408553	1.022974	-3.385579	25618.430105
HLA B*5301	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.581063	1.195398	-3.385665	38112.149992
HLA A*0201	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.002362	0.616515	-3.385846	10054.530552
HLA B*7301	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.594091	1.208137	-3.385954	39272.752744
HLA A*6801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.179532	0.793337	-3.386195	15119.302739
HLA A*0219	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.328548	0.942253	-3.386295	21308.253233
HLA B*4402	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.118732	0.732333	-3.386399	13144.128320
HLA A*1101	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.455629	1.069099	-3.386530	28551.514078
HLA A*8001	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.404124	1.017549	-3.386575	25358.510089
HLA B*4402	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.335718	0.949124	-3.386595	21662.993911
HLA A*2602	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.484476	1.097819	-3.386657	30512.382538
HLA B*4801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.409680	1.022974	-3.386707	25685.041130
HLA B*7301	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.620434	1.233662	-3.386772	41728.595662
HLA A*6901	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.369269	0.982334	-3.386935	23402.870177
HLA B*0802	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.468812	1.081848	-3.386964	29431.480158
HLA B*5801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.342668	0.955683	-3.386985	22012.443501
HLA A*2402	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.541787	1.154698	-3.387089	34816.660142
HLA B*0803	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.509754	1.122659	-3.387095	32341.058480
HLA A*2501	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.352590	0.965301	-3.387289	22521.127508
HLA A*0202	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.195269	0.807959	-3.387310	15677.204146
HLA A*3002	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.562089	1.174655	-3.387434	36482.871045
HLA B*7301	1:333-341	9	VAVVAVLAV	0.995617	0.194384	-4.577542	1.190001	-3.387540	37804.332214
HLA A*2301	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.542553	1.154939	-3.387614	34878.117812
HLA A*6801	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.532199	1.144551	-3.387648	34056.409553
HLA B*1509	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.542621	1.154939	-3.387682	34883.590157
HLA B*7301	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.607317	1.219563	-3.387753	40487.092920
HLA A*2603	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.568858	1.181092	-3.387766	37055.943403
HLA B*1801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.456884	1.069099	-3.387784	28634.115254
HLA B*0803	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.490636	1.102823	-3.387814	30948.276637
HLA A*0212	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.349078	0.961256	-3.387821	22339.716084
HLA B*7301	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.532382	1.144551	-3.387831	34070.783415
HLA B*1509	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.373228	0.985326	-3.387902	23617.178156
HLA B*3901	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.457910	1.069720	-3.388191	28701.889865
HLA A*0301	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.342588	0.954333	-3.388255	22008.394987
HLA A*8001	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.403391	1.014994	-3.388397	25315.743932
HLA A*8001	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.411283	1.022881	-3.388401	25779.982266
HLA B*1501	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.175448	0.786863	-3.388585	14977.811419
HLA B*4601	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.293508	0.904921	-3.388586	19656.565147
HLA B*0801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.383014	0.994371	-3.388643	24155.365358
HLA B*7301	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.569887	1.181170	-3.388717	37143.852737
HLA B*5801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.283330	0.894591	-3.388739	19201.257025
HLA A*2301	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.515240	1.126330	-3.388910	32752.184905
HLA B*3901	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.420041	1.031103	-3.388938	26305.193110
HLA A*3201	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.570084	1.181092	-3.388992	37160.735880
HLA B*7301	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.627708	1.238694	-3.389014	42433.394478
HLA A*2902	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.310473	0.921444	-3.389029	20439.640890

HLA B*1509	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.418211	1.029142	-3.389069	26194.568306
HLA A*2603	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.625863	1.236758	-3.389105	42253.572011
HLA A*0250	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.563877	1.174655	-3.389222	36633.377912
HLA B*2705	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.462990	1.073598	-3.389392	29039.563239
HLA A*3101	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.350657	0.961256	-3.389400	22421.078710
HLA A*0203	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.222664	0.833148	-3.389516	16697.967399
HLA A*8001	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.373686	0.984065	-3.389621	23642.105733
HLA B*1501	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.331912	0.942253	-3.389659	21473.968511
HLA A*6802	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-3.981794	0.592081	-3.389713	9589.465618
HLA B*3801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.364171	0.974301	-3.389870	23129.739472
HLA B*4601	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.375209	0.985326	-3.389882	23725.131134
HLA A*1101	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.419055	1.029142	-3.389913	26245.491526
HLA B*4403	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.648327	1.258359	-3.389968	44496.602813
HLA A*2402	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.585448	1.195398	-3.390050	38498.835029
HLA A*3101	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.413035	1.022974	-3.390062	25884.234762
HLA A*6802	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.344494	0.954333	-3.390160	22105.167196
HLA A*0101	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.364507	0.974301	-3.390206	23147.639889
HLA B*1509	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.351883	0.961636	-3.390247	22484.484472
HLA B*4001	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.391291	1.001026	-3.390264	24620.158607
HLA B*0802	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.463932	1.073598	-3.390334	29102.629049
HLA B*5101	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.413277	1.022881	-3.390396	25898.661958
HLA B*5101	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.345020	0.954621	-3.390399	22131.970811
HLA A*2403	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.413341	1.022881	-3.390460	25902.445174
HLA A*0202	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.452222	1.061692	-3.390530	28328.422462
HLA A*0101	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.375862	0.985326	-3.390535	23760.839371
HLA A*3001	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.244136	0.853416	-3.390720	17544.280095
HLA B*4801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.433102	1.042359	-3.390743	27108.299893
HLA A*0201	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.374929	0.984065	-3.390864	23709.862360
HLA A*2301	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.540220	1.149326	-3.390894	34691.254236
HLA A*0219	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.300049	0.909118	-3.390930	19954.855917
HLA A*8001	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.397630	1.006578	-3.391052	24982.146852
HLA A*1101	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.461103	1.069720	-3.391384	28913.684897
HLA B*5301	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.523600	1.132158	-3.391442	33388.718053
HLA A*6901	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.244878	0.853416	-3.391462	17574.298131
HLA B*4801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.418237	1.026649	-3.391588	26196.127159
HLA B*3501	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.453505	1.061692	-3.391813	28412.222645
HLA B*0803	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.504924	1.112976	-3.391948	31983.330695
HLA A*2501	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.474655	1.082637	-3.392018	29830.138738
HLA B*1502	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.567479	1.175404	-3.392075	36938.455014
HLA A*3101	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.386498	0.994371	-3.392127	24349.940088
HLA B*0702	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.299431	0.907250	-3.392181	19926.484320
HLA A*2603	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.495054	1.102823	-3.392231	31264.645019
HLA B*5801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.353946	0.961636	-3.392310	22591.537178
HLA A*2402	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.567777	1.175404	-3.392373	36963.842519
HLA A*0219	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.479162	1.086732	-3.392430	30141.272647
HLA A*6801	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.602054	1.209597	-3.392456	39999.424972
HLA B*1509	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.521072	1.128536	-3.392535	33194.925550
HLA A*0206	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.337011	0.944464	-3.392547	21727.546817
HLA B*5801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.346958	0.954333	-3.392625	22230.970065
HLA B*5301	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.535885	1.143250	-3.392635	34346.714639
HLA A*0250	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-3.566448	0.173777	-3.392671	3685.087028
HLA B*5801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.354002	0.961256	-3.392746	22594.470594
HLA A*0250	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.572182	1.179436	-3.392746	37340.694891
HLA A*0301	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.367061	0.974301	-3.392760	23284.161750
HLA B*1801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.490679	1.097819	-3.392860	30951.290465
HLA A*0212	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.393913	1.001026	-3.392886	24769.250860
HLA B*4403	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.542302	1.149326	-3.392975	34857.934172
HLA B*3501	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.339327	0.946270	-3.393057	21843.754485
HLA B*0803	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.408141	1.014994	-3.393147	25594.187831
HLA B*0702	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.258352	0.865145	-3.393207	18128.099907
HLA A*0201	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.766619	0.373369	-3.393250	5842.775129
HLA B*4501	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.632085	1.238694	-3.393391	42863.227106
HLA A*6801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.287256	0.893801	-3.393455	19375.621879
HLA B*4403	1:549-557	9	SVIELQVSK	0.982858	0.255246	-4.631577	1.238104	-3.393474	42813.169133
HLA A*2402	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.548535	1.154939	-3.393595	35361.837911

HLA B*0801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.377779	0.984065	-3.393714	23865.962734
HLA B*4501	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.613388	1.219563	-3.393824	41057.042635
HLA B*3801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.537112	1.143250	-3.393861	34443.845543
HLA A*2403	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.423054	1.029142	-3.393912	26488.266311
HLA B*4001	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.376294	0.982334	-3.393960	23784.503152
HLA A*3002	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.455763	1.061692	-3.394071	28560.319685
HLA B*0803	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.469822	1.075727	-3.394095	29500.024903
HLA B*3801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.463314	1.069099	-3.394215	29061.251247
HLA A*2501	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.430896	1.036678	-3.394218	26970.941999
HLA B*3801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.507428	1.112976	-3.394453	32168.309571
HLA A*2602	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.633170	1.238694	-3.394476	42970.492109
HLA B*4601	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.312675	0.918162	-3.394513	20543.513828
HLA B*4501	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.310884	0.916314	-3.394570	20459.000887
HLA B*1503	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.178343	0.783751	-3.394592	15077.971696
HLA B*4403	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.549625	1.154927	-3.394698	35450.714294
HLA B*5101	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.339001	0.944277	-3.394723	21827.334711
HLA A*2902	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.377067	0.982334	-3.394733	23826.873779
HLA A*2902	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.437113	1.042359	-3.394754	27359.795843
HLA A*1101	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.468373	1.073598	-3.394774	29401.720878
HLA A*0301	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.282787	0.887960	-3.394827	19177.276501
HLA B*5801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.299494	0.904590	-3.394904	19929.395134
HLA A*6801	1:180-188	9	AQYLSPEQA	1.287462	-0.050704	-4.631669	1.236758	-3.394911	42822.203051
HLA A*2403	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.417889	1.022974	-3.394916	26175.161268
HLA B*4601	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.337189	0.942253	-3.394936	21736.481969
HLA A*0212	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.349578	0.954621	-3.394957	22365.473119
HLA B*5401	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.431676	1.036678	-3.394998	27019.427583
HLA A*3201	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.549764	1.154698	-3.395066	35462.031381
HLA A*2501	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.369445	0.974301	-3.395144	23412.367624
HLA A*3001	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-3.637839	0.242669	-3.395170	4343.493741
HLA A*0101	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.396251	1.001026	-3.395224	24902.939256
HLA A*2902	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.426406	1.031103	-3.395303	26693.544737
HLA B*1501	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.418199	1.022881	-3.395318	26193.859767
HLA A*0203	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.357181	0.961636	-3.395545	22760.459372
HLA B*1501	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.379651	0.984065	-3.395587	23969.087328
HLA B*4801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.391552	0.995952	-3.395600	24634.947395
HLA A*2301	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.493162	1.097502	-3.395660	31128.784764
HLA A*0301	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.351455	0.955683	-3.395772	22462.357148
HLA B*4501	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.413341	1.017549	-3.395792	25902.445174
HLA B*4801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.381348	0.985326	-3.396022	24062.892223
HLA B*1501	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.397099	1.001026	-3.396072	24951.621470
HLA A*6901	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.288304	0.892112	-3.396191	19422.428028
HLA A*6801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.516556	1.120342	-3.396214	32851.559344
HLA A*0212	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.340869	0.944464	-3.396405	21921.413227
HLA B*5701	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.370733	0.974301	-3.396432	23481.879367
HLA B*3501	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.303784	0.907250	-3.396534	20127.242423
HLA A*0201	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.397562	1.001026	-3.396535	24978.227790
HLA B*4601	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.397571	1.001026	-3.396545	24978.768314
HLA A*2403	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.407242	1.010656	-3.396585	25541.211894
HLA A*2403	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.378954	0.982334	-3.396620	23930.606229
HLA B*0801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.216076	0.819348	-3.396728	16446.581931
HLA A*6802	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.379118	0.982334	-3.396784	23939.670280
HLA A*6802	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.358126	0.961256	-3.396869	22810.012123
HLA B*4002	1:445-453	9	TAAGFGRFK	0.989482	0.244180	-4.630706	1.233662	-3.397044	42727.326328
HLA B*1502	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.551984	1.154927	-3.397057	35643.789739
HLA A*0206	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.080026	0.682948	-3.397078	12023.374493
HLA A*8001	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.423834	1.026649	-3.397185	26535.884191
HLA A*2902	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.431967	1.034768	-3.397199	27037.559006
HLA A*1101	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.428500	1.031103	-3.397396	26822.523865
HLA A*0301	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.366248	0.968816	-3.397432	23240.618717
HLA B*4501	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.294812	0.897363	-3.397449	19715.672448
HLA A*2501	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.471058	1.073598	-3.397460	29584.089774
HLA B*3801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.523853	1.126330	-3.397524	33408.231713
HLA B*4402	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.415157	1.017549	-3.397608	26010.991972
HLA A*2301	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.520282	1.122659	-3.397623	33134.641185
HLA A*0219	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.382997	0.985326	-3.397671	24154.450631

HLA A*2601	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.381815	0.984065	-3.397750	24088.811510
HLA B*0802	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.427104	1.029142	-3.397962	26736.468720
HLA B*0702	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.471641	1.073598	-3.398043	29623.807980
HLA A*2601	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.229884	0.831818	-3.398066	16977.884557
HLA B*0801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.316295	0.918162	-3.398134	20715.493561
HLA B*5401	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.251609	0.853416	-3.398193	17848.809898
HLA A*3201	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.547628	1.149326	-3.398302	35288.071759
HLA A*0301	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.327592	0.929186	-3.398406	21261.387804
HLA B*0702	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.808229	0.409720	-3.398509	6430.260265
HLA B*5701	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.131372	0.732827	-3.398545	13532.312538
HLA B*3501	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.467666	1.069099	-3.398566	29353.882763
HLA A*3301	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.593979	1.195398	-3.398581	39262.555928
HLA A*0201	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.303679	0.904921	-3.398757	20122.343142
HLA B*3801	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.496313	1.097502	-3.398810	31355.434696
HLA B*1501	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.273889	0.875034	-3.398855	18788.384110
HLA B*5101	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.405552	1.006578	-3.398974	25442.056946
HLA A*2501	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.394961	0.995952	-3.399009	24829.086527
HLA A*2402	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.517740	1.118640	-3.399100	32941.254109
HLA A*3001	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.197905	0.798791	-3.399114	15772.652527
HLA A*2603	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.594077	1.194908	-3.399169	39271.477997
HLA B*4402	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.422212	1.022974	-3.399239	26437.015064
HLA B*1501	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.345650	0.946270	-3.399380	22164.082128
HLA A*3002	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.094823	0.695361	-3.399462	12440.087380
HLA A*0212	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.414518	1.014994	-3.399524	25972.745208
HLA A*0101	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.354162	0.954621	-3.399541	22602.784006
HLA B*5301	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.594622	1.194908	-3.399715	39320.798349
HLA A*1101	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.461421	1.061692	-3.399729	28934.809287
HLA B*1503	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.293804	0.894030	-3.399773	19669.968535
HLA B*1801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.430894	1.031103	-3.399790	26970.796089
HLA A*0301	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.298773	0.898882	-3.399891	19896.323149
HLA B*1517	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.304531	0.904590	-3.399942	20161.898020
HLA A*0212	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.410679	1.010656	-3.400022	25744.164192
HLA B*3901	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.485498	1.085412	-3.400087	30584.271938
HLA B*5801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.346392	0.946270	-3.400122	22202.004585
HLA B*5301	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.575556	1.175404	-3.400152	37631.909544
HLA B*5801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.356260	0.956046	-3.400214	22712.242943
HLA A*1101	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.361177	0.960920	-3.400258	22970.872810
HLA A*0101	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.260422	0.860149	-3.400274	18214.706693
HLA B*0802	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.374642	0.974301	-3.400341	23694.218861
HLA A*3201	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.344834	0.944464	-3.400371	22122.514042
HLA B*5801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.349566	0.949124	-3.400442	22364.868153
HLA B*1509	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.411118	1.010656	-3.400462	25770.221436
HLA B*3901	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-3.971809	0.571232	-3.400577	9371.499690
HLA A*0201	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.308866	0.908065	-3.400801	20364.146540
HLA A*3001	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-3.994204	0.593391	-3.400813	9867.437543
HLA B*1517	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.174739	0.773768	-3.400970	14953.360851
HLA B*2705	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.462788	1.061692	-3.401096	29026.055711
HLA B*4801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.385321	0.984065	-3.401256	24284.032476
HLA B*0802	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.436039	1.034768	-3.401271	27292.237239
HLA A*2402	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.527730	1.126330	-3.401400	33707.779122
HLA A*0202	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.483301	1.081848	-3.401454	30429.959759
HLA A*0101	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.383789	0.982334	-3.401455	24198.527565
HLA A*2301	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.534511	1.133041	-3.401470	34238.186491
HLA A*8001	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.432764	1.031103	-3.401661	27087.190099
HLA B*4601	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.384012	0.982334	-3.401678	24210.967340
HLA B*3801	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.515503	1.113773	-3.401731	32772.035715
HLA B*1517	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.295587	0.893801	-3.401786	19750.901554
HLA A*0201	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.356439	0.954621	-3.401817	22721.583038
HLA A*0202	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.563283	1.161199	-3.402083	36583.272034
HLA A*3201	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.557026	1.154927	-3.402099	36060.012085
HLA B*5301	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.535227	1.133041	-3.402187	34294.726687
HLA A*2402	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.471291	1.069099	-3.402192	29599.938636
HLA B*4601	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.322338	0.920120	-3.402218	21005.748458
HLA A*6802	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.417311	1.014994	-3.402318	26140.349676
HLA A*0201	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.358389	0.956046	-3.402343	22823.837071

HLA A*6802	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.184268	0.781690	-3.402578	15285.101427
HLA B*5401	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.210573	0.807959	-3.402615	16239.518900
HLA A*0202	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.535728	1.133041	-3.402687	34334.267497
HLA A*6801	1:489-497	9	GSGPATKDI	1.136230	0.120187	-4.659113	1.256417	-3.402696	45615.594651
HLA A*0202	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.413362	1.010656	-3.402706	25903.706369
HLA B*5301	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.357402	0.954621	-3.402781	22772.036682
HLA A*3201	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.321182	0.918327	-3.402855	20949.912525
HLA A*2602	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.583989	1.181092	-3.402896	38369.713624
HLA A*0301	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.357724	0.954621	-3.403103	22788.920543
HLA A*0206	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.413794	1.010656	-3.403138	25929.504264
HLA A*0206	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.485801	1.082637	-3.403164	30605.623407
HLA A*0101	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.345459	0.942253	-3.403206	22154.371932
HLA B*4001	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.372025	0.968816	-3.403209	23551.852316
HLA B*0803	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.485853	1.082637	-3.403216	30609.266231
HLA A*0301	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.364509	0.961256	-3.403253	23147.765116
HLA A*2902	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.399232	0.995952	-3.403280	25074.489839
HLA B*4002	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.479063	1.075727	-3.403336	30134.424866
HLA B*0803	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.501157	1.097819	-3.403339	31707.168754
HLA A*0211	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.486022	1.082637	-3.403385	30621.191230
HLA B*5701	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.404455	1.001026	-3.403429	25377.860797
HLA B*5401	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.529777	1.126330	-3.403447	33866.985426
HLA A*2602	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.308044	0.904590	-3.403454	20325.624300
HLA A*2402	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.526156	1.122659	-3.403497	33585.822196
HLA A*2601	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.404537	1.001026	-3.403511	25382.666452
HLA A*3002	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.477122	1.073598	-3.403524	30000.067542
HLA A*2602	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.609831	1.206278	-3.403552	40722.135377
HLA B*0802	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.426486	1.022881	-3.403605	26698.455099
HLA B*2705	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.434738	1.031103	-3.403634	27210.562713
HLA A*0201	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.378023	0.974301	-3.403722	23879.394182
HLA B*5801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.348042	0.944277	-3.403764	22286.482385
HLA B*4403	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.386101	0.982334	-3.403767	24327.687811
HLA A*3101	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.298388	0.894591	-3.403797	19878.678526
HLA B*1517	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.473542	1.069720	-3.403822	29753.743679
HLA B*1517	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.398351	0.994371	-3.403980	25023.672574
HLA A*0219	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.435116	1.031103	-3.404012	27234.273223
HLA A*0211	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.309000	0.904921	-3.404079	20370.427071
HLA A*0211	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.473918	1.069720	-3.404198	29779.509141
HLA B*4002	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.585419	1.181170	-3.404249	38496.335817
HLA B*5801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.333578	0.929186	-3.404392	21556.492473
HLA B*2705	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.197844	0.793337	-3.404507	15770.434147
HLA B*4001	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.388730	0.984065	-3.404665	24475.406174
HLA A*1101	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.279831	0.875034	-3.404797	19047.205959
HLA B*5301	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.579461	1.174655	-3.404806	37971.792609
HLA B*7301	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.441511	1.036678	-3.404833	27638.284837
HLA A*6801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-3.870330	0.465424	-3.404906	7418.739795
HLA B*5401	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.433680	1.028753	-3.404927	27144.400522
HLA B*4403	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.641386	1.236390	-3.404997	43791.162711
HLA B*0803	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.441699	1.036678	-3.405021	27650.249031
HLA B*5401	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.560355	1.154927	-3.405428	36337.503631
HLA A*3301	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.641866	1.236390	-3.405476	43839.518078
HLA B*4801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.428406	1.022881	-3.405524	26816.720218
HLA A*2402	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.560550	1.154927	-3.405623	36353.823590
HLA B*1509	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.310884	0.905205	-3.405679	20459.000887
HLA B*2705	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.354850	0.949124	-3.405726	22638.640033
HLA B*3901	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.448289	1.042359	-3.405930	28073.034058
HLA A*0250	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.152658	0.746693	-3.405966	14212.103242
HLA A*8001	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.350584	0.944464	-3.406120	22417.318863
HLA A*0202	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.509266	1.103143	-3.406123	32304.686947
HLA A*0219	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.324587	0.918327	-3.406260	21114.782768
HLA B*3501	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.417048	1.010656	-3.406392	26124.515838
HLA A*8001	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.300241	0.893801	-3.406441	19963.710073
HLA B*1501	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.321955	0.915512	-3.406443	20987.233503
HLA A*2603	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.506007	1.099547	-3.406460	32063.195355
HLA A*0301	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.368163	0.961636	-3.406527	23343.314220
HLA A*0201	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.355659	0.949124	-3.406535	22680.809811

HLA B*4601	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.361173	0.954621	-3.406552	22970.624271
HLA A*8001	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.371882	0.965301	-3.406581	23544.081410
HLA B*3801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.429498	1.022881	-3.406617	26884.265240
HLA B*5801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.271770	0.865145	-3.406625	18696.925384
HLA A*0250	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.279890	0.873123	-3.406768	19049.782215
HLA B*5701	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.367768	0.960920	-3.406848	23322.108021
HLA B*5301	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.568054	1.161199	-3.406855	36987.446546
HLA B*5801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.361730	0.954621	-3.407108	23000.094802
HLA A*2301	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.351406	0.944277	-3.407129	22459.805397
HLA B*1517	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.493862	1.086732	-3.407131	31179.009414
HLA A*2603	1:502-510	9	GQTVDVAQK	1.016309	0.208397	-4.631883	1.224706	-3.407177	42843.289608
HLA A*6802	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.180979	0.773768	-3.407211	15169.771737
HLA A*0216	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.363261	0.956046	-3.407215	23081.365080
HLA A*8001	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.392562	0.985326	-3.407236	24692.321206
HLA A*0250	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.582678	1.175404	-3.407273	38254.060923
HLA B*1517	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.314550	0.907250	-3.407300	20632.393771
HLA B*0803	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.492803	1.085412	-3.407391	31103.029723
HLA B*0803	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.389790	0.982334	-3.407456	24535.195648
HLA A*2301	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.526116	1.118640	-3.407476	33582.733513
HLA B*0802	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.444171	1.036678	-3.407493	27808.060865
HLA B*4001	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.361849	0.954333	-3.407516	23006.441503
HLA A*8001	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.449939	1.042359	-3.407579	28179.850906
HLA A*0212	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.154331	0.746693	-3.407638	14266.951570
HLA B*3901	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.414217	1.006578	-3.407639	25954.766196
HLA B*5401	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.562601	1.154939	-3.407662	36525.922713
HLA B*1517	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.391735	0.984065	-3.407670	24645.344831
HLA A*0101	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.368639	0.960920	-3.407720	23368.964104
HLA B*3501	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.450171	1.042359	-3.407812	28194.947486
HLA A*0216	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.494701	1.086732	-3.407969	31239.284570
HLA A*2403	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.369617	0.961636	-3.407981	23421.615507
HLA B*3501	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.189672	0.781690	-3.407982	15476.478204
HLA B*1502	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.569177	1.161155	-3.408022	37083.217158
HLA B*5801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.326525	0.918327	-3.408198	21209.232005
HLA A*0201	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.393528	0.985326	-3.408201	24747.284786
HLA B*1502	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.562984	1.154698	-3.408286	36558.145913
HLA A*0201	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.352755	0.944464	-3.408291	22529.657699
HLA B*2705	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.404260	0.995952	-3.408308	25366.468168
HLA A*0212	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.195203	0.786863	-3.408339	15674.829592
HLA A*0203	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.941195	0.532852	-3.408344	8733.640386
HLA B*3501	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.216367	0.807959	-3.408408	16457.618431
HLA A*6901	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.781928	0.373369	-3.408559	6052.411060
HLA B*5101	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.491257	1.082637	-3.408619	30992.508877
HLA A*0101	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.374074	0.965301	-3.408773	23663.218848
HLA B*5701	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.419482	1.010656	-3.408826	26271.345559
HLA A*2601	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.364713	0.955683	-3.409030	23158.662415
HLA A*2403	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.374337	0.965301	-3.409036	23677.560916
HLA B*1517	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-3.694781	0.285730	-3.409051	4952.007782
HLA B*4402	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.424123	1.014988	-3.409135	26553.547479
HLA A*1101	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.424127	1.014988	-3.409139	26553.834784
HLA B*3901	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.438316	1.029142	-3.409174	27435.683787
HLA B*4601	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.383484	0.974301	-3.409182	24181.515072
HLA B*5701	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.403731	0.994371	-3.409361	25335.610252
HLA A*0301	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.358539	0.949124	-3.409415	22831.740802
HLA B*3501	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.297455	0.887960	-3.409495	19836.030386
HLA A*0219	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.253860	0.844164	-3.409696	17941.554583
HLA A*2603	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.646121	1.236390	-3.409731	44271.138299
HLA B*0803	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.371400	0.961636	-3.409764	23517.984855
HLA A*3201	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.542938	1.133041	-3.409898	34909.076171
HLA B*3801	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.530423	1.120342	-3.410081	33917.407499
HLA B*3901	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.491933	1.081848	-3.410086	31040.834332
HLA A*2402	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.543190	1.133041	-3.410149	34929.289424
HLA B*1503	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.304047	0.893801	-3.410247	20139.441367
HLA B*1801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.472022	1.061692	-3.410330	29649.781726
HLA B*7301	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.375634	0.965301	-3.410333	23748.373922
HLA A*2601	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.384635	0.974301	-3.410334	24245.701574

HLA A*0250	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.565362	1.154939	-3.410422	36758.843625
HLA A*0201	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.328849	0.918327	-3.410522	21323.013579
HLA B*4601	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.379365	0.968816	-3.410549	23953.272794
HLA B*4002	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.565334	1.154698	-3.410636	36756.457368
HLA B*4403	1:386-394	9	TLQKPDSTI	0.975553	0.274011	-4.660243	1.249564	-3.410680	45734.448146
HLA A*2501	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.417262	1.006578	-3.410684	26137.380101
HLA A*6801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-3.832673	0.421976	-3.410697	6802.563325
HLA A*3201	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.537074	1.126330	-3.410744	34440.864274
HLA B*4001	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.366819	0.956046	-3.410773	23271.190996
HLA A*2403	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.329041	0.918162	-3.410880	21332.474799
HLA B*3501	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.437529	1.026649	-3.410880	27386.006773
HLA B*1801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.425889	1.014994	-3.410896	26661.793630
HLA A*0202	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.176012	0.765110	-3.410902	14997.270841
HLA A*3301	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.620690	1.209597	-3.411092	41753.209349
HLA A*0101	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.365764	0.954333	-3.411430	23214.732934
HLA B*1502	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.554730	1.143250	-3.411480	35869.921074
HLA A*0250	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.305288	0.893801	-3.411487	20197.050338
HLA B*1501	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.385833	0.974301	-3.411532	24312.688886
HLA A*6801	1:84-92	9	AGPLPYIVM	1.248846	0.009513	-4.669966	1.258359	-3.411607	46769.810686
HLA A*6801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.285143	0.873492	-3.411652	19281.617509
HLA A*0202	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.566607	1.154927	-3.411680	36864.391341
HLA A*0216	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.360900	0.949124	-3.411776	22956.213644
HLA A*0203	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.158485	0.746693	-3.411792	14404.065132
HLA A*0202	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.243619	0.831818	-3.411801	17523.411742
HLA A*3002	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.102699	0.690866	-3.411833	12667.733102
HLA A*0301	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.367883	0.956046	-3.411837	23328.291172
HLA A*2501	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.441055	1.029142	-3.411914	27609.293163
HLA A*1101	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.333679	0.921765	-3.411915	21561.507641
HLA B*1509	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.473659	1.061692	-3.411967	29761.792990
HLA A*0250	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.573195	1.161199	-3.411996	37427.862361
HLA A*1101	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.418634	1.006578	-3.412056	26220.088478
HLA A*0219	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.454443	1.042359	-3.412083	28473.617966
HLA A*0202	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.309486	0.897363	-3.412124	20393.251612
HLA B*4001	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.330338	0.918162	-3.412177	21396.274304
HLA B*0702	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.454718	1.042359	-3.412358	28491.646248
HLA B*1801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.482164	1.069720	-3.412445	30350.386590
HLA B*4002	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.618763	1.206278	-3.412485	41568.397783
HLA A*0216	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.300885	0.888375	-3.412510	19993.324416
HLA A*3301	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.435489	1.022974	-3.412516	27257.709471
HLA A*1101	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.427532	1.014994	-3.412538	26762.806406
HLA A*3101	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.320663	0.908065	-3.412598	20924.880080
HLA A*0219	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.419247	1.006578	-3.412669	26257.136896
HLA A*2602	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.462407	1.049687	-3.412720	29000.628361
HLA A*0219	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.374015	0.961256	-3.412759	23660.018680
HLA A*0203	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-3.831423	0.418508	-3.412915	6783.013279
HLA A*0250	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.367563	0.954621	-3.412942	23311.133813
HLA A*2902	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.427992	1.014994	-3.412998	26791.199084
HLA A*2501	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.482113	1.069099	-3.413013	30346.774576
HLA A*6802	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.407404	0.994371	-3.413033	25550.747757
HLA B*4601	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.357517	0.944464	-3.413053	22778.073998
HLA A*3101	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.328658	0.915512	-3.413146	21313.671860
HLA A*0301	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.359472	0.946270	-3.413202	22880.829821
HLA A*0301	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.334990	0.921765	-3.413226	21626.694095
HLA A*0219	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.329697	0.916314	-3.413382	21364.697475
HLA B*4501	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.623136	1.209597	-3.413538	41989.014040
HLA B*5701	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.378918	0.965301	-3.413617	23928.664379
HLA B*2705	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.456014	1.042359	-3.413655	28576.856845
HLA B*4601	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.374647	0.960920	-3.413727	23694.475228
HLA A*8001	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.382555	0.968816	-3.413740	24129.896614
HLA B*0702	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.382577	0.968816	-3.413761	24131.071503
HLA B*1801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.358252	0.944464	-3.413788	22816.676677
HLA B*1801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.414819	1.001026	-3.413792	25990.736675
HLA A*2601	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.343037	0.929186	-3.413851	22031.147769
HLA B*1509	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.428852	1.014988	-3.413864	26844.298731
HLA B*4403	1:381-389	9	GFKIRTLQK	0.984702	0.253992	-4.652572	1.238694	-3.413878	44933.719979

HLA B*5401	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.546075	1.132158	-3.413917	35162.109199
HLA A*1101	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.450683	1.036678	-3.414006	28228.218977
HLA B*4403	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.595205	1.181170	-3.414035	39373.588602
HLA B*5701	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.420624	1.006578	-3.414046	26340.509224
HLA A*3002	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.437035	1.022881	-3.414154	27354.911835
HLA A*1101	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.456548	1.042359	-3.414188	28611.972063
HLA A*0203	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.308887	0.894591	-3.414297	20365.138074
HLA B*4002	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.244974	0.830662	-3.414313	17578.196638
HLA A*3001	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.179480	0.765110	-3.414370	15117.503383
HLA A*6901	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.336184	0.921765	-3.414419	21686.210833
HLA A*6901	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.161253	0.746693	-3.414560	14496.153190
HLA B*4001	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.379875	0.965301	-3.414574	23981.409154
HLA A*0212	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.400132	0.985326	-3.414806	25126.497730
HLA B*0802	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.484582	1.069720	-3.414862	30519.811530
HLA A*2402	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.564269	1.149326	-3.414943	36666.489347
HLA A*8001	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.331292	0.916286	-3.415006	21443.321049
HLA A*6801	1:330-338	9	GRWVAVVAV	1.015320	0.241749	-4.672169	1.257069	-3.415101	47007.746157
HLA B*0702	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.416158	1.001026	-3.415131	26071.006365
HLA A*3001	1:159-167	9	IARAIADSG	0.805700	-0.564762	-3.656076	0.240938	-3.415138	4529.767407
HLA B*4402	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.333482	0.918327	-3.415155	21551.711656
HLA A*3001	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.285214	0.869990	-3.415224	19284.747105
HLA B*5101	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.430248	1.014994	-3.415254	26930.700942
HLA A*2301	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.543989	1.128536	-3.415452	34993.596166
HLA A*0211	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-3.466463	0.050897	-3.415566	2927.271908
HLA B*3801	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.502412	1.086732	-3.415680	31798.899421
HLA B*5101	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.502530	1.086732	-3.415798	31807.502011
HLA B*1509	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.263657	0.847787	-3.415870	18350.902304
HLA B*7301	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.596979	1.181092	-3.415887	39534.737577
HLA A*0206	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.502696	1.086732	-3.415965	31819.721687
HLA A*3301	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.513478	1.097502	-3.415976	32619.564867
HLA A*3301	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.591493	1.175404	-3.416089	39038.472202
HLA B*0802	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.401452	0.985326	-3.416126	25203.007521
HLA B*0801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.412084	0.995952	-3.416132	25827.584355
HLA A*3101	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.304111	0.887960	-3.416151	20142.383289
HLA A*0212	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.331694	0.915512	-3.416182	21463.167252
HLA A*2501	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.458547	1.042359	-3.416188	28743.999991
HLA B*4402	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.417232	1.001026	-3.416205	26135.541961
HLA A*3001	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.245559	0.829345	-3.416214	17601.891522
HLA A*0211	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.203158	0.786863	-3.416295	15964.605248
HLA A*3001	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.248160	0.831818	-3.416343	17707.621080
HLA B*0702	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.331269	0.914880	-3.416389	21442.161021
HLA B*4601	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.372114	0.955683	-3.416431	23556.694504
HLA B*5701	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.321156	0.904590	-3.416567	20948.665858
HLA B*4801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.427264	1.010656	-3.416607	26746.306140
HLA B*1517	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.490263	1.073598	-3.416665	30921.667230
HLA A*3301	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.622950	1.206278	-3.416672	41971.072557
HLA A*2603	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.592118	1.175404	-3.416714	39094.690195
HLA A*1101	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.372413	0.955683	-3.416729	23572.884831
HLA B*5701	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.359258	0.942253	-3.417005	22869.568363
HLA A*0219	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.411405	0.994371	-3.417034	25787.235563
HLA A*0250	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.520416	1.103143	-3.417273	33144.860281
HLA A*0201	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.373085	0.955683	-3.417401	23609.385696
HLA B*4402	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.333710	0.916286	-3.417424	21563.024084
HLA A*2603	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.596908	1.179436	-3.417472	39528.321741
HLA B*1517	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.359754	0.942253	-3.417501	22895.688574
HLA A*2301	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.446356	1.028753	-3.417603	27948.321238
HLA B*0802	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.444274	1.026649	-3.417625	27814.680948
HLA B*1503	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-3.813430	0.395731	-3.417699	6507.741763
HLA B*2705	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.446859	1.029142	-3.417717	27980.696201
HLA B*3801	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.515550	1.097819	-3.417732	32775.581769
HLA A*6801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-3.634240	0.216497	-3.417742	4307.643847
HLA A*3001	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.290949	0.873123	-3.417827	19541.101517
HLA B*5401	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.491447	1.073598	-3.417849	31006.092802
HLA B*4501	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.572819	1.154939	-3.417880	37395.479484
HLA B*1502	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.413846	0.995952	-3.417894	25932.590514

HLA B*0803	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.360212	0.942253	-3.417959	22919.854630
HLA A*0101	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.386794	0.968816	-3.417978	24366.543786
HLA B*1501	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.386799	0.968816	-3.417983	24366.807428
HLA A*1101	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.336362	0.918327	-3.418035	21695.128986
HLA B*5401	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.546599	1.128536	-3.418063	35204.554551
HLA A*2603	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.428737	1.010656	-3.418081	26837.183665
HLA B*4402	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.373846	0.955683	-3.418162	23650.804613
HLA A*0219	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.433199	1.014994	-3.418205	27114.313328
HLA B*5401	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.522559	1.104337	-3.418222	33308.795098
HLA A*0301	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.360482	0.942253	-3.418229	22934.118362
HLA B*4403	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.424954	1.006578	-3.418376	26604.448923
HLA B*0802	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.449572	1.031103	-3.418469	28156.078759
HLA B*0801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.310581	0.892112	-3.418469	20444.728028
HLA B*5301	1:521-529	9	SQASVDSPR	0.518283	0.661153	-4.597909	1.179436	-3.418473	39619.524269
HLA A*0250	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.184015	0.765110	-3.418904	15276.173439
HLA A*6801	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.580218	1.161155	-3.419063	38037.996522
HLA B*4002	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.638722	1.219563	-3.419159	43523.334439
HLA B*3801	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.486426	1.067242	-3.419185	30649.697538
HLA A*3201	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.563774	1.144551	-3.419223	36624.658920
HLA A*0250	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.568550	1.149326	-3.419224	37029.691327
HLA A*2601	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.373909	0.954621	-3.419288	23654.259467
HLA A*6801	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.614255	1.194908	-3.419347	41139.084579
HLA A*0202	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.272780	0.853416	-3.419365	18740.469778
HLA A*0219	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.401711	0.982334	-3.419377	25218.009987
HLA B*4501	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.547931	1.128536	-3.419395	35312.707042
HLA A*2402	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.434409	1.014988	-3.419421	27189.961657
HLA A*0211	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.501282	1.081848	-3.419434	31716.261268
HLA B*4601	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.316824	0.897363	-3.419461	20740.724331
HLA B*5801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.363964	0.944464	-3.419500	23118.730712
HLA B*5301	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.517369	1.097819	-3.419550	32913.109191
HLA A*2301	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.504980	1.085412	-3.419568	31987.483595
HLA B*5701	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.339868	0.920120	-3.419747	21870.951028
HLA B*4601	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.375852	0.956046	-3.419806	23760.325202
HLA B*0803	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.434836	1.014988	-3.419848	27216.746072
HLA B*1517	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.442895	1.022974	-3.419921	27726.492610
HLA A*0301	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.213284	0.793337	-3.419948	16341.219541
HLA A*3002	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.369145	0.949124	-3.420021	23396.160972
HLA A*2902	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.203788	0.783751	-3.420037	15987.768323
HLA A*3301	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.615028	1.194908	-3.420120	41212.371325
HLA B*1501	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.074350	0.654207	-3.420143	11867.248008
HLA A*6802	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.170782	0.750403	-3.420379	14817.750606
HLA B*5301	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.569713	1.149326	-3.420387	37128.985848
HLA B*4001	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.405726	0.985326	-3.420400	25452.244250
HLA B*3901	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.482336	1.061692	-3.420644	30362.374990
HLA A*3201	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.616090	1.195398	-3.420692	41313.270008
HLA B*1517	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.455486	1.034768	-3.420717	28542.093540
HLA B*4001	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.382422	0.961636	-3.420786	24122.456977
HLA A*2301	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.489903	1.069099	-3.420804	30896.083553
HLA B*1517	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.252763	0.831818	-3.420945	17896.283923
HLA B*4601	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.350217	0.929186	-3.421032	22398.407911
HLA A*0301	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.329142	0.908065	-3.421077	21337.437848
HLA A*0211	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.482808	1.061692	-3.421116	30395.408621
HLA B*4001	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.319220	0.898050	-3.421170	20855.489803
HLA A*2301	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.525646	1.104337	-3.421309	33546.417390
HLA A*0250	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.309275	0.887960	-3.421315	20383.324758
HLA A*6901	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.365806	0.944464	-3.421342	23216.993649
HLA A*6901	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.382297	0.960920	-3.421377	24115.541479
HLA B*4403	1:65-73	9	ALNHPAIVA	1.328579	-0.133671	-4.616301	1.194908	-3.421393	41333.389924
HLA A*6802	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.329485	0.908065	-3.421420	21354.297749
HLA A*0101	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.377577	0.956046	-3.421531	23854.861666
HLA B*0702	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.444434	1.022881	-3.421553	27824.915086
HLA B*4801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.428272	1.006578	-3.421694	26808.452190
HLA A*0101	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.383538	0.961636	-3.421902	24184.524104
HLA A*2601	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.383662	0.961636	-3.422026	24191.459385
HLA B*2705	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.219045	0.796898	-3.422147	16559.430696

HLA A*0301	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.342330	0.920120	-3.422210	21995.301956
HLA A*2902	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.407577	0.985326	-3.422251	25560.978582
HLA A*0216	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.423498	1.001026	-3.422471	26515.363595
HLA A*1101	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.457314	1.034768	-3.422545	28662.477343
HLA A*6901	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.120485	0.697848	-3.422636	13197.282281
HLA A*3101	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.396944	0.974301	-3.422643	24942.714017
HLA B*4002	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.543009	1.120342	-3.422667	34914.742258
HLA B*5401	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.525792	1.102823	-3.422969	33557.671186
HLA B*4001	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.339442	0.916314	-3.423128	21849.545695
HLA B*1801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.452305	1.029142	-3.423163	28333.786847
HLA B*5101	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.505025	1.081848	-3.423177	31990.771690
HLA A*0301	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.367493	0.944277	-3.423215	23307.350800
HLA A*0101	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.331426	0.908065	-3.423361	21449.934410
HLA B*3901	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.458155	1.034768	-3.423386	28718.042909
HLA A*2301	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.485085	1.061692	-3.423393	30555.165273
HLA A*0206	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.454520	1.031103	-3.423417	28478.701711
HLA A*2902	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.429996	1.006578	-3.423418	26915.116398
HLA B*4001	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.384863	0.961256	-3.423606	24258.428069
HLA A*0211	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-3.882261	0.458556	-3.423705	7625.368284
HLA A*0250	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.578674	1.154927	-3.423747	37903.038162
HLA B*0803	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.491062	1.067242	-3.423820	30978.595719
HLA B*2705	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.446819	1.022974	-3.423845	27978.122987
HLA B*4403	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.598692	1.174655	-3.424037	39690.962897
HLA B*0803	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.409389	0.985326	-3.424063	25667.816708
HLA A*3201	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.452847	1.028753	-3.424094	28369.217272
HLA B*0702	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.378547	0.954333	-3.424214	23908.219793
HLA B*7301	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.557313	1.133041	-3.424272	36083.819782
HLA A*2501	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.368778	0.944464	-3.424314	23376.424282
HLA B*7301	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.556476	1.132158	-3.424318	36014.392090
HLA B*0803	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.378655	0.954333	-3.424322	23914.170211
HLA A*0101	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.368809	0.944464	-3.424345	23378.068370
HLA A*3301	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.567624	1.143250	-3.424374	36950.846735
HLA A*2902	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.342551	0.918162	-3.424389	22006.490062
HLA B*0702	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.453550	1.029142	-3.424408	28415.143228
HLA B*1502	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.522242	1.097819	-3.424423	33284.477400
HLA A*2403	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.378785	0.954333	-3.424451	23921.286786
HLA A*1101	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.442080	1.017549	-3.424531	27674.492387
HLA A*0250	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.493644	1.069099	-3.424545	31163.326586
HLA B*0801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.299684	0.875034	-3.424650	19938.130129
HLA B*5101	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.856952	0.432298	-3.424654	7193.697497
HLA A*3001	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.251269	0.826538	-3.424730	17834.814176
HLA A*2601	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.393652	0.968816	-3.424836	24754.381447
HLA B*1801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.393758	0.968816	-3.424942	24760.408511
HLA A*3101	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.343291	0.918327	-3.424964	22044.023625
HLA A*2501	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.367303	0.942253	-3.425050	23297.139733
HLA B*5301	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.580133	1.154698	-3.425435	38030.589115
HLA B*4402	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.410850	0.985326	-3.425524	25754.333135
HLA A*2403	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.409647	0.984065	-3.425582	25683.095858
HLA A*0211	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.499191	1.073598	-3.425593	31563.920810
HLA A*0101	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.343953	0.918327	-3.425626	22077.679405
HLA B*5701	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.330566	0.904921	-3.425645	21407.505143
HLA B*3501	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.299144	0.873492	-3.425652	19913.337050
HLA B*1517	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.295820	0.869990	-3.425830	19761.482556
HLA B*5401	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.528973	1.103143	-3.425830	33804.383267
HLA B*0803	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.495552	1.069720	-3.425832	31300.522901
HLA A*6901	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.347285	0.921444	-3.425841	22247.693477
HLA B*5801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.335007	0.909118	-3.425888	21627.513097
HLA A*6901	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.300991	0.875034	-3.425957	19998.192283
HLA B*3801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.508619	1.082637	-3.425982	32256.662366
HLA A*2403	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.368245	0.942253	-3.425992	23347.734604
HLA A*0203	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.191129	0.765110	-3.426018	15528.475498
HLA A*2603	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.570658	1.144551	-3.426107	37209.820922
HLA B*4601	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.391500	0.965301	-3.426199	24632.015578
HLA B*4001	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.273875	0.847664	-3.426211	18787.774261
HLA A*2601	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.333510	0.907250	-3.426260	21553.110810

HLA A*0216	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.436972	1.010656	-3.426316	27350.916477
HLA A*6901	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.208097	0.781690	-3.426407	16147.184284
HLA A*0216	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.299586	0.873123	-3.426463	19933.600395
HLA B*4403	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.632792	1.206278	-3.426514	42933.081442
HLA A*1101	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.158556	0.732039	-3.426517	14406.403054
HLA A*2603	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.632874	1.206278	-3.426596	42941.211424
HLA B*1502	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.512120	1.085412	-3.426709	32517.725535
HLA A*6801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.502466	1.075727	-3.426739	31802.856323
HLA B*1517	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.320813	0.894030	-3.426783	20932.126216
HLA B*4001	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.376059	0.949124	-3.426935	23771.639479
HLA A*0101	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.345100	0.918162	-3.426938	22136.042056
HLA B*4601	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.388222	0.961256	-3.426966	24446.822484
HLA A*3201	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.512393	1.085412	-3.426981	32538.138345
HLA A*0101	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.347240	0.920120	-3.427120	22245.406801
HLA B*1501	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.208924	0.781690	-3.427234	16177.962356
HLA A*3101	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.412594	0.985326	-3.427267	25857.922347
HLA A*3002	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.442303	1.014994	-3.427309	27688.719057
HLA B*5401	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.292483	0.865145	-3.427338	19610.255615
HLA B*5701	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.411409	0.984065	-3.427344	25787.514576
HLA A*3002	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.553706	1.126330	-3.427376	35785.413976
HLA B*3801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.555931	1.128536	-3.427395	35969.218987
HLA A*0212	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.345734	0.918327	-3.427407	22168.399136
HLA A*0203	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.256994	0.829510	-3.427485	18071.503395
HLA A*6802	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.347736	0.920120	-3.427616	22270.814133
HLA B*5801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.349155	0.921444	-3.427711	22343.704668
HLA A*8001	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.423674	0.995952	-3.427722	26526.124166
HLA B*0702	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.281145	0.853416	-3.427729	19104.894333
HLA A*0219	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.315710	0.887960	-3.427750	20687.607285
HLA A*2403	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.402070	0.974301	-3.427769	25238.891903
HLA A*6802	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.428796	1.001026	-3.427769	26840.813565
HLA A*3001	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-3.968304	0.540402	-3.427902	9296.161575
HLA B*1503	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.326828	0.898882	-3.427946	21224.038579
HLA B*0801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.315917	0.887960	-3.427957	20697.458384
HLA B*4402	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.402336	0.974301	-3.428035	25254.325596
HLA B*0802	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.293263	0.865145	-3.428118	19645.508915
HLA B*5801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.343112	0.914880	-3.428233	22034.962053
HLA B*4501	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.634535	1.206278	-3.428257	43105.767105
HLA B*3901	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.224271	0.795837	-3.428434	16759.870421
HLA B*5301	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-3.999820	0.571232	-3.428588	9995.848273
HLA B*3501	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.451520	1.022881	-3.428639	28282.636669
HLA B*4002	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.636859	1.208137	-3.428722	43337.017442
HLA B*1517	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.225807	0.796898	-3.428909	16819.272997
HLA B*5701	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.222349	0.793337	-3.429012	16685.867009
HLA B*1502	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.603797	1.174655	-3.429142	40160.310867
HLA A*3201	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.572399	1.143250	-3.429148	37359.284346
HLA B*4002	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.584120	1.154939	-3.429181	38381.339635
HLA B*3901	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.384900	0.955683	-3.429217	24260.527926
HLA A*2601	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.383761	0.954333	-3.429427	24196.956680
HLA B*1517	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.375761	0.946270	-3.429491	23755.312643
HLA A*3201	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.294715	0.865145	-3.429570	19711.299889
HLA A*8001	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.390859	0.961256	-3.429602	24595.663412
HLA B*0803	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.503241	1.073598	-3.429643	31859.683510
HLA A*0211	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.345180	0.915512	-3.429668	22140.114051
HLA B*0702	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.412032	0.982334	-3.429698	25824.510602
HLA A*3001	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.292573	0.862842	-3.429731	19614.287423
HLA B*4403	1:611-619	9	GTGVNRDGI	1.069446	0.140151	-4.639429	1.209597	-3.429832	43594.264554
HLA B*4002	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.213214	0.783381	-3.429833	16338.567630
HLA A*2902	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.245259	0.815296	-3.429962	17589.707033
HLA A*2601	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.344856	0.914880	-3.429976	22123.591192
HLA A*3301	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.584912	1.154927	-3.429985	38451.377734
HLA A*2601	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.329091	0.898882	-3.430209	21334.898470
HLA B*1509	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.472578	1.042359	-3.430219	29687.821389
HLA B*5701	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.412596	0.982334	-3.430262	25858.062236
HLA A*2902	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.229059	0.798791	-3.430268	16945.676332
HLA A*0202	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.499426	1.069099	-3.430327	31581.001161

HLA B*5101	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.457156	1.026649	-3.430508	28652.090150
HLA A*2902	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.346827	0.916314	-3.430512	22224.236129
HLA A*8001	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.404852	0.974301	-3.430551	25401.073656
HLA B*3501	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.325287	0.894591	-3.430696	21148.850354
HLA B*3801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.512545	1.081848	-3.430698	32549.582159
HLA A*0250	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.304226	0.873492	-3.430734	20147.723432
HLA A*0216	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.185227	0.754459	-3.430768	15318.876495
HLA B*3501	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.246072	0.815296	-3.430775	17622.662661
HLA B*4601	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.379964	0.949124	-3.430840	23986.339658
HLA A*2601	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.024250	0.593391	-3.430859	10574.250644
HLA A*8001	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.413212	0.982334	-3.430878	25894.739206
HLA B*4001	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.373136	0.942253	-3.430883	23612.195795
HLA B*1502	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.559467	1.128536	-3.430931	36263.271612
HLA B*1801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.325660	0.894591	-3.431070	21167.049837
HLA B*5801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.306120	0.875034	-3.431086	20235.766785
HLA B*5801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.346723	0.915512	-3.431212	22218.946610
HLA A*0219	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.400036	0.968816	-3.431220	25120.925154
HLA B*5801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.349442	0.918162	-3.431280	22358.456525
HLA A*3101	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.349470	0.918162	-3.431308	22359.908054
HLA B*1509	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.296531	0.865145	-3.431386	19793.902071
HLA B*4403	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.446513	1.014994	-3.431519	27958.453294
HLA A*0216	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.462664	1.031103	-3.431560	29017.734434
HLA B*1517	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.468283	1.036678	-3.431605	29395.677217
HLA A*1101	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.432661	1.001026	-3.431634	27080.743164
HLA A*0301	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.347153	0.915512	-3.431642	22240.954475
HLA A*3002	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.144614	0.712902	-3.431712	13951.269143
HLA B*1517	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.454628	1.022881	-3.431747	28485.789657
HLA A*6901	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.376210	0.944277	-3.431932	23779.871428
HLA A*0216	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.474329	1.042359	-3.431969	29807.715663
HLA A*0219	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.433015	1.001026	-3.431989	27102.874278
HLA B*3901	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.397317	0.965301	-3.432016	24964.178281
HLA B*4501	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.640292	1.208137	-3.432154	43680.903865
HLA B*4002	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.581557	1.149326	-3.432230	38155.472922
HLA A*2403	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.438840	1.006578	-3.432262	27468.802314
HLA B*1801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.467083	1.034768	-3.432314	29314.526459
HLA A*2601	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.376830	0.944464	-3.432366	23813.858360
HLA A*2501	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.455298	1.022881	-3.432417	28529.743448
HLA B*1501	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.326245	0.893801	-3.432445	21195.582388
HLA B*1517	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.439143	1.006578	-3.432565	27487.978814
HLA A*6801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.003828	0.571232	-3.432596	10088.529697
HLA B*4402	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.374894	0.942253	-3.432641	23707.938423
HLA A*0301	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.350861	0.918162	-3.432699	22431.633906
HLA A*3001	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-3.713328	0.280603	-3.432725	5168.067212
HLA A*0250	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.337373	0.904590	-3.432783	21745.656077
HLA B*5801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.349146	0.916286	-3.432860	22343.221165
HLA A*0202	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-3.708023	0.275124	-3.432899	5105.320556
HLA B*1509	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.502624	1.069720	-3.432904	31814.385758
HLA B*4001	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.393873	0.960920	-3.432953	24766.972984
HLA A*0201	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.394597	0.961636	-3.432961	24808.275250
HLA B*3501	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.394270	0.961256	-3.433014	24789.627070
HLA B*0801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.388737	0.955683	-3.433054	24475.803405
HLA B*1501	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.377351	0.944277	-3.433074	23842.475875
HLA A*6901	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.382236	0.949124	-3.433112	24112.149695
HLA A*3201	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.594322	1.161199	-3.433122	39293.579465
HLA B*4601	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.377466	0.944277	-3.433189	23848.796986
HLA B*0802	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.417283	0.984065	-3.433218	26138.652735
HLA B*4501	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.842982	0.409720	-3.433263	6965.978561
HLA B*5701	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.418618	0.985326	-3.433291	26219.095562
HLA A*0212	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.394972	0.961636	-3.433337	24829.758149
HLA B*4801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.434594	1.001026	-3.433568	27201.584620
HLA A*2902	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.188121	0.754459	-3.433662	15421.317558
HLA A*6802	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.180368	0.746693	-3.433675	15148.449373
HLA A*0101	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.308737	0.875034	-3.433703	20358.088213
HLA B*4402	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.388042	0.954333	-3.433708	24436.641000
HLA A*2602	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.382915	0.949124	-3.433791	24149.877512

HLA A*0201	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.188272	0.754459	-3.433813	15426.657850
HLA A*0206	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.419158	0.985326	-3.433832	26251.739619
HLA B*7301	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.588777	1.154927	-3.433850	38795.093978
HLA A*3002	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.456825	1.022974	-3.433851	28630.242831
HLA B*0802	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.448914	1.014994	-3.433920	28113.461091
HLA A*2501	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.448982	1.014988	-3.433995	28117.872068
HLA A*0203	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.435022	1.001026	-3.433995	27228.380485
HLA A*6801	1:354-362	9	GGITRDVQV	1.280221	-0.073943	-4.640315	1.206278	-3.434037	43683.267017
HLA A*0219	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.349684	0.915512	-3.434172	22370.918544
HLA A*2301	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.537321	1.103143	-3.434178	34460.433564
HLA B*4801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.383340	0.949124	-3.434216	24173.536411
HLA A*3101	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.388869	0.954621	-3.434247	24483.219566
HLA A*6802	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.408597	0.974301	-3.434296	25621.063505
HLA B*4601	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.352625	0.918327	-3.434298	22522.955134
HLA A*3101	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.390365	0.956046	-3.434319	24567.736717
HLA B*5801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.356084	0.921765	-3.434319	22703.029509
HLA B*7301	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-3.892467	0.458095	-3.434372	7806.690944
HLA B*5401	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.557087	1.122659	-3.434428	36065.084539
HLA A*6801	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.615521	1.181092	-3.434429	41259.218346
HLA B*0803	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.428814	0.994371	-3.434444	26841.975237
HLA B*7301	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.555022	1.120342	-3.434680	35893.991632
HLA B*1509	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.089307	0.654485	-3.434822	12283.067546
HLA B*7301	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.603508	1.168679	-3.434829	40133.596428
HLA B*3901	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.216297	0.781429	-3.434868	16454.947631
HLA A*0203	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.390577	0.955683	-3.434893	24579.701416
HLA A*0212	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.308425	0.873492	-3.434933	20343.445527
HLA B*0803	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.464148	1.029142	-3.435007	29117.117318
HLA A*0301	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.353476	0.918327	-3.435149	22567.106855
HLA B*0702	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.431138	0.995952	-3.435186	26985.974897
HLA A*6801	1:596-604	9	GGSQHNRVV	1.229811	0.006579	-4.671606	1.236390	-3.435216	46946.752155
HLA B*4501	1:348-356	9	IAINTFGGI	0.883060	0.298110	-4.616590	1.181170	-3.435420	41360.902991
HLA B*5301	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.590440	1.154939	-3.435501	38943.971940
HLA A*2602	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.610265	1.174655	-3.435610	40762.911693
HLA B*0702	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.419767	0.984065	-3.435702	26288.548322
HLA A*3101	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.168687	0.732827	-3.435859	14746.418006
HLA B*4002	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.568950	1.133041	-3.435909	37063.762501
HLA B*7301	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.343171	0.907250	-3.435921	22037.942422
HLA A*3101	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.168268	0.732333	-3.435935	14732.224626
HLA A*0250	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.518591	1.082637	-3.435953	33005.828808
HLA A*0202	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.554651	1.118640	-3.436010	35863.323903
HLA A*2902	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.446783	1.010656	-3.436127	27975.852701
HLA A*0219	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.420265	0.984065	-3.436200	26318.715862
HLA A*3201	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.512068	1.075727	-3.436341	32513.855585
HLA B*0801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.382638	0.946270	-3.436368	24134.465949
HLA B*4402	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.420478	0.984065	-3.436414	26331.675753
HLA A*0101	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.392146	0.955683	-3.436463	24668.688381
HLA B*5801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.356627	0.920120	-3.436506	22731.418866
HLA B*1502	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.559178	1.122659	-3.436519	36239.149464
HLA A*2602	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.555268	1.118640	-3.436628	35914.386588
HLA B*3801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.539886	1.103143	-3.436743	34664.614500
HLA A*6901	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.344818	0.908065	-3.436753	22121.676296
HLA A*2501	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.365952	0.929186	-3.436766	23224.782239
HLA A*2602	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.310050	0.873256	-3.436794	20419.746864
HLA A*3002	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.539637	1.102823	-3.436815	34644.741836
HLA A*0301	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.341773	0.904921	-3.436852	21967.118889
HLA A*0301	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.341482	0.904590	-3.436892	21952.387710
HLA B*3901	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.432853	0.995952	-3.436901	27092.759142
HLA A*3002	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.342107	0.905205	-3.436902	21984.000606
HLA B*1509	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.486675	1.049687	-3.436988	30667.278593
HLA A*1101	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.459884	1.022881	-3.437003	28832.616867
HLA B*5401	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.536564	1.099547	-3.437017	34400.456284
HLA B*4402	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.405905	0.968816	-3.437089	25462.711132
HLA A*0216	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.307245	0.869990	-3.437255	20288.272475
HLA B*5101	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.454828	1.017549	-3.437279	28498.891592
HLA B*5401	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-3.979732	0.542449	-3.437282	9544.024787

HLA A*2402	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.541625	1.104337	-3.437288	34803.666122
HLA B*5801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.331146	0.893801	-3.437346	21436.129884
HLA A*2603	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.586676	1.149326	-3.437350	38607.916800
HLA B*4403	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.598530	1.161155	-3.437374	39676.149726
HLA A*0101	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.381665	0.944277	-3.437388	24080.472615
HLA A*3002	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.353687	0.916286	-3.437402	22578.097229
HLA A*0216	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.332016	0.894591	-3.437425	21479.080678
HLA B*5801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.344708	0.907250	-3.437458	22116.052247
HLA B*4002	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.406659	0.968816	-3.437843	25506.967440
HLA A*2603	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.354141	0.916286	-3.437855	22601.683526
HLA A*3002	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.520515	1.082637	-3.437878	33152.392157
HLA B*2705	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.282052	0.844164	-3.437887	19144.831186
HLA A*2403	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.393614	0.955683	-3.437931	24752.238844
HLA B*4501	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.587377	1.149326	-3.438050	38670.208634
HLA B*1501	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.271300	0.833148	-3.438153	18676.706665
HLA B*7301	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.556871	1.118640	-3.438230	36047.139059
HLA B*0801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.360076	0.921765	-3.438311	22912.664114
HLA A*0212	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.267894	0.829510	-3.438384	18530.773365
HLA B*1501	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.360167	0.921765	-3.438403	22917.498868
HLA B*5401	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.536388	1.097819	-3.438569	34386.501416
HLA B*1509	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.439744	1.001026	-3.438718	27526.074159
HLA B*4402	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.360233	0.921444	-3.438789	22920.970602
HLA A*3301	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.506209	1.067242	-3.438967	32078.116242
HLA B*5101	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-3.960019	0.521039	-3.438981	9120.515367
HLA B*3501	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.171064	0.732039	-3.439025	14827.373216
HLA B*0702	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.445618	1.006578	-3.439040	27900.885580
HLA A*2403	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.385384	0.946270	-3.439114	24287.579831
HLA B*1517	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.481490	1.042359	-3.439131	30303.299985
HLA A*0202	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.343726	0.904590	-3.439136	22066.096978
HLA A*6901	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.271007	0.831818	-3.439189	18664.081071
HLA A*2301	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.506500	1.067242	-3.439259	32099.642304
HLA B*5801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.338169	0.898882	-3.439287	21785.573168
HLA B*0802	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.421641	0.982334	-3.439308	26402.283717
HLA B*4002	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.553116	1.113773	-3.439344	35736.854577
HLA B*1801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.423455	0.984065	-3.439390	26512.781707
HLA A*0211	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.333486	0.894030	-3.439456	21551.944842
HLA B*4801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.357651	0.918162	-3.439489	22785.099012
HLA A*0250	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.572626	1.133041	-3.439586	37378.894121
HLA A*0203	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.423662	0.984065	-3.439597	26525.406658
HLA B*4402	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.348800	0.909118	-3.439682	22325.459699
HLA A*2601	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.388876	0.949124	-3.439752	24483.616924
HLA B*5401	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.450470	1.010656	-3.439813	28214.325647
HLA B*5701	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.408646	0.968816	-3.439831	25623.974420
HLA B*5801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.347898	0.908065	-3.439833	22279.128987
HLA B*4002	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.614537	1.174655	-3.439882	41165.800197
HLA A*2601	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.401163	0.961256	-3.439907	25186.242606
HLA A*0101	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.386293	0.946270	-3.440024	24338.482233
HLA A*3002	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.558699	1.118640	-3.440058	36199.177369
HLA A*8001	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.394472	0.954333	-3.440139	24801.163139
HLA A*3201	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.614880	1.174655	-3.440225	41198.327593
HLA B*1502	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.489929	1.049687	-3.440242	30897.922196
HLA A*2301	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.490000	1.049687	-3.440312	30902.937232
HLA A*0250	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.359002	0.918327	-3.440675	22856.086659
HLA B*5101	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.483062	1.042359	-3.440702	30413.172875
HLA B*3801	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.516678	1.075727	-3.440951	32860.802256
HLA A*0203	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.385262	0.944277	-3.440985	24280.748350
HLA A*0216	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.402059	0.960920	-3.441139	25238.209215
HLA B*5101	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.350306	0.909118	-3.441188	22403.012955
HLA A*2902	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.415747	0.974301	-3.441446	26046.335825
HLA B*5701	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.395858	0.954333	-3.441525	24880.450818
HLA A*2501	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.442634	1.001026	-3.441608	27709.847913
HLA A*2602	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.478311	1.036678	-3.441633	30082.302348
HLA A*0201	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.385922	0.944277	-3.441645	24317.687500
HLA A*0301	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.357961	0.916286	-3.441675	22801.375784
HLA A*6802	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.403370	0.961636	-3.441734	25314.511364

HLA A*0201	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.402655	0.960920	-3.441735	25272.913175
HLA B*1501	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.403377	0.961636	-3.441741	25314.922213
HLA B*0803	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.425828	0.984065	-3.441763	26658.043723
HLA A*3001	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.261169	0.819348	-3.441821	18246.069237
HLA B*1503	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.268502	0.826538	-3.441964	18556.756167
HLA B*4402	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.403619	0.961636	-3.441983	25329.032089
HLA B*1509	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.363485	0.921444	-3.442040	23093.230553
HLA B*5101	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.478734	1.036678	-3.442056	30111.610161
HLA A*1101	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.357625	0.915512	-3.442113	22783.743139
HLA A*3002	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.357625	0.915512	-3.442113	22783.743139
HLA A*2601	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.388403	0.946270	-3.442133	24457.008209
HLA A*2603	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.603374	1.161199	-3.442175	40121.222592
HLA A*3001	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.271744	0.829510	-3.442235	18695.812786
HLA A*3101	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.404025	0.961636	-3.442389	25352.748901
HLA A*6801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.330893	0.888375	-3.442517	21423.609097
HLA A*1101	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.396916	0.954333	-3.442582	24941.094822
HLA A*6901	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.351704	0.909118	-3.442586	22475.241841
HLA B*3501	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.443790	1.001026	-3.442764	27783.700500
HLA B*0802	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.485221	1.042359	-3.442862	30564.754181
HLA A*0219	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.337471	0.894591	-3.442880	21750.597585
HLA A*0301	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.364380	0.921444	-3.442936	23140.878664
HLA B*1509	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.361264	0.918327	-3.442937	22975.471255
HLA A*2403	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.239850	0.796898	-3.442952	17372.010837
HLA A*3002	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.546096	1.103143	-3.442953	35163.821249
HLA A*6901	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.337596	0.894591	-3.443005	21756.834900
HLA B*4801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.372258	0.929186	-3.443072	23564.469572
HLA A*2501	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.425502	0.982334	-3.443168	26638.005086
HLA B*3901	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.385483	0.942253	-3.443230	24293.098969
HLA A*0212	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.224684	0.781429	-3.443255	16775.835772
HLA B*3501	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.176228	0.732827	-3.443401	15004.736987
HLA A*3201	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.546251	1.102823	-3.443429	35176.378827
HLA B*5801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.348669	0.905205	-3.443464	22318.697141
HLA B*0802	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.439455	0.995952	-3.443503	27507.763952
HLA B*1503	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.316631	0.873123	-3.443509	20731.525560
HLA A*3101	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.359808	0.916286	-3.443522	22898.537604
HLA A*3101	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.303761	0.860149	-3.443612	20126.153590
HLA A*0216	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.976527	0.532852	-3.443675	9473.857783
HLA B*0801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.306538	0.862842	-3.443696	20255.262410
HLA A*2902	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.014936	0.571232	-3.443704	10349.902101
HLA A*6901	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.240750	0.796898	-3.443852	17408.042743
HLA B*4001	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.360160	0.916286	-3.443875	22917.126928
HLA B*7301	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.412720	0.968816	-3.443905	25865.477429
HLA B*0803	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.525778	1.081848	-3.443930	33556.581944
HLA A*6901	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.106435	0.662443	-3.443992	12777.167430
HLA A*0216	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.429505	0.985326	-3.444179	26884.701566
HLA B*4402	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.398809	0.954621	-3.444188	25050.084685
HLA A*3002	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.317804	0.873492	-3.444312	20787.566641
HLA A*8001	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.393607	0.949124	-3.444483	24751.837127
HLA B*0702	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.352588	0.908065	-3.444523	22521.005671
HLA B*5701	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.399157	0.954621	-3.444536	25070.149408
HLA B*3501	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.166619	0.722004	-3.444615	14676.381542
HLA B*4801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.419419	0.974301	-3.445118	26267.508462
HLA A*3301	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.494840	1.049687	-3.445152	31249.257225
HLA A*0212	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.365275	0.920120	-3.445155	23188.625087
HLA B*4001	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.275818	0.830662	-3.445157	18872.018669
HLA A*3002	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.389625	0.944464	-3.445161	24525.906119
HLA A*3001	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.232069	0.786863	-3.445205	17063.518878
HLA B*1502	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.394348	0.949124	-3.445224	24794.053066
HLA A*3002	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.439660	0.994371	-3.445289	27520.713813
HLA A*3301	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.626425	1.181092	-3.445333	42308.239672
HLA A*6901	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.199921	0.754459	-3.445462	15846.034385
HLA A*0101	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.394594	0.949124	-3.445470	24808.141040
HLA B*7301	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.600456	1.154939	-3.445517	39852.548428
HLA A*2301	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.528160	1.082637	-3.445523	33741.166675
HLA A*2501	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.354738	0.909118	-3.445619	22632.762115

HLA B*1517	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.401739	0.956046	-3.445693	25219.647160
HLA B*1801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.362009	0.916314	-3.445695	23014.906497
HLA A*3201	1:116-124	9	IEVIADACQ	1.170936	0.004468	-4.621101	1.175404	-3.445697	41792.757108
HLA B*2705	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.452333	1.006578	-3.445755	28335.626298
HLA A*0101	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.350863	0.904921	-3.445942	22431.755259
HLA A*0201	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.340554	0.894591	-3.445963	21905.527602
HLA B*5101	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.430043	0.984065	-3.445978	26918.028711
HLA B*4403	1:145-153	9	MISATNAVK	0.938735	0.280828	-4.665586	1.219563	-3.446023	46300.552340
HLA A*0212	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.340152	0.894030	-3.446122	21885.272365
HLA A*2301	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.527977	1.081848	-3.446129	33726.931872
HLA A*3101	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.178225	0.732039	-3.446187	15073.893740
HLA A*2602	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.601187	1.154927	-3.446260	39919.655802
HLA A*6801	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.641675	1.195398	-3.446277	43820.311765
HLA B*0801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.390609	0.944277	-3.446332	24581.563115
HLA B*5701	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.407629	0.961256	-3.446373	25564.020968
HLA A*2403	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.334365	0.887960	-3.446405	21595.595004
HLA A*0250	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.245129	0.798696	-3.446433	17584.474101
HLA B*4601	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.261740	0.815296	-3.446444	18270.071349
HLA A*2403	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.364798	0.918327	-3.446471	23163.173143
HLA A*2602	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.607700	1.161155	-3.446544	40522.810668
HLA A*3301	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.092606	0.645932	-3.446674	12376.718606
HLA B*3501	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.401206	0.954333	-3.446872	25188.695311
HLA A*6802	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.322096	0.875034	-3.447062	20994.046925
HLA B*5801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.341172	0.894030	-3.447141	21936.716988
HLA B*1501	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.403299	0.956046	-3.447253	25310.403236
HLA B*1801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.457972	1.010656	-3.447315	28705.927274
HLA B*4002	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.457986	1.010656	-3.447329	28706.859064
HLA B*3501	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.453952	1.006578	-3.447374	28441.441985
HLA B*4001	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.179715	0.732333	-3.447382	15125.683998
HLA B*4002	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.363729	0.916314	-3.447415	23106.227118
HLA B*1502	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.484133	1.036678	-3.447455	30488.292037
HLA A*8001	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.458223	1.010656	-3.447567	28722.548744
HLA B*4601	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.409243	0.961636	-3.447608	25659.208829
HLA A*3101	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.352231	0.904590	-3.447641	22502.494189
HLA A*6802	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.431787	0.984065	-3.447722	27026.298546
HLA B*1801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.529629	1.081848	-3.447781	33855.444745
HLA B*0803	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.482597	1.034768	-3.447828	30380.613002
HLA B*7301	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.591129	1.143250	-3.447878	39005.750883
HLA B*1517	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.357031	0.909118	-3.447912	22752.580316
HLA B*4002	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.629078	1.181092	-3.447985	42567.439210
HLA B*5701	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.403741	0.955683	-3.448057	25336.158509
HLA A*2601	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.366337	0.918162	-3.448175	23245.396916
HLA B*5101	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.212608	0.764421	-3.448187	16315.778959
HLA A*0212	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.432313	0.984065	-3.448248	27059.069277
HLA B*4501	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.484998	1.036678	-3.448320	30549.049783
HLA B*1502	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.355576	0.907250	-3.448326	22676.515695
HLA A*2403	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.409344	0.960920	-3.448424	25665.178503
HLA B*4001	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.404114	0.955683	-3.448431	25357.961348
HLA B*1502	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.603459	1.154939	-3.448519	40129.037202
HLA B*7301	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.546033	1.097502	-3.448530	35158.685350
HLA B*5301	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.574967	1.126330	-3.448637	37580.844523
HLA B*1509	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.302121	0.853416	-3.448705	20050.298478
HLA B*0801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.378040	0.929186	-3.448854	23880.298493
HLA B*1801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-3.739309	0.290447	-3.448862	5486.668968
HLA A*3101	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.195565	0.746693	-3.448872	15687.894093
HLA B*5301	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.466505	1.017549	-3.448956	29275.539676
HLA B*1517	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.393457	0.944464	-3.448993	24743.268710
HLA A*0201	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.395447	0.946270	-3.449177	24856.906881
HLA A*2403	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.324293	0.875034	-3.449259	21100.509015
HLA B*1517	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.346648	0.897363	-3.449286	22215.100477
HLA A*0219	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.398424	0.949124	-3.449300	25027.869560
HLA B*0803	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.472334	1.022974	-3.449360	29671.122873
HLA A*6802	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.410301	0.960920	-3.449381	25721.750990
HLA B*4403	1:56-64	9	FRREAQNAA	1.299708	-0.104310	-4.644805	1.195398	-3.449407	44137.220164
HLA B*3501	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.405522	0.956046	-3.449476	25440.267706

HLA B*5101	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.314740	0.865145	-3.449594	20641.436889
HLA A*0203	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.297424	0.847787	-3.449637	19834.635395
HLA B*4601	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.371109	0.921444	-3.449664	23502.213664
HLA B*5701	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.337626	0.887960	-3.449666	21758.365081
HLA A*2301	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.519425	1.069720	-3.449705	33069.277762
HLA B*4002	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.535192	1.085412	-3.449781	34291.943840
HLA B*5401	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.536609	1.086732	-3.449877	34403.992416
HLA A*0202	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.344515	0.894591	-3.449924	22106.243501
HLA B*7301	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.517329	1.067242	-3.450087	32910.082374
HLA B*1517	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.432588	0.982334	-3.450254	27076.201926
HLA A*2301	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.479465	1.029142	-3.450323	30162.314851
HLA B*0803	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.473253	1.022881	-3.450371	29733.951636
HLA A*2603	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.526187	1.075727	-3.450459	33588.184321
HLA B*4801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.406161	0.955683	-3.450477	25477.730358
HLA A*1101	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.444988	0.994371	-3.450618	27860.462784
HLA A*0301	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.323898	0.873256	-3.450642	21081.340290
HLA A*3001	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.281377	0.830662	-3.450716	19115.129255
HLA B*3501	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.446671	0.995952	-3.450719	27968.589024
HLA A*3301	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.595311	1.144551	-3.450760	39383.175072
HLA B*0702	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.338761	0.887960	-3.450801	21815.293521
HLA B*4801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.419743	0.968816	-3.450927	26287.126179
HLA B*4801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.411973	0.960920	-3.451053	25821.018145
HLA B*5801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.349111	0.898050	-3.451060	22341.408124
HLA B*1501	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.215437	0.764363	-3.451074	16422.398749
HLA B*0802	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.466063	1.014988	-3.451075	29245.779857
HLA B*5101	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.407131	0.956046	-3.451085	25534.718489
HLA A*0211	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.487796	1.036678	-3.451118	30746.518227
HLA B*1509	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.412469	0.961256	-3.451213	25850.509320
HLA A*2402	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.518464	1.067242	-3.451222	32996.188091
HLA A*3301	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.612424	1.161155	-3.451269	40966.076795
HLA A*0101	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.366802	0.915512	-3.451290	23270.309751
HLA B*4001	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.397644	0.946270	-3.451374	24982.957769
HLA A*0250	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.570070	1.118640	-3.451430	37159.529686
HLA B*0801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.367751	0.916286	-3.451466	23321.224848
HLA A*2902	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.412742	0.961256	-3.451485	25866.736824
HLA A*2601	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.359577	0.908065	-3.451513	22886.400723
HLA A*2301	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.525118	1.073598	-3.451519	33505.608692
HLA B*5701	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.316728	0.865145	-3.451582	20736.124436
HLA A*8001	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.393875	0.942253	-3.451622	24767.106970
HLA B*0702	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.349099	0.897363	-3.451736	22340.803809
HLA A*6802	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.398076	0.946270	-3.451806	25007.838676
HLA B*2705	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.366748	0.914880	-3.451868	23267.414466
HLA A*0101	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.344038	0.892112	-3.451926	22081.979585
HLA B*1517	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.453047	1.001026	-3.452021	28382.265589
HLA A*1101	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.413341	0.961256	-3.452084	25902.445174
HLA A*0216	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.467095	1.014994	-3.452101	29315.319412
HLA B*0802	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.469674	1.017549	-3.452126	29489.972328
HLA A*6801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.861891	0.409720	-3.452171	7275.968141
HLA B*5101	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.462859	1.010656	-3.452202	29030.766926
HLA A*0301	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.340612	0.888375	-3.452237	21908.490464
HLA B*1509	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.534111	1.081848	-3.452264	34206.712752
HLA A*0101	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.381486	0.929186	-3.452301	24070.573926
HLA A*0216	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.045846	0.593391	-3.452455	11113.377494
HLA B*7301	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.566269	1.113773	-3.452496	36835.684277
HLA A*3301	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.470118	1.017549	-3.452570	29520.140332
HLA A*2403	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.357209	0.904590	-3.452620	22761.936999
HLA B*2705	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.453677	1.001026	-3.452650	28423.445470
HLA A*0201	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.372880	0.920120	-3.452760	23598.276309
HLA B*0802	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.453801	1.001026	-3.452775	28431.596326
HLA A*8001	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.361899	0.909118	-3.452780	23009.055360
HLA B*1501	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.357385	0.904590	-3.452796	22771.174339
HLA A*3002	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.607723	1.154927	-3.452796	40525.002966
HLA B*4601	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.399150	0.946270	-3.452880	25069.742531
HLA B*4001	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.397383	0.944464	-3.452919	24967.960064
HLA B*5701	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.397397	0.944277	-3.453120	24968.770520

HLA A*2403	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.409300	0.956046	-3.453254	25662.540569
HLA A*0202	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.447634	0.994371	-3.453263	28030.693730
HLA A*0101	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.244422	0.790996	-3.453427	17555.863256
HLA B*0702	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.348096	0.894591	-3.453505	22289.255608
HLA A*0219	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.415246	0.961636	-3.453610	26016.339752
HLA B*3501	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.422541	0.968816	-3.453726	26457.045634
HLA B*5401	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.496092	1.042359	-3.453733	31339.493583
HLA B*4001	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.408414	0.954621	-3.453793	25610.254431
HLA A*2902	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.347832	0.894030	-3.453802	22275.754469
HLA B*4402	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.237200	0.783381	-3.453819	17266.323459
HLA B*3501	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.375298	0.921444	-3.453854	23730.008948
HLA A*0202	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.077245	0.623337	-3.453908	11946.607189
HLA B*0803	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.496292	1.042359	-3.453932	31353.908068
HLA B*7301	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.615112	1.161155	-3.453957	41220.398463
HLA A*2402	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.439314	0.985326	-3.453988	27498.836563
HLA A*0250	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.527634	1.073598	-3.454035	33700.303381
HLA B*4501	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.369584	0.915512	-3.454072	23419.841657
HLA B*4402	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.370540	0.916314	-3.454226	23471.464859
HLA A*2501	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.438297	0.984065	-3.454232	27434.496421
HLA B*7301	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.269566	0.815296	-3.454270	18602.288604
HLA B*4001	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.241175	0.786863	-3.454312	17425.096871
HLA B*4801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.409067	0.954621	-3.454446	25648.799930
HLA A*3101	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.374570	0.920120	-3.454449	23690.245518
HLA A*3301	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.629141	1.174655	-3.454486	42573.657363
HLA A*0211	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.152367	0.697848	-3.454519	14202.572587
HLA A*0101	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.376451	0.921765	-3.454687	23793.125707
HLA B*2705	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.236166	0.781429	-3.454737	17225.272423
HLA A*0212	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.348758	0.893801	-3.454957	22323.285796
HLA B*0803	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.465652	1.010656	-3.454996	29218.105085
HLA A*0212	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.411059	0.956046	-3.455013	25766.736320
HLA A*2601	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.399361	0.944277	-3.455084	25081.951710
HLA A*0201	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.343493	0.888375	-3.455118	22054.282004
HLA A*3301	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.609852	1.154698	-3.455154	40724.118146
HLA A*0206	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.229714	0.774481	-3.455233	16971.272755
HLA A*8001	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.399540	0.944277	-3.455262	25092.266314
HLA A*0219	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.360184	0.904921	-3.455262	22918.366752
HLA B*0801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.288466	0.833148	-3.455318	19429.679431
HLA B*4403	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.035231	0.579907	-3.455324	10845.038380
HLA A*3301	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.588375	1.133041	-3.455334	38759.221579
HLA A*0250	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.330387	0.875034	-3.455353	21398.705223
HLA B*0803	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.451590	0.995952	-3.455638	28287.227219
HLA A*2602	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.610359	1.154698	-3.455661	40771.733561
HLA B*1509	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.451640	0.995952	-3.455688	28290.441048
HLA A*0202	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.130987	0.675193	-3.455794	13520.311700
HLA B*1501	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.361006	0.905205	-3.455801	22961.802900
HLA A*1101	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.466467	1.010656	-3.455811	29273.005747
HLA B*0802	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.462438	1.006578	-3.455860	29002.668005
HLA A*6801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.456933	1.001026	-3.455907	28637.368494
HLA B*4501	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.600510	1.144551	-3.455959	39857.507487
HLA B*1509	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.318823	0.862842	-3.455982	20836.430942
HLA A*0219	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.329133	0.873123	-3.456010	21336.976121
HLA B*5701	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.405167	0.949124	-3.456043	25419.494209
HLA A*2603	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.611017	1.154939	-3.456078	40833.540117
HLA A*2902	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.410726	0.954621	-3.456105	25746.949805
HLA A*3001	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.264078	0.807959	-3.456119	18368.681377
HLA B*1517	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.344550	0.888375	-3.456175	22108.037459
HLA A*3101	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.400494	0.944277	-3.456216	25147.439914
HLA A*0301	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.365381	0.909118	-3.456262	23194.270929
HLA B*1503	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-3.989129	0.532852	-3.456278	9752.804049
HLA B*4601	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.372603	0.916314	-3.456289	23583.216757
HLA B*4801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.400755	0.944464	-3.456291	25162.545429
HLA B*4402	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.412354	0.956046	-3.456308	25843.657657
HLA B*0802	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.425234	0.968816	-3.456418	26621.581765
HLA A*2301	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.440491	0.984065	-3.456426	27573.469252
HLA A*8001	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.372805	0.916314	-3.456491	23594.191413

HLA B*5701	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.373021	0.916314	-3.456707	23605.937396
HLA B*5701	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.375063	0.918327	-3.456736	23717.174748
HLA B*1517	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.310191	0.853416	-3.456775	20426.376053
HLA A*1101	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.479754	1.022974	-3.456780	30182.392028
HLA B*1517	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.411478	0.954621	-3.456856	25791.560614
HLA B*5701	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.351484	0.894591	-3.456893	22463.815422
HLA B*0801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.412948	0.956046	-3.456902	25879.054140
HLA A*0219	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.132410	0.675193	-3.457218	13564.709329
HLA A*3301	1:269-277	9	MRADLVRVH	1.336203	-0.186877	-4.606609	1.149326	-3.457283	40421.218333
HLA B*1517	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.406572	0.949124	-3.457448	25501.862326
HLA A*2501	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.373787	0.916314	-3.457473	23647.606123
HLA A*6901	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.330763	0.873256	-3.457507	21417.235581
HLA A*3002	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.544419	1.086732	-3.457687	35028.257320
HLA A*3101	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.351493	0.893801	-3.457692	22464.301534
HLA B*4001	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.379489	0.921765	-3.457725	23960.141760
HLA B*0801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.249307	0.791452	-3.457855	17754.431421
HLA A*0211	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.458975	1.001026	-3.457948	28772.315266
HLA A*2601	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.374264	0.916314	-3.457950	23673.590367
HLA B*0801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.305744	0.847787	-3.457957	20218.258643
HLA B*5701	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.387149	0.929186	-3.457963	24386.456784
HLA A*3201	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.472959	1.014994	-3.457965	29713.851261
HLA A*0216	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.378178	0.920120	-3.458058	23887.921906
HLA B*3801	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.475644	1.017549	-3.458096	29898.156196
HLA B*1517	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.468812	1.010656	-3.458156	29431.480158
HLA A*2402	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.533937	1.075727	-3.458210	34193.021458
HLA A*0211	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.321055	0.862842	-3.458214	20943.793236
HLA A*3002	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.527335	1.069099	-3.458236	33677.157341
HLA A*2501	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.266256	0.807959	-3.458297	18461.031084
HLA A*0101	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.365566	0.907250	-3.458316	23204.185844
HLA B*5101	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.352355	0.894030	-3.458325	22508.947122
HLA A*3001	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.275045	0.816673	-3.458372	18838.459115
HLA B*2705	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-3.916493	0.458095	-3.458398	8250.738452
HLA B*4001	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.387748	0.929186	-3.458562	24420.121646
HLA B*3901	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.459647	1.001026	-3.458620	28816.867063
HLA A*0211	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.489767	1.031103	-3.458664	30886.390699
HLA B*4601	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.375016	0.916286	-3.458730	23714.608741
HLA A*2402	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.520473	1.061692	-3.458781	33149.164001
HLA A*0301	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.364034	0.905205	-3.458829	23122.483110
HLA B*5801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.356197	0.897363	-3.458834	22708.925676
HLA B*5801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.328924	0.869990	-3.458934	21326.705263
HLA A*2602	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.520686	1.061692	-3.458994	33165.487349
HLA B*5801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.351119	0.892112	-3.459007	22444.986671
HLA B*1801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.485665	1.026649	-3.459016	30596.021678
HLA A*3002	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.427865	0.968816	-3.459049	26783.373607
HLA B*2705	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.374617	0.915512	-3.459105	23692.808889
HLA A*3002	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.474120	1.014988	-3.459132	29793.367295
HLA B*4601	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.374649	0.915512	-3.459138	23694.603413
HLA A*2601	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.375465	0.916286	-3.459179	23739.125446
HLA A*2601	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.312621	0.853416	-3.459205	20540.957810
HLA A*6801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.364128	0.904921	-3.459207	23127.487254
HLA B*3501	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-3.638849	0.179592	-3.459257	4353.609565
HLA B*5301	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.508977	1.049687	-3.459289	32283.198030
HLA A*0101	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.353946	0.894591	-3.459355	22591.537178
HLA B*5301	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.579734	1.120342	-3.459392	37995.629177
HLA A*0201	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.206231	0.746693	-3.459539	16077.973581
HLA B*5401	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.486222	1.026649	-3.459573	30635.275334
HLA A*2902	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.367864	0.908065	-3.459799	23327.281566
HLA A*2601	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.353678	0.893801	-3.459877	22577.608655
HLA A*2902	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.380039	0.920120	-3.459919	23990.492447
HLA A*0301	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.358081	0.898050	-3.460031	22807.667651
HLA A*2402	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.483102	1.022974	-3.460128	30415.970046
HLA A*2402	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.546871	1.086732	-3.460140	35226.654002
HLA A*0211	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.546930	1.086732	-3.460198	35231.418632
HLA B*0803	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.491414	1.031103	-3.460311	31003.744537
HLA B*7301	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.586672	1.126330	-3.460342	38607.499073

HLA B*1801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.467001	1.006578	-3.460423	29308.976393
HLA B*1501	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.292316	0.831818	-3.460499	19602.724720
HLA A*2603	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.558031	1.097502	-3.460529	36143.603348
HLA B*3901	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.414877	0.954333	-3.460544	25994.252087
HLA B*1517	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.491771	1.031103	-3.460668	31029.249499
HLA B*1502	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.621902	1.161199	-3.460703	41869.926382
HLA B*2705	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.405172	0.944464	-3.460708	25419.769244
HLA A*2902	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.193116	0.732333	-3.460783	15599.708584
HLA B*7301	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.589348	1.128536	-3.460811	38846.127665
HLA A*2402	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.589421	1.128536	-3.460884	38852.642961
HLA A*3001	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.308556	0.847664	-3.460892	20349.609585
HLA B*4801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.359063	0.898050	-3.461013	22859.301756
HLA A*2403	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.405501	0.944464	-3.461037	25439.029075
HLA A*0216	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.376585	0.915512	-3.461074	23800.463774
HLA A*0211	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.216306	0.755176	-3.461129	16455.303713
HLA A*6801	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.635797	1.174655	-3.461142	43231.176196
HLA A*0219	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.358591	0.897363	-3.461228	22834.458342
HLA A*0203	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.314707	0.853416	-3.461291	20639.873597
HLA B*7301	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.622541	1.161199	-3.461342	41931.582906
HLA A*2402	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.564521	1.103143	-3.461378	36687.720187
HLA B*1801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.503747	1.042359	-3.461387	31896.761901
HLA A*3201	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.584054	1.122659	-3.461395	38375.526190
HLA B*4002	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.622576	1.161155	-3.461421	41934.985723
HLA A*8001	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.417126	0.955683	-3.461442	26129.180168
HLA A*0212	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.405808	0.944277	-3.461531	25457.063990
HLA B*0702	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.410841	0.949124	-3.461717	25753.775828
HLA B*1501	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.350182	0.888375	-3.461807	22396.590391
HLA A*2403	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.416454	0.954621	-3.461833	26088.783621
HLA A*0301	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.353972	0.892112	-3.461859	22592.881613
HLA A*2501	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.377382	0.915512	-3.461870	23844.152741
HLA B*4002	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.559462	1.097502	-3.461960	36262.879253
HLA B*7301	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.404244	0.942253	-3.461991	25365.507578
HLA A*3001	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.174899	0.712902	-3.461996	14958.862793
HLA B*1503	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.463209	1.001026	-3.462182	29054.177291
HLA B*4001	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.377699	0.915512	-3.462187	23861.573322
HLA B*4501	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.350269	0.887960	-3.462309	22401.073874
HLA B*3501	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.406800	0.944464	-3.462336	25515.248176
HLA B*0801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.370411	0.908065	-3.462346	23464.482107
HLA B*4403	1:434-442	9	TLTYAEAVK	0.998576	0.209561	-4.670584	1.208137	-3.462446	46836.402174
HLA B*4403	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.595496	1.133041	-3.462456	39400.010300
HLA B*5701	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.424188	0.961636	-3.462553	26557.570033
HLA B*1509	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.493686	1.031103	-3.462583	31166.361356
HLA A*6801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.489246	1.026649	-3.462597	30849.318552
HLA A*0301	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.217171	0.754459	-3.462711	16488.096208
HLA B*1503	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.209422	0.746693	-3.462729	16196.527448
HLA B*5701	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.407197	0.944464	-3.462733	25538.586702
HLA B*0702	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.371936	0.909118	-3.462817	23547.011123
HLA B*1503	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.409109	0.946270	-3.462839	25651.297681
HLA A*0212	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.418545	0.955683	-3.462861	26214.698816
HLA A*2902	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.351296	0.888375	-3.462920	22454.095385
HLA A*0101	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.384419	0.921444	-3.462974	24233.637253
HLA A*2402	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.545652	1.082637	-3.463015	35127.885704
HLA A*0101	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.361908	0.898882	-3.463026	23009.553271
HLA A*0212	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.423979	0.960920	-3.463059	26544.786168
HLA A*0301	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.316479	0.853416	-3.463063	20724.236750
HLA A*0301	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.357705	0.894591	-3.463114	22787.934280
HLA A*6801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-3.825897	0.362756	-3.463140	6697.252585
HLA B*5301	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.585835	1.122659	-3.463176	38533.215652
HLA A*0211	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.424186	0.960920	-3.463266	26557.426360
HLA A*1101	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.351291	0.887960	-3.463331	22453.852438
HLA A*0219	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.419424	0.956046	-3.463378	26267.792672
HLA A*1101	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.371595	0.908065	-3.463530	23528.547291
HLA A*0216	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.337107	0.873492	-3.463615	21732.366640
HLA A*3002	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.549078	1.085412	-3.463666	35406.056672
HLA B*5301	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.563257	1.099547	-3.463709	36581.095073

HLA A*0101	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.372923	0.909118	-3.463804	23600.574374
HLA B*5401	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.470476	1.006578	-3.463898	29544.424820
HLA A*3101	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.369119	0.905205	-3.463914	23394.768736
HLA A*0202	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.311740	0.847787	-3.463953	20499.328437
HLA B*4001	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.408235	0.944277	-3.463958	25599.726899
HLA A*0211	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.384167	0.920120	-3.464047	24219.613474
HLA A*2601	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.384172	0.920120	-3.464052	24219.875526
HLA B*4402	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.425321	0.961256	-3.464065	26626.911031
HLA A*0250	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.470685	1.006578	-3.464107	29558.653299
HLA B*1517	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.363022	0.898882	-3.464140	23068.632095
HLA B*3901	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.490846	1.026649	-3.464197	30963.181205
HLA B*1503	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.352252	0.887960	-3.464292	22503.589840
HLA B*3801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.549710	1.085412	-3.464298	35457.619206
HLA B*7301	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.546329	1.081848	-3.464481	35182.659298
HLA B*4801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.426127	0.961636	-3.464491	26676.365583
HLA B*5701	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.420636	0.956046	-3.464590	26341.221730
HLA B*7301	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.567455	1.102823	-3.464633	36936.456739
HLA A*3001	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.219116	0.754459	-3.464657	16562.118455
HLA B*1503	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.219844	0.755176	-3.464668	16589.917519
HLA B*1502	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.406938	0.942253	-3.464685	25523.393521
HLA A*3101	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.386268	0.921444	-3.464823	24337.033923
HLA A*0219	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.280179	0.815296	-3.464883	19062.462471
HLA B*4403	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.645989	1.181092	-3.464897	44257.728221
HLA B*2705	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.372991	0.908065	-3.464926	23604.277282
HLA A*0101	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.381242	0.916286	-3.464957	24057.034944
HLA B*4801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.421129	0.956046	-3.465083	26371.164384
HLA A*3002	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.471669	1.006578	-3.465091	29625.731181
HLA A*2501	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.480191	1.014994	-3.465197	30212.778024
HLA A*2501	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.496322	1.031103	-3.465219	31356.113221
HLA B*5101	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.426479	0.961256	-3.465223	26698.021795
HLA A*0101	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.380157	0.914880	-3.465277	23996.982620
HLA A*0216	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.364161	0.898882	-3.465279	23129.238960
HLA A*2403	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.363353	0.898050	-3.465303	23086.235431
HLA A*0250	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.547177	1.081848	-3.465329	35251.437114
HLA A*3002	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.494548	1.029142	-3.465407	31228.301432
HLA A*1101	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.372690	0.907250	-3.465440	23587.937785
HLA B*7301	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.249213	0.783751	-3.465462	17750.589856
HLA A*0201	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.875184	0.409720	-3.465465	7502.122908
HLA A*0216	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.187520	0.722004	-3.465516	15399.974870
HLA B*2705	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.439848	0.974301	-3.465547	27532.627111
HLA A*3101	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.372845	0.907250	-3.465595	23596.361426
HLA B*4801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.407972	0.942253	-3.465719	25584.220528
HLA A*3201	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.466836	1.001026	-3.465810	29297.879412
HLA A*2403	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.360461	0.894591	-3.465870	22933.001750
HLA B*0702	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.426876	0.960920	-3.465956	26722.442191
HLA A*0101	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.363445	0.897363	-3.466082	23091.106810
HLA A*3201	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.569267	1.103143	-3.466124	37090.841353
HLA B*1509	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.382511	0.916286	-3.466225	24127.416480
HLA B*4501	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.580302	1.113773	-3.466529	38045.405372
HLA A*3001	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.264031	0.797462	-3.466569	18366.694034
HLA B*1801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.448928	0.982334	-3.466595	28114.373650
HLA A*2403	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.386860	0.920120	-3.466739	24370.235034
HLA A*0301	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.364114	0.897363	-3.466752	23126.736563
HLA A*0202	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.299908	0.833148	-3.466760	19948.379755
HLA B*5801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.355367	0.888375	-3.466992	22665.600031
HLA B*3501	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.375096	0.908065	-3.467031	23718.971118
HLA B*4501	1:612-620	9	TGVNRDGII	1.054444	0.126648	-4.648188	1.181092	-3.467096	44482.402499
HLA B*4801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.267233	0.799991	-3.467242	18502.624677
HLA A*3101	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.413566	0.946270	-3.467296	25915.901086
HLA A*8001	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.423378	0.956046	-3.467332	26508.048900
HLA A*2601	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.382870	0.915512	-3.467358	24147.395325
HLA B*4002	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.484930	1.017549	-3.467381	30544.257417
HLA A*3101	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.396594	0.929186	-3.467408	24922.616458
HLA A*2602	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.541038	1.073598	-3.467439	34756.626945
HLA A*3101	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.364814	0.897363	-3.467452	23164.050331

HLA A*0201	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.341061	0.873492	-3.467569	21931.139962
HLA A*3101	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.376736	0.909118	-3.467617	23808.705704
HLA A*0301	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.361772	0.894030	-3.467742	23002.334614
HLA A*2902	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.355715	0.887960	-3.467755	22683.754819
HLA A*3101	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.416924	0.949124	-3.467800	26117.026383
HLA A*0202	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.158490	0.690572	-3.467918	14404.220982
HLA A*3301	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.266625	0.798696	-3.467929	18476.717669
HLA B*1503	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.423984	0.956046	-3.467938	26545.073378
HLA B*0801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.362002	0.894030	-3.467972	23014.532975
HLA B*7301	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.377177	0.909118	-3.468059	23832.932885
HLA B*0803	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.469089	1.001026	-3.468063	29450.274239
HLA A*6801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.383011	0.914880	-3.468132	24155.234681
HLA B*5401	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.537328	1.069099	-3.468229	34460.992849
HLA A*0212	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.276281	0.807959	-3.468323	18892.142210
HLA A*2603	1:266-274	9	AAEMRADLV	0.998847	0.162308	-4.629529	1.161155	-3.468374	42611.676925
HLA B*5401	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.550231	1.081848	-3.468383	35500.229225
HLA B*5401	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.551136	1.082637	-3.468498	35574.246417
HLA A*3201	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.423126	0.954621	-3.468505	26492.708940
HLA A*0201	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.390351	0.921765	-3.468587	24566.939278
HLA B*1801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.454017	0.985326	-3.468691	28445.750532
HLA A*6801	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.623427	1.154698	-3.468729	42017.190823
HLA A*3002	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.550607	1.081848	-3.468759	35530.970897
HLA B*1502	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.385055	0.916286	-3.468770	24269.191759
HLA A*3001	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.292530	0.823629	-3.468901	19612.377516
HLA A*3101	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.367852	0.898882	-3.468970	23326.650585
HLA B*5701	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.415317	0.946270	-3.469047	26020.562460
HLA B*4601	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.342344	0.873256	-3.469088	21996.015920
HLA A*2602	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.595560	1.126330	-3.469230	39405.765762
HLA B*5701	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.391209	0.921765	-3.469444	24615.497316
HLA A*0211	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.454941	0.985326	-3.469614	28506.292993
HLA A*0203	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.184668	0.714935	-3.469733	15299.165313
HLA A*6901	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.368884	0.898882	-3.470002	23382.115848
HLA A*2902	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.260998	0.790996	-3.470002	18238.864887
HLA B*4601	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.358034	0.887960	-3.470074	22805.200045
HLA B*1509	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.414574	0.944464	-3.470110	25976.117659
HLA B*3501	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.419271	0.949124	-3.470147	26258.557416
HLA A*2602	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.598694	1.128536	-3.470158	39691.177622
HLA B*1801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.385753	0.915512	-3.470241	24308.217313
HLA A*0219	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.431176	0.960920	-3.470256	26988.310856
HLA A*3201	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.455693	0.985326	-3.470366	28555.684817
HLA B*1801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.419529	0.949124	-3.470405	26274.188214
HLA B*5101	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.464780	0.994371	-3.470410	29159.521146
HLA A*0250	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.540133	1.069720	-3.470413	34684.310925
HLA B*0802	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.481145	1.010656	-3.470488	30279.210753
HLA A*6801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.116434	0.645932	-3.470502	13074.768075
HLA B*5301	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.499708	1.029142	-3.470566	31601.509783
HLA A*0211	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.481234	1.010656	-3.470577	30285.436066
HLA A*2501	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.426681	0.956046	-3.470635	26710.445953
HLA A*0212	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.045188	0.574537	-3.470651	11096.556039
HLA B*0702	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.432005	0.961256	-3.470749	27039.899430
HLA B*1503	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.345852	0.875034	-3.470818	22174.396376
HLA A*2301	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.456212	0.985326	-3.470886	28589.845997
HLA B*4402	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.436253	0.965301	-3.470952	27305.676512
HLA B*5801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.344618	0.873492	-3.471126	22111.506190
HLA B*5301	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.599671	1.128536	-3.471135	39780.603757
HLA A*3002	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.513516	1.042359	-3.471156	32622.388481
HLA A*0202	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.359554	0.888375	-3.471179	22885.162628
HLA A*3001	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-3.980681	0.509478	-3.471203	9564.906973
HLA A*3101	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.004091	0.532852	-3.471239	10094.644266
HLA B*1501	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.387546	0.916286	-3.471260	24408.762816
HLA A*3001	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.245080	0.773768	-3.471312	17582.476484
HLA B*4601	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.378676	0.907250	-3.471426	23915.334597
HLA A*6802	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.376071	0.904590	-3.471481	23772.282498
HLA B*4001	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.391756	0.920120	-3.471636	24646.544817
HLA A*2403	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.387229	0.915512	-3.471717	24390.942749

HLA B*0802	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.426117	0.954333	-3.471784	26675.788324
HLA A*2403	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.401037	0.929186	-3.471851	25178.885922
HLA B*5701	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.387522	0.915512	-3.472010	24407.442365
HLA A*2902	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.376759	0.904590	-3.472170	23809.993764
HLA A*6901	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.291527	0.819348	-3.472179	19567.124767
HLA B*3501	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.390600	0.918162	-3.472438	24581.031186
HLA A*2602	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.627435	1.154939	-3.472496	42406.773876
HLA A*0201	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.369859	0.897363	-3.472496	23434.670103
HLA B*4601	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.332674	0.860149	-3.472525	21511.641177
HLA B*2705	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.457880	0.985326	-3.472554	28699.871373
HLA B*7301	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.541721	1.069099	-3.472622	34811.386622
HLA B*2705	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.390793	0.918162	-3.472631	24591.938019
HLA A*3301	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.414962	0.942253	-3.472709	25999.315117
HLA A*2902	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.421992	0.949124	-3.472868	26423.574478
HLA A*0301	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.338094	0.865145	-3.472948	21781.802053
HLA A*2603	1:39-47	9	VKVLRADLA	1.257059	-0.082404	-4.647646	1.174655	-3.472991	44426.848255
HLA A*2601	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.391345	0.918327	-3.473018	24623.222221
HLA B*5101	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.366852	0.893801	-3.473051	23272.953587
HLA B*4001	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.394554	0.921444	-3.473110	24805.859587
HLA B*1502	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.576484	1.103143	-3.473341	37712.411387
HLA B*5801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.205404	0.732039	-3.473366	16047.385735
HLA A*0206	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-3.995177	0.521798	-3.473379	9889.562352
HLA B*0801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.281347	0.807959	-3.473388	19113.784962
HLA A*3002	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.484067	1.010656	-3.473411	30483.674115
HLA B*0802	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.429197	0.955683	-3.473514	26865.655250
HLA A*2301	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.488538	1.014988	-3.473550	30799.125121
HLA B*1801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.053463	0.579907	-3.473556	11310.012812
HLA A*3002	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.204305	0.730675	-3.473630	16006.807903
HLA A*3001	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.264642	0.790996	-3.473646	18392.546274
HLA A*2601	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.378613	0.904921	-3.473692	23911.841611
HLA B*3901	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.378759	0.904921	-3.473838	23919.863301
HLA B*2705	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.435095	0.961256	-3.473838	27232.947246
HLA A*8001	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.378507	0.904590	-3.473918	23906.021100
HLA A*2402	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.559345	1.085412	-3.473933	36253.071672
HLA B*2705	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.339099	0.865145	-3.473954	21832.294780
HLA B*1517	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.289330	0.815296	-3.474034	19468.399329
HLA B*2705	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.428659	0.954621	-3.474038	26832.392948
HLA A*0212	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.379022	0.904921	-3.474101	23934.360920
HLA A*1101	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.368757	0.894591	-3.474166	23375.286135
HLA A*2601	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.383305	0.909118	-3.474187	24171.574848
HLA A*2902	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.430243	0.956046	-3.474197	26930.409560
HLA A*2603	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.628932	1.154698	-3.474234	42553.163926
HLA A*0250	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.382330	0.908065	-3.474265	24117.368021
HLA A*2403	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.396093	0.921765	-3.474329	24893.914508
HLA B*1501	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.334563	0.860149	-3.474414	21605.410935
HLA B*0801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.389493	0.914880	-3.474614	24518.477028
HLA B*5301	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.577485	1.102823	-3.474663	37799.424119
HLA A*0203	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.337633	0.862842	-3.474792	21758.718215
HLA B*4801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.436105	0.961256	-3.474849	27296.371695
HLA A*0201	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.396396	0.921444	-3.474952	24911.293429
HLA A*0250	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.395128	0.920120	-3.475007	24838.625264
HLA B*5101	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.506145	1.031103	-3.475042	32073.431030
HLA B*4601	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.389928	0.914880	-3.475048	24543.028127
HLA A*2902	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.328672	0.853416	-3.475257	21314.363699
HLA B*2705	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.350332	0.875034	-3.475298	22404.346170
HLA B*5101	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.301902	0.826538	-3.475364	20040.213315
HLA A*2602	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.551098	1.075727	-3.475371	35571.167307
HLA A*2603	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.457715	0.982334	-3.475382	28689.005012
HLA B*5701	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.390551	0.914880	-3.475671	24578.238751
HLA B*1517	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.257391	0.781690	-3.475701	18088.033207
HLA B*3801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.537410	1.061692	-3.475718	34467.518522
HLA A*0202	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.257260	0.781429	-3.475831	18082.554198
HLA B*4001	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.390743	0.914880	-3.475864	24589.144345
HLA B*2705	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.380789	0.904921	-3.475867	24031.929896
HLA A*2902	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.422168	0.946270	-3.475898	26434.297799

HLA B*5101	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.430313	0.954333	-3.475980	26934.780630
HLA A*2601	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.397790	0.921765	-3.476025	24991.338786
HLA A*6901	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.240571	0.764421	-3.476151	17400.886870
HLA B*4001	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.375054	0.898882	-3.476171	23716.661525
HLA A*2402	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.491203	1.014994	-3.476209	30988.652798
HLA A*8001	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.394566	0.918327	-3.476239	24806.530581
HLA B*0702	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.370319	0.894030	-3.476289	23459.531959
HLA B*4801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.341522	0.865145	-3.476376	21954.406723
HLA A*8001	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.384449	0.908065	-3.476384	24235.341630
HLA B*1502	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.491414	1.014988	-3.476426	31003.744537
HLA A*0101	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.370319	0.893801	-3.476519	23459.531959
HLA A*2602	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.589691	1.112976	-3.476715	38876.822159
HLA B*3501	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.459170	0.982334	-3.476836	28785.237535
HLA A*8001	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.368999	0.892112	-3.476887	23388.314908
HLA A*0219	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.421207	0.944277	-3.476929	26375.872752
HLA B*1517	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.462288	0.985326	-3.476961	28992.628065
HLA A*3001	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.207801	0.730675	-3.477126	16136.181370
HLA A*0101	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.371247	0.894030	-3.477217	23509.716379
HLA B*0803	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.451546	0.974301	-3.477245	28284.319784
HLA B*1509	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.431610	0.954333	-3.477277	27015.335074
HLA A*0211	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.347283	0.869990	-3.477293	22247.573120
HLA A*2601	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.398866	0.921444	-3.477421	25053.337333
HLA B*4001	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.372023	0.894591	-3.477432	23551.724903
HLA B*4601	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.375488	0.898050	-3.477438	23740.409741
HLA A*2403	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.241882	0.764363	-3.477520	17453.494607
HLA A*2301	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.519989	1.042359	-3.477629	33112.241918
HLA A*0250	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.153030	0.675193	-3.477837	14224.256408
HLA B*4601	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.376740	0.898882	-3.477858	23808.963311
HLA B*5801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.351300	0.873256	-3.478044	22454.338335
HLA A*0216	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.439735	0.961636	-3.478099	27525.478514
HLA A*0216	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.386209	0.908065	-3.478144	24333.742629
HLA B*5701	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.394528	0.916286	-3.478243	24804.383465
HLA B*1509	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.297607	0.819348	-3.478260	19843.006809
HLA A*0219	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.372326	0.894030	-3.478296	23568.166816
HLA B*7301	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.591295	1.112976	-3.478320	39020.735953
HLA B*4601	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.386385	0.908065	-3.478320	24343.617846
HLA B*1517	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-3.590972	0.112336	-3.478636	3899.165536
HLA B*1801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.383563	0.904921	-3.478642	24185.963338
HLA A*0211	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.473048	0.994371	-3.478678	29719.960337
HLA A*1101	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.396840	0.918162	-3.478679	24936.777482
HLA B*4403	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.253167	0.774481	-3.478686	17912.944182
HLA A*6801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.421052	0.942253	-3.478799	26366.456857
HLA B*0803	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.496491	1.017549	-3.478943	31368.329183
HLA B*4402	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.425239	0.946270	-3.478969	26621.869806
HLA B*4002	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.623554	1.144551	-3.479003	42029.467266
HLA A*0216	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.423328	0.944277	-3.479051	26505.037553
HLA A*0201	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.308683	0.829510	-3.479173	20355.555266
HLA B*0702	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.383789	0.904590	-3.479199	24198.527565
HLA B*4601	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.400978	0.921765	-3.479213	25175.480778
HLA A*0206	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-3.901273	0.421976	-3.479297	7966.597147
HLA A*0206	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.480390	1.001026	-3.479364	30226.674280
HLA B*5301	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.494473	1.014988	-3.479485	31222.895767
HLA A*0219	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.435330	0.955683	-3.479646	27247.683955
HLA A*0206	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.387715	0.908065	-3.479650	24418.272174
HLA A*3001	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.252345	0.772678	-3.479667	17879.058807
HLA B*4402	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.327486	0.847787	-3.479699	21256.212455
HLA B*2705	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.303392	0.823629	-3.479763	20109.066647
HLA A*2902	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.372013	0.892112	-3.479901	23551.215260
HLA B*4002	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.462266	0.982334	-3.479933	28991.216477
HLA A*3301	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.592935	1.112976	-3.479960	39168.360804
HLA A*2501	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.448790	0.968816	-3.479974	28105.401439
HLA A*2403	1:10-18	9	RYELGEILG	0.929933	-0.507247	-3.902678	0.422686	-3.479992	7992.411728
HLA B*4501	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.606349	1.126330	-3.480019	40396.952771
HLA B*5301	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.583248	1.103143	-3.480106	38304.382898
HLA A*2301	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.422393	0.942253	-3.480140	26448.030000

HLA B*4403	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.635205	1.154939	-3.480266	43172.279632
HLA A*0101	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.350330	0.869990	-3.480340	22404.224966
HLA A*0301	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.355379	0.875034	-3.480345	22666.213131
HLA A*0216	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.374520	0.894030	-3.480490	23687.554277
HLA B*4402	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.441497	0.960920	-3.480577	27637.387732
HLA A*2603	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.554206	1.073598	-3.480608	35826.673504
HLA B*4403	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.606997	1.126330	-3.480667	40457.315703
HLA A*3101	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.372869	0.892112	-3.480756	23597.637997
HLA B*0702	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.385899	0.904921	-3.480978	24316.371976
HLA A*3301	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.354500	0.873492	-3.481008	22620.398979
HLA A*6901	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.354176	0.873123	-3.481054	22603.517689
HLA B*5801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.354232	0.873123	-3.481110	22606.452661
HLA A*2603	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.624386	1.143250	-3.481135	42110.035054
HLA B*1502	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.594190	1.112976	-3.481214	39281.677129
HLA B*1502	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.389397	0.908065	-3.481332	24513.039299
HLA B*4402	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.403144	0.921765	-3.481379	25301.367702
HLA A*0212	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.380417	0.898882	-3.481535	24011.397080
HLA A*6901	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-3.385396	-0.096147	-3.481544	2428.826175
HLA A*0212	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.376254	0.894591	-3.481663	23782.315836
HLA B*5101	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.379186	0.897363	-3.481824	23943.426393
HLA A*3002	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.335286	0.853416	-3.481870	21641.440871
HLA A*0201	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.396812	0.914880	-3.481932	24935.158672
HLA A*6901	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.193892	0.711889	-3.482003	15627.583047
HLA B*1801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.504919	1.022881	-3.482038	31982.984644
HLA A*6802	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.403910	0.921765	-3.482145	25346.029169
HLA B*4403	1:82-90	9	TPAGPLPYI	1.120142	0.024409	-4.626721	1.144551	-3.482170	42337.088747
HLA A*3001	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-3.940740	0.458556	-3.482183	8724.479077
HLA B*3801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.555877	1.073598	-3.482279	35964.743707
HLA B*1502	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.914646	0.432298	-3.482348	8215.729371
HLA A*2501	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.444067	0.961636	-3.482432	27801.442358
HLA B*0802	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.438490	0.956046	-3.482444	27446.669363
HLA A*3001	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.119206	0.636741	-3.482465	13158.500043
HLA A*0250	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.438518	0.956046	-3.482472	27448.451222
HLA B*4501	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.544165	1.061692	-3.482473	35007.797407
HLA B*3901	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.299163	0.816673	-3.482490	19914.198900
HLA B*4402	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.389743	0.907250	-3.482492	24532.541138
HLA B*4002	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.651193	1.168679	-3.482514	44791.254563
HLA A*2902	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.377123	0.894591	-3.482533	23829.967598
HLA B*1517	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-3.867826	0.385288	-3.482537	7376.079483
HLA A*0206	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.352534	0.869990	-3.482544	22518.203614
HLA A*1101	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.468011	0.985326	-3.482685	29377.235831
HLA B*1517	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.377281	0.894591	-3.482690	23838.606635
HLA A*2403	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.431866	0.949124	-3.482742	27031.270119
HLA A*6802	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.145201	0.662443	-3.482758	13970.150613
HLA B*1509	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.352856	0.869990	-3.482866	22534.899276
HLA A*2902	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.390170	0.907250	-3.482920	24556.707769
HLA A*3301	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.637865	1.154939	-3.482925	43437.477642
HLA A*0216	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.438699	0.955683	-3.483015	27459.887571
HLA A*6801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-3.693456	0.210423	-3.483033	4936.921355
HLA A*0211	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.213754	0.730675	-3.483079	16358.909947
HLA A*8001	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.404596	0.921444	-3.483152	25386.099619
HLA A*0203	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.205160	0.722004	-3.483156	16038.359559
HLA B*0801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.432313	0.949124	-3.483189	27059.069277
HLA B*0801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.336712	0.853416	-3.483296	21712.623904
HLA A*6802	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.346416	0.862842	-3.483574	22203.205721
HLA B*4001	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.265025	0.781429	-3.483596	18408.772193
HLA B*1801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.448898	0.965301	-3.483597	28112.396476
HLA B*0702	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.439357	0.955683	-3.483673	27501.514476
HLA B*4402	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.399218	0.915512	-3.483706	25073.675951
HLA A*8001	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.438349	0.954621	-3.483727	27437.761802
HLA A*0202	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.570465	1.086732	-3.483733	37193.317900
HLA B*0802	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.445470	0.961636	-3.483834	27891.377937
HLA B*4601	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.357468	0.873492	-3.483976	22775.486381
HLA B*4601	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.377845	0.893801	-3.484044	23869.578149
HLA A*2601	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.388643	0.904590	-3.484053	24470.507523

HLA B*5301	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.545821	1.061692	-3.484129	35141.571103
HLA B*1517	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.445555	0.961256	-3.484298	27896.810479
HLA A*6802	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.433474	0.949124	-3.484350	27131.480956
HLA B*3901	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.445282	0.960920	-3.484362	27879.309407
HLA A*3101	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.382422	0.898050	-3.484371	24122.456977
HLA A*2601	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.382436	0.898050	-3.484385	24123.239989
HLA B*3901	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.468540	0.984065	-3.484475	29413.016311
HLA A*2501	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.438868	0.954333	-3.484535	27470.585610
HLA A*0216	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.406309	0.921765	-3.484544	25486.415235
HLA B*3801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.554286	1.069720	-3.484567	35833.263934
HLA A*3201	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.499581	1.014988	-3.484593	31592.279255
HLA A*0212	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.357757	0.873123	-3.484634	22790.646606
HLA B*0702	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.402968	0.918327	-3.484641	25291.103965
HLA A*2902	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.281579	0.796898	-3.484681	19124.024647
HLA B*5801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.324591	0.839877	-3.484714	21115.011226
HLA B*4801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.430988	0.946270	-3.484718	26976.633082
HLA A*0219	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.431096	0.946270	-3.484826	26983.347184
HLA B*4002	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.511507	1.026649	-3.484858	32471.843522
HLA B*1517	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.399895	0.914880	-3.485015	25112.772392
HLA A*8001	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.414264	0.929186	-3.485078	25957.574596
HLA A*3201	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.235546	0.750403	-3.485143	17200.688663
HLA A*0101	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.389766	0.904590	-3.485176	24533.868357
HLA B*4002	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.646638	1.161199	-3.485438	44323.860096
HLA B*4403	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.570855	1.085412	-3.485443	37226.734049
HLA B*1501	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.359115	0.873492	-3.485623	22862.022577
HLA B*3801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.496334	1.010656	-3.485678	31356.961398
HLA B*1509	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.454501	0.968816	-3.485686	28477.469205
HLA A*0250	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.486753	1.001026	-3.485726	30672.753999
HLA B*4601	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.377840	0.892112	-3.485728	23869.319887
HLA B*4801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.430036	0.944277	-3.485759	26917.591844
HLA B*4001	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.404182	0.918327	-3.485855	25361.939989
HLA B*0802	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.446837	0.960920	-3.485917	27979.333882
HLA B*5401	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.481899	0.995952	-3.485947	30331.838539
HLA A*0203	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.355952	0.869990	-3.485963	22696.152582
HLA B*1801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.339388	0.853416	-3.485973	21846.827181
HLA A*0203	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.407467	0.921444	-3.486023	25554.480151
HLA A*2902	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.447664	0.961636	-3.486029	28032.665158
HLA B*5301	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.590424	1.104337	-3.486087	38942.497190
HLA B*4501	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.654835	1.168679	-3.486156	45168.423063
HLA A*6802	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.315543	0.829345	-3.486198	20679.662657
HLA A*0202	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.509101	1.022881	-3.486220	32292.455729
HLA B*5401	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.380847	0.894591	-3.486257	24035.180367
HLA B*3801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.471584	0.985326	-3.486258	29619.961954
HLA B*3901	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.440950	0.954621	-3.486328	27602.572636
HLA B*3901	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.447606	0.961256	-3.486349	28028.874074
HLA B*0702	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.380159	0.893801	-3.486358	23997.112441
HLA A*3101	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.301663	0.815296	-3.486367	20029.158002
HLA A*6802	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.430678	0.944277	-3.486400	26957.375800
HLA B*2705	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.045038	0.558588	-3.486449	11092.714711
HLA B*4001	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.359946	0.873492	-3.486454	22905.847605
HLA A*3001	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.270257	0.783751	-3.486506	18631.899223
HLA B*5401	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.548403	1.061692	-3.486711	35351.126531
HLA B*4002	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.605388	1.118640	-3.486747	40307.667484
HLA A*0202	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.517876	1.031103	-3.486773	32951.591826
HLA B*5701	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.404972	0.918162	-3.486810	25408.082889
HLA B*1503	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.283809	0.796898	-3.486911	19222.459564
HLA B*5401	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.396157	0.909118	-3.487038	24897.550953
HLA A*2603	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.605679	1.118640	-3.487039	40334.715997
HLA A*0201	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.385262	0.898050	-3.487212	24280.748350
HLA A*1101	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.429498	0.942253	-3.487245	26884.265240
HLA A*6901	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.385304	0.898050	-3.487254	24283.112876
HLA B*4801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.278774	0.791452	-3.487322	19000.892883
HLA B*4501	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.379473	0.892112	-3.487361	23959.234425
HLA A*2601	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.392665	0.905205	-3.487460	24698.199545
HLA A*3001	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-3.833561	0.346054	-3.487506	6816.488379

HLA A*0206	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.431784	0.944277	-3.487507	27026.152337
HLA B*2705	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.429829	0.942253	-3.487576	26904.780230
HLA A*1101	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.461900	0.974301	-3.487599	28966.759873
HLA B*4403	1:90-98	9	IVMEYVDGV	0.902945	0.210828	-4.601436	1.113773	-3.487663	39942.554224
HLA B*1501	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.286415	0.798696	-3.487718	19338.132646
HLA B*5301	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.557477	1.069720	-3.487757	36097.487032
HLA A*2902	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.386658	0.898882	-3.487776	24358.899408
HLA B*4402	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.408000	0.920120	-3.487880	25585.881476
HLA A*6802	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.009692	0.521798	-3.487894	10225.679845
HLA B*5301	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.574694	1.086732	-3.487962	37557.268169
HLA B*5301	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.561636	1.073598	-3.488037	36444.798845
HLA A*8001	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.409903	0.921765	-3.488139	25698.245079
HLA A*8001	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.449786	0.961636	-3.488150	28169.943407
HLA A*3201	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.549865	1.061692	-3.488173	35470.281704
HLA B*1502	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.570961	1.082637	-3.488323	37235.797815
HLA A*6802	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.307701	0.819348	-3.488353	20309.576570
HLA A*2603	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.525047	1.036678	-3.488369	33500.171284
HLA A*2301	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.505932	1.017549	-3.488383	32057.645169
HLA A*0202	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.437515	0.949124	-3.488391	27385.117856
HLA A*6801	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.571069	1.082637	-3.488431	37245.065278
HLA B*4402	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.332596	0.844164	-3.488432	21507.801126
HLA B*4501	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.649640	1.161199	-3.488441	44631.369910
HLA B*2705	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.395811	0.907250	-3.488561	24877.758954
HLA B*0803	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.495155	1.006578	-3.488576	31271.918810
HLA A*0301	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.262356	0.773768	-3.488587	18295.985544
HLA B*3801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.519725	1.031103	-3.488622	33092.185036
HLA B*0702	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.380735	0.892112	-3.488622	24028.939850
HLA B*5801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.342128	0.853416	-3.488712	21985.071011
HLA A*6901	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.403630	0.914880	-3.488751	25329.717235
HLA A*6801	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.632045	1.143250	-3.488795	42859.285237
HLA B*4501	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.632066	1.143250	-3.488816	42861.372064
HLA A*6802	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.410378	0.921444	-3.488934	25726.343410
HLA B*3501	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.700340	0.211378	-3.488962	5015.799872
HLA B*2705	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.444728	0.955683	-3.489044	27843.737662
HLA A*3002	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.431375	0.942253	-3.489122	27000.724030
HLA B*7301	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.471500	0.982334	-3.489166	29614.193850
HLA A*0250	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.377570	0.888375	-3.489195	23854.474513
HLA B*3901	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.333397	0.844164	-3.489233	21547.514739
HLA A*3101	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.333402	0.844164	-3.489238	21547.747880
HLA B*5101	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.458084	0.968816	-3.489269	28713.382444
HLA A*6801	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.571153	1.081848	-3.489306	37252.319685
HLA A*2602	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.531666	1.042359	-3.489306	34014.612425
HLA A*6901	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.394538	0.905205	-3.489333	24804.920226
HLA A*0203	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.179950	0.690572	-3.489378	15133.869039
HLA B*3501	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-3.915506	0.426123	-3.489383	8232.012791
HLA A*8001	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.377424	0.887960	-3.489464	23846.474750
HLA B*4001	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.394075	0.904590	-3.489485	24778.498510
HLA B*7301	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.589056	1.099547	-3.489509	38820.077401
HLA A*0203	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.435811	0.946270	-3.489541	27277.919142
HLA A*3301	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.587440	1.097819	-3.489621	38675.857488
HLA B*7301	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.587501	1.097819	-3.489682	38681.297905
HLA A*2403	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.411156	0.921444	-3.489711	25772.452157
HLA A*2402	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.559434	1.069720	-3.489714	36260.525192
HLA A*3301	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.565491	1.075727	-3.489764	36769.782623
HLA A*2601	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.383843	0.894030	-3.489813	24201.538713
HLA A*3001	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.286013	0.796188	-3.489825	19320.251385
HLA B*1517	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.450756	0.960920	-3.489836	28232.953432
HLA B*1801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.419043	0.929186	-3.489857	26244.781610
HLA A*0206	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.451600	0.961636	-3.489964	28287.839349
HLA B*5401	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.474094	0.984065	-3.490029	29791.594381
HLA A*2603	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.486095	0.995952	-3.490143	30626.327036
HLA A*3002	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.271650	0.781429	-3.490221	18691.767532
HLA B*2705	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.419466	0.929186	-3.490280	26270.350702
HLA B*0801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.394871	0.904590	-3.490282	24823.982793
HLA B*0802	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.451562	0.961256	-3.490306	28285.390910

HLA A*2501	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.444937	0.954621	-3.490315	27857.147097
HLA B*2705	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.446454	0.956046	-3.490408	27954.672247
HLA A*0206	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.343857	0.853416	-3.490441	22072.782999
HLA B*4801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.411891	0.921444	-3.490447	25816.129498
HLA A*2902	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.405963	0.915512	-3.490452	25466.155126
HLA B*4501	1:128-136	9	FSHQNGIIH	1.313839	-0.180798	-4.623509	1.133041	-3.490469	42025.147368
HLA B*4801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.406017	0.915512	-3.490506	25469.324012
HLA A*2403	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.395445	0.904921	-3.490524	24856.772408
HLA B*4002	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.593379	1.102823	-3.490557	39208.429722
HLA B*1501	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.283997	0.793337	-3.490660	19230.780674
HLA B*4601	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.385269	0.894591	-3.490678	24281.142422
HLA A*2501	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.216658	0.725976	-3.490682	16468.662337
HLA B*0802	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.412462	0.921765	-3.490698	25850.089778
HLA A*0201	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.395908	0.905205	-3.490703	24883.277589
HLA A*0211	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.379095	0.888375	-3.490719	23938.375206
HLA B*5301	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.573442	1.082637	-3.490804	37449.128862
HLA A*0101	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.364326	0.873492	-3.490834	23137.999482
HLA B*1502	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.572782	1.081848	-3.490934	37392.242738
HLA B*3801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.520080	1.029142	-3.490938	33119.228864
HLA B*4501	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.645916	1.154927	-3.490990	44250.306532
HLA B*5101	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.446682	0.955683	-3.490999	27969.345569
HLA B*7301	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-3.847658	0.356622	-3.491035	7041.377183
HLA B*5101	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.492117	1.001026	-3.491090	31053.935439
HLA B*5701	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.400238	0.909118	-3.491119	25132.615396
HLA B*5401	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.520299	1.029142	-3.491157	33135.895992
HLA A*8001	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.411337	0.920120	-3.491216	25783.190204
HLA B*4001	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.379179	0.887960	-3.491219	23943.037802
HLA A*2602	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.476587	0.985326	-3.491260	29963.086629
HLA B*5301	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.514265	1.022974	-3.491292	32678.735326
HLA B*5701	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.396497	0.905205	-3.491292	24917.089099
HLA B*1501	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-3.917428	0.426123	-3.491304	8268.522552
HLA B*4402	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.396307	0.904921	-3.491386	24906.172797
HLA B*0702	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.379924	0.888375	-3.491549	23984.133781
HLA A*2402	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.520905	1.029142	-3.491763	33182.177757
HLA B*0702	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.409972	0.918162	-3.491810	25702.277110
HLA B*4403	1:329-337	9	VGRWVAVVA	1.430600	-0.275902	-4.646670	1.154698	-3.491973	44327.217243
HLA A*0219	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.436448	0.944464	-3.491984	27317.940082
HLA B*7301	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.574739	1.082637	-3.492101	37561.128800
HLA A*0203	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.154599	0.662443	-3.492156	14275.753103
HLA A*2403	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.436455	0.944277	-3.492178	27318.383447
HLA A*0212	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.390250	0.898050	-3.492200	24561.225053
HLA A*2403	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.321640	0.829345	-3.492295	20972.024843
HLA A*6901	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.279235	0.786863	-3.492371	19021.050942
HLA B*7301	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-3.804939	0.312328	-3.492611	6381.742437
HLA A*0206	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.274322	0.781690	-3.492632	18807.095747
HLA A*0301	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.366194	0.873492	-3.492702	23237.727126
HLA A*2301	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.515715	1.022974	-3.492741	32787.995978
HLA A*0212	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-3.589679	0.096922	-3.492757	3887.581050
HLA A*0212	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.414701	0.921765	-3.492937	25983.707275
HLA B*1517	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.226155	0.733042	-3.493113	16832.744969
HLA B*4001	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.387163	0.894030	-3.493133	24387.248365
HLA A*6801	1:318-326	9	DDTDRDRSI	1.189328	-0.034401	-4.648207	1.154927	-3.493280	44484.327700
HLA A*2402	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.575286	1.081848	-3.493438	37608.504612
HLA A*8001	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.411668	0.918162	-3.493506	25802.864979
HLA A*2601	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.385680	0.892112	-3.493568	24304.141007
HLA B*1801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.268286	0.774481	-3.493804	18547.522585
HLA B*5401	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.413942	0.920120	-3.493822	25938.343142
HLA B*4501	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.593394	1.099547	-3.493846	39209.702422
HLA B*5701	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.415291	0.921444	-3.493847	26019.014054
HLA A*8001	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.409380	0.915512	-3.493868	25667.261274
HLA A*8001	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.408919	0.914880	-3.494039	25640.059718
HLA B*1517	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.409596	0.915512	-3.494084	25680.039301
HLA A*2902	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.369180	0.875034	-3.494146	23398.059608
HLA A*0203	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.399399	0.905205	-3.494194	25084.122853
HLA A*0101	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.392301	0.898050	-3.494251	24677.497975

HLA B*4403	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.591810	1.097502	-3.494308	39066.993780
HLA A*0201	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.393316	0.898882	-3.494434	24735.238513
HLA A*0203	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.416205	0.921765	-3.494440	26073.827342
HLA A*0212	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.391885	0.897363	-3.494523	24653.879337
HLA B*1502	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.598884	1.104337	-3.494547	39708.574147
HLA A*0212	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.309865	0.815296	-3.494569	20411.021711
HLA B*1502	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.463455	0.968816	-3.494639	29070.685867
HLA B*1801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.450366	0.955683	-3.494683	28207.610446
HLA A*0219	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.241384	0.746693	-3.494692	17433.488729
HLA B*3901	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.423920	0.929186	-3.494735	26541.196302
HLA A*0211	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.338958	0.844164	-3.494794	21825.209312
HLA B*0803	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.463683	0.968816	-3.494867	29085.944981
HLA B*4801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.409758	0.914880	-3.494878	25689.626996
HLA A*2501	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.444023	0.949124	-3.494899	27798.584853
HLA B*5101	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.460204	0.965301	-3.494903	28853.838125
HLA A*0201	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.364908	0.869990	-3.494919	23169.063471
HLA B*1509	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.450672	0.955683	-3.494988	28227.455430
HLA A*1101	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.388805	0.893801	-3.495004	24479.643637
HLA A*6802	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.342852	0.847787	-3.495065	22021.734081
HLA A*3001	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.250242	0.755176	-3.495065	17792.700309
HLA B*4001	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.402592	0.907250	-3.495342	25269.221906
HLA B*5801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.358215	0.862842	-3.495373	22814.701792
HLA B*5401	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.518356	1.022974	-3.495382	32987.977850
HLA A*3001	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.157888	0.662443	-3.495446	14384.285928
HLA A*2501	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.451205	0.955683	-3.495522	28262.141304
HLA B*5701	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.394418	0.898882	-3.495536	24798.077385
HLA A*2301	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.449878	0.954333	-3.495544	28175.887488
HLA A*1101	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.450277	0.954621	-3.495656	28201.812240
HLA A*2603	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.600068	1.104337	-3.495731	39816.990652
HLA B*1509	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.450380	0.954621	-3.495759	28208.526061
HLA A*0301	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.368924	0.873123	-3.495801	23384.266356
HLA B*3501	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.268577	0.772678	-3.495899	18559.968924
HLA B*2705	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.416047	0.920120	-3.495927	26064.378268
HLA A*0301	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.356079	0.860149	-3.495930	22702.783869
HLA A*6901	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.210916	0.714935	-3.495981	16252.350650
HLA B*1503	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.193586	0.697387	-3.496199	15616.596257
HLA A*0206	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-3.763800	0.267585	-3.496215	5804.967464
HLA A*2602	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.565935	1.069720	-3.496215	36807.397814
HLA A*0301	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.280043	0.783751	-3.496292	19056.482112
HLA A*2403	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.361459	0.865145	-3.496314	22985.790036
HLA B*4402	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.388460	0.892112	-3.496347	24460.183848
HLA A*2403	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.344059	0.847664	-3.496395	22083.054760
HLA A*0216	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.359272	0.862842	-3.496430	22870.310706
HLA B*5701	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.390266	0.893801	-3.496466	24562.155185
HLA A*2402	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.570143	1.073598	-3.496545	37165.762106
HLA B*4002	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.533226	1.036678	-3.496548	34137.018292
HLA B*0801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.289983	0.793337	-3.496646	19497.700840
HLA A*3002	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.401250	0.904590	-3.496661	25191.284537
HLA A*0301	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.329831	0.833148	-3.496683	21371.286588
HLA A*0206	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.218707	0.722004	-3.496703	16546.535525
HLA B*4402	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.414901	0.918162	-3.496739	25995.658386
HLA B*0801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.394853	0.898050	-3.496802	24822.908456
HLA A*2902	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.415216	0.918327	-3.496889	26014.510124
HLA B*3801	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.519982	1.022974	-3.497008	33111.704521
HLA B*4402	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.441708	0.944464	-3.497244	27650.847376
HLA A*8001	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.391281	0.894030	-3.497251	24619.625843
HLA B*0702	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.453411	0.956046	-3.497365	28406.075031
HLA A*0212	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.443668	0.946270	-3.497398	27775.885649
HLA B*3901	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.466427	0.968816	-3.497612	29270.313688
HLA A*2602	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.584414	1.086732	-3.497682	38407.303262
HLA B*4002	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.626246	1.128536	-3.497710	42290.848148
HLA B*4402	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.395360	0.897363	-3.497997	24851.931874
HLA B*0801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.371492	0.873492	-3.498000	23522.947337
HLA B*1502	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.342302	0.844164	-3.498138	21993.874096
HLA B*4403	1:458-466	9	PSTPELVGK	1.142224	0.018975	-4.659365	1.161199	-3.498166	45642.007253

HLA B*5701	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.405515	0.907250	-3.498265	25439.854822
HLA B*1503	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.327824	0.829510	-3.498315	21272.778007
HLA A*2301	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-3.791707	0.293372	-3.498335	6190.232667
HLA A*0301	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.368339	0.869990	-3.498349	23352.787497
HLA B*0801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.280052	0.781690	-3.498362	19056.894490
HLA A*3301	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.513405	1.014988	-3.498417	32614.094811
HLA B*0802	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.447742	0.949124	-3.498618	28037.670174
HLA A*0206	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.454325	0.955683	-3.498642	28465.917052
HLA B*1509	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.482768	0.984065	-3.498703	30392.613341
HLA A*0211	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.541099	1.042359	-3.498739	34761.516056
HLA B*0801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.420222	0.921444	-3.498778	26316.153123
HLA A*3201	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.454478	0.955683	-3.498794	28475.928647
HLA B*4601	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.403402	0.904590	-3.498813	25316.428718
HLA A*0219	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.372307	0.873492	-3.498815	23567.146829
HLA B*7301	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.585560	1.086732	-3.498829	38508.833500
HLA A*0202	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.220897	0.722004	-3.498892	16630.174110
HLA B*5101	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.445237	0.946270	-3.498968	27876.443899
HLA A*2602	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.602293	1.103143	-3.499150	40021.503093
HLA B*1503	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.460852	0.961636	-3.499216	28896.952819
HLA B*3501	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.290232	0.790996	-3.499237	19508.884969
HLA A*2501	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.387637	0.888375	-3.499262	24413.913259
HLA B*5101	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.419417	0.920120	-3.499296	26267.366358
HLA B*2705	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.387278	0.887960	-3.499318	24393.713905
HLA B*4403	1:201-209	9	SLGCVLYEV	1.046700	0.073642	-4.619675	1.120342	-3.499333	41655.743026
HLA A*0211	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.514338	1.014994	-3.499344	32684.216224
HLA B*1801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.298094	0.798696	-3.499398	19865.240389
HLA A*3001	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.282787	0.783381	-3.499406	19177.276501
HLA B*1801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.460392	0.960920	-3.499472	28866.328512
HLA A*2301	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.534283	1.034768	-3.499514	34220.224400
HLA A*3002	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.290622	0.790996	-3.499627	19526.412629
HLA B*4601	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.404866	0.905205	-3.499661	25401.898171
HLA A*2602	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.482101	0.982334	-3.499767	30345.953724
HLA B*4801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.418117	0.918327	-3.499790	26188.900531
HLA B*1503	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.154016	0.654207	-3.499809	14256.612846
HLA A*0219	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.232649	0.732827	-3.499822	17086.335120
HLA B*5401	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.391975	0.892112	-3.499862	24658.948099
HLA A*0250	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.510527	1.010656	-3.499871	32398.672084
HLA A*0216	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.404883	0.904921	-3.499961	25402.860140
HLA A*2603	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.612969	1.112976	-3.499994	41017.525364
HLA B*4501	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.618686	1.118640	-3.500045	41560.977391
HLA B*5301	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.329669	0.829510	-3.500159	21363.310553
HLA A*3101	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.329612	0.829345	-3.500267	21360.536977
HLA A*0250	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.409457	0.909118	-3.500339	25671.843965
HLA B*4001	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.365637	0.865145	-3.500491	23207.952112
HLA A*0212	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.408639	0.908065	-3.500575	25623.558555
HLA A*2501	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.415467	0.914880	-3.500587	26029.573194
HLA A*2602	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.623420	1.122659	-3.500761	42016.508903
HLA B*5701	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.408943	0.908065	-3.500878	25641.446855
HLA B*1801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.422351	0.921444	-3.500907	26445.454669
HLA B*1502	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.562672	1.061692	-3.500980	36531.851230
HLA B*1502	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.587767	1.086732	-3.501035	38704.951688
HLA A*0101	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.406353	0.905205	-3.501148	25489.035064
HLA A*6802	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.117684	0.616515	-3.501168	13112.452258
HLA A*8001	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.408466	0.907250	-3.501216	25613.302682
HLA A*2301	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.532502	1.031103	-3.501399	34080.184989
HLA B*1517	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.216348	0.714935	-3.501413	16456.906175
HLA B*5801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.361563	0.860149	-3.501414	22991.262113
HLA B*0702	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.374675	0.873256	-3.501419	23696.013492
HLA B*1801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.374544	0.873123	-3.501421	23688.835782
HLA A*0206	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.389935	0.888375	-3.501560	24543.426455
HLA A*2301	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.528381	1.026649	-3.501732	33758.329419
HLA B*4001	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.399143	0.897363	-3.501780	25069.335660
HLA A*6901	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.300643	0.798791	-3.501852	19982.186867
HLA B*4403	1:487-495	9	IVGSGPATK	0.962871	0.205808	-4.670541	1.168679	-3.501862	46831.841561
HLA B*7301	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.551704	1.049687	-3.502017	35620.850478

HLA B*4501	1:243-251	9	LSADLDAVV	0.948699	0.148803	-4.599615	1.097502	-3.502113	39775.439085
HLA B*1509	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.394237	0.892112	-3.502125	24787.749613
HLA A*0216	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.217072	0.714935	-3.502137	16484.350285
HLA B*1502	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.571325	1.069099	-3.502226	37267.034348
HLA B*4001	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.410291	0.908065	-3.502226	25721.194389
HLA B*5301	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.587654	1.085412	-3.502242	38694.902297
HLA A*2301	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.411438	0.909118	-3.502319	25789.188722
HLA A*3101	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.276281	0.773768	-3.502513	18892.142210
HLA B*1509	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.467983	0.965301	-3.502682	29375.328762
HLA A*0101	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.342605	0.839877	-3.502728	22009.228444
HLA B*5801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.346973	0.844164	-3.502808	22231.691680
HLA A*3101	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.372822	0.869990	-3.502832	23595.084923
HLA A*2403	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.300359	0.797462	-3.502897	19969.110876
HLA A*6801	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.605740	1.102823	-3.502917	40340.389761
HLA B*1509	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.509540	1.006578	-3.502962	32325.140898
HLA B*1503	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.373125	0.869990	-3.503135	23611.557107
HLA B*5801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.351051	0.847787	-3.503264	22441.465625
HLA A*0202	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.459029	0.955683	-3.503345	28775.895554
HLA B*2705	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.401431	0.898050	-3.503381	25201.780441
HLA A*0203	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.376541	0.873123	-3.503418	23798.017500
HLA B*4501	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.532610	1.029142	-3.503468	34088.667066
HLA A*1101	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.363659	0.860149	-3.503510	23102.477358
HLA B*4002	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.646830	1.143250	-3.503580	44343.527006
HLA B*5701	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.376837	0.873256	-3.503581	23814.244854
HLA A*0219	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.423714	0.920120	-3.503594	26528.563836
HLA B*1801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.499630	0.995952	-3.503678	31595.868584
HLA A*2602	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-3.969159	0.465424	-3.503735	9314.485609
HLA B*0802	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.469040	0.965301	-3.503739	29446.928652
HLA B*0702	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.295202	0.791452	-3.503750	19733.385894
HLA A*2402	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.448043	0.944277	-3.503765	28057.092026
HLA A*0202	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.518811	1.014994	-3.503818	33022.617517
HLA A*2301	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.526739	1.022881	-3.503857	33630.912940
HLA B*7301	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.577574	1.073598	-3.503976	37807.195564
HLA A*2602	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.606912	1.102823	-3.504090	40449.437165
HLA B*2705	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.465802	0.961636	-3.504167	29228.223105
HLA A*2601	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.377438	0.873256	-3.504182	23847.248804
HLA B*4801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.409140	0.904921	-3.504219	25653.101763
HLA A*0101	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.367065	0.862842	-3.504224	23284.413680
HLA B*4501	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.202115	0.697848	-3.504267	15926.304431
HLA A*2501	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.411623	0.907250	-3.504373	25800.212893
HLA B*3801	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.531026	1.026649	-3.504378	33964.597076
HLA A*0206	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.295427	0.790996	-3.504432	19743.637077
HLA A*2403	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.330991	0.826538	-3.504453	21428.477423
HLA B*1517	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.425979	0.921444	-3.504534	26667.275213
HLA A*3002	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.424684	0.920120	-3.504564	26587.902452
HLA B*5101	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.374605	0.869990	-3.504615	23692.168020
HLA A*0212	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.393011	0.888375	-3.504635	24717.848692
HLA B*1509	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.453771	0.949124	-3.504647	28429.596843
HLA B*0702	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.286379	0.781690	-3.504689	19336.563453
HLA B*4402	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.379729	0.875034	-3.504695	23973.366823
HLA B*4501	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.572063	1.067242	-3.504821	37330.393852
HLA B*0702	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.410091	0.905205	-3.504886	25709.369459
HLA A*2301	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.519897	1.014994	-3.504903	33105.256446
HLA A*6901	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.142321	0.637402	-3.504918	13877.799850
HLA B*0702	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.403943	0.898882	-3.505061	25347.948911
HLA A*2602	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.423234	0.918162	-3.505073	26499.302601
HLA B*4402	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.378571	0.873492	-3.505079	23909.513236
HLA B*5701	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.397228	0.892112	-3.505116	24959.046778
HLA A*3101	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.380152	0.875034	-3.505118	23996.722979
HLA A*3101	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.128463	0.623337	-3.505126	13441.983474
HLA B*4801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.425250	0.920120	-3.505130	26622.589922
HLA A*2603	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.574370	1.069099	-3.505270	37529.239703
HLA B*3801	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.487735	0.982334	-3.505401	30742.193814
HLA A*3002	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.540260	1.034768	-3.505492	34694.444872
HLA A*8001	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.296491	0.790996	-3.505496	19792.081747

HLA A*3101	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.393946	0.888375	-3.505571	24771.126916
HLA B*0803	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.403637	0.898050	-3.505587	25330.128331
HLA A*3301	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.631920	1.126330	-3.505591	42846.998207
HLA B*4801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.412890	0.907250	-3.505640	25875.554306
HLA A*0301	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.368517	0.862842	-3.505675	23362.391007
HLA B*5401	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.540455	1.034768	-3.505687	34710.026897
HLA B*0702	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.427200	0.921444	-3.505756	26742.399672
HLA B*5701	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.252638	0.746693	-3.505946	17891.153362
HLA B*1801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.394559	0.888375	-3.506184	24806.127983
HLA A*2902	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.450496	0.944277	-3.506218	28216.004697
HLA A*2403	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.321521	0.815296	-3.506224	20966.239369
HLA A*3002	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.452549	0.946270	-3.506279	28349.732727
HLA A*2403	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.413576	0.907250	-3.506326	25916.461901
HLA B*7301	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.568078	1.061692	-3.506386	36989.447580
HLA A*3301	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.588290	1.081848	-3.506443	38751.673723
HLA B*2705	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.321746	0.815296	-3.506450	20977.131000
HLA B*4001	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.411449	0.904921	-3.506528	25789.886315
HLA B*4402	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.421533	0.914880	-3.506654	26395.714197
HLA A*0216	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.297690	0.790996	-3.506694	19846.764361
HLA A*0301	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.305565	0.798791	-3.506774	20209.947583
HLA A*0250	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.568538	1.061692	-3.506846	37028.689708
HLA B*4801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.423164	0.916286	-3.506878	26495.002201
HLA B*4601	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.381914	0.875034	-3.506880	24094.285480
HLA B*1502	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.580483	1.073598	-3.506885	38061.256923
HLA A*1101	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.468544	0.961636	-3.506909	29413.334555
HLA B*4001	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.400736	0.893801	-3.506935	25161.456440
HLA A*3301	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.635517	1.128536	-3.506981	43203.353924
HLA B*3901	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.360421	0.853416	-3.507005	22930.892742
HLA A*3101	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.261703	0.754459	-3.507244	18268.489992
HLA A*6801	1:402-410	9	TDPAANTSV	1.153412	-0.027082	-4.633605	1.126330	-3.507275	43013.519773
HLA B*4501	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.620488	1.112976	-3.507512	41733.788168
HLA B*3801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.501895	0.994371	-3.507524	31761.075660
HLA B*3801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.549893	1.042359	-3.507534	35472.584462
HLA B*3501	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.429364	0.921765	-3.507600	26875.976387
HLA B*1801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.395635	0.887960	-3.507675	24867.667058
HLA B*1502	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.538794	1.031103	-3.507691	34577.521841
HLA B*5701	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.401760	0.894030	-3.507730	25220.875109
HLA B*1502	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.294624	0.786863	-3.507760	19707.141526
HLA A*2902	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.413054	0.905205	-3.507849	25885.355033
HLA A*8001	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.402660	0.894591	-3.508069	25273.186624
HLA A*6801	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.636805	1.128536	-3.508269	43331.625463
HLA B*4002	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.640440	1.132158	-3.508282	43695.793860
HLA B*5701	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.406485	0.898050	-3.508435	25496.758234
HLA A*3101	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.381893	0.873256	-3.508637	24093.112382
HLA A*0202	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.494067	0.985326	-3.508740	31193.687591
HLA A*0101	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.382001	0.873256	-3.508745	24099.108817
HLA B*0801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.407683	0.898882	-3.508801	25567.202032
HLA A*2403	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.407777	0.898882	-3.508895	25572.735260
HLA A*8001	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.397315	0.888375	-3.508940	24964.043228
HLA B*0802	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.425262	0.916286	-3.508976	26623.310058
HLA A*3101	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.382471	0.873492	-3.508979	24125.197629
HLA A*0216	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.455256	0.946270	-3.508986	28526.965414
HLA A*2602	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.608574	1.099547	-3.509026	40604.444079
HLA A*0211	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.235292	0.725976	-3.509316	17190.641786
HLA B*5801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.357089	0.847664	-3.509426	22755.657748
HLA A*0201	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.317388	0.807959	-3.509429	20767.671026
HLA A*8001	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.374626	0.865145	-3.509480	23693.321596
HLA A*0201	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.382786	0.873123	-3.509663	24142.692932
HLA A*3301	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.546493	1.036678	-3.509815	35195.985221
HLA A*8001	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.456087	0.946270	-3.509817	28581.649773
HLA A*2403	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.403886	0.894030	-3.509856	25344.658014
HLA A*0212	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.431488	0.921444	-3.510044	27007.736345
HLA A*2601	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.380084	0.869990	-3.510094	23992.958506
HLA B*5701	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.385182	0.875034	-3.510148	24276.282651
HLA A*0216	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.200827	0.690572	-3.510256	15879.158921

HLA B*1502	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.466324	0.956046	-3.510278	29263.347154
HLA A*6802	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.222180	0.711889	-3.510291	16679.368929
HLA B*3801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.475600	0.965301	-3.510299	29895.083185
HLA B*0702	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.358097	0.847787	-3.510310	22808.531376
HLA A*2402	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.545112	1.034768	-3.510343	35084.204153
HLA A*0219	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.418500	0.908065	-3.510435	26212.004401
HLA B*0801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.370590	0.860149	-3.510441	23474.131549
HLA A*0250	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.597237	1.086732	-3.510506	39558.271219
HLA B*4403	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.572281	1.061692	-3.510589	37349.180233
HLA A*3001	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.306470	0.795837	-3.510633	20252.084876
HLA A*2403	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.425582	0.914880	-3.510702	26642.905231
HLA A*3101	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.358506	0.847787	-3.510719	22830.011627
HLA B*5401	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.310736	0.799991	-3.510745	20452.029176
HLA A*2602	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.592825	1.081848	-3.510977	39158.402935
HLA B*5801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.301987	0.790996	-3.510991	20044.116647
HLA A*1101	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.440299	0.929186	-3.511113	27561.240073
HLA B*3501	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.410082	0.898882	-3.511200	25708.813125
HLA A*0216	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.432682	0.921444	-3.511237	27082.061730
HLA A*0206	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.495312	0.984065	-3.511247	31283.255764
HLA B*4501	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.643482	1.132158	-3.511324	44002.992966
HLA A*3201	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.244154	0.732827	-3.511327	17545.039412
HLA B*0802	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.457624	0.946270	-3.511354	28682.952682
HLA B*4402	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.440555	0.929186	-3.511369	27577.497121
HLA A*3301	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.630076	1.118640	-3.511436	42665.422988
HLA B*5301	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.593375	1.081848	-3.511527	39208.005497
HLA B*0801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.405334	0.893801	-3.511533	25429.259766
HLA B*5101	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.341064	0.829510	-3.511554	21931.258608
HLA B*4403	1:506-514	9	DVAQKNLNV	1.046483	0.085675	-4.643715	1.132158	-3.511557	44026.566358
HLA B*5801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.233633	0.722004	-3.511629	17125.109389
HLA A*2301	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.518236	1.006578	-3.511658	32978.877579
HLA B*3901	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.460852	0.949124	-3.511728	28896.952819
HLA B*5401	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-3.825666	0.313851	-3.511816	6693.702850
HLA B*1517	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.480654	0.968816	-3.511838	30244.994401
HLA A*0211	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.385123	0.873123	-3.512001	24272.999574
HLA B*4002	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.534927	1.022881	-3.512045	34270.986981
HLA B*4801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.433892	0.921765	-3.512127	27157.620078
HLA A*2602	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.594780	1.082637	-3.512142	39335.053250
HLA B*1501	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.338726	0.826538	-3.512188	21813.523318
HLA B*3501	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.377377	0.865145	-3.512232	23843.894754
HLA A*0211	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.406908	0.894591	-3.512317	25521.598561
HLA B*4402	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.382501	0.869990	-3.512512	24126.894379
HLA B*0702	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.311244	0.798696	-3.512548	20475.942079
HLA B*5301	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.406393	0.893801	-3.512593	25491.379351
HLA A*2601	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.387659	0.875034	-3.512625	24415.101977
HLA B*4402	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.410698	0.898050	-3.512647	25745.278401
HLA B*3501	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.387708	0.875034	-3.512674	24417.875877
HLA A*0301	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.356838	0.844164	-3.512674	22742.489262
HLA B*3901	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.419973	0.907250	-3.512723	26301.066497
HLA A*6801	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.586416	1.073598	-3.512817	38584.739794
HLA A*2402	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.539475	1.026649	-3.512827	34631.811979
HLA B*1501	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.386056	0.873123	-3.512934	24325.187348
HLA A*3002	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.406739	0.893801	-3.512938	25511.659527
HLA A*2601	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.407559	0.894591	-3.512968	25559.872349
HLA A*2403	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.421038	0.908065	-3.512973	26365.601033
HLA A*0250	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.434749	0.921765	-3.512985	27211.298753
HLA A*0211	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.410348	0.897363	-3.512985	25724.534177
HLA A*2902	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.373486	0.860149	-3.513338	23631.236633
HLA B*3901	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.459637	0.946270	-3.513368	28816.243486
HLA A*0206	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-3.729944	0.216497	-3.513446	5369.621962
HLA A*1101	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.459767	0.946270	-3.513497	28824.818859
HLA B*5401	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.401499	0.887960	-3.513539	25205.734578
HLA A*0219	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.435485	0.921765	-3.513720	27257.414550
HLA A*0202	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.514780	1.001026	-3.513753	32717.474915
HLA B*1501	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.344520	0.830662	-3.513858	22106.482687
HLA A*3201	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.543072	1.029142	-3.513931	34919.842522

HLA A*2501	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.367467	0.853416	-3.514051	23305.963849
HLA B*4501	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.479474	0.965301	-3.514173	30162.967557
HLA B*0801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.340718	0.826538	-3.514180	21913.824626
HLA A*6901	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.286891	0.772678	-3.514214	19359.381594
HLA B*2705	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.264719	0.750403	-3.514316	18395.830121
HLA A*8001	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.413284	0.898882	-3.514402	25899.082288
HLA A*0219	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.435870	0.921444	-3.514426	27281.608654
HLA A*2601	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.264968	0.750403	-3.514565	18406.382202
HLA B*7301	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.543709	1.029142	-3.514567	34971.075350
HLA B*3501	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.387969	0.873256	-3.514712	24432.543159
HLA B*5801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.322773	0.807959	-3.514814	21026.782155
HLA B*7301	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.541491	1.026649	-3.514842	34792.935590
HLA B*4403	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.633499	1.118640	-3.514859	43003.049621
HLA A*2501	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.433036	0.918162	-3.514875	27104.193923
HLA A*3002	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.354968	0.839877	-3.515091	22644.764488
HLA B*0803	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.431441	0.916314	-3.515127	27004.814326
HLA A*0301	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.362970	0.847787	-3.515183	23065.886686
HLA A*0212	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.430109	0.914880	-3.515229	26922.106480
HLA A*0216	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.280348	0.765110	-3.515238	19069.888975
HLA B*7301	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.499419	0.984065	-3.515354	31580.488616
HLA B*4402	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.346033	0.830662	-3.515371	22183.635299
HLA A*3101	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.409499	0.894030	-3.515469	25674.343960
HLA B*5801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.262163	0.746693	-3.515470	18287.871045
HLA A*1101	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.380669	0.865145	-3.515523	24025.300296
HLA B*1509	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.433708	0.918162	-3.515547	27146.162758
HLA A*6802	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.306601	0.790996	-3.515606	20258.221252
HLA A*0211	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.227527	0.711889	-3.515638	16886.010025
HLA A*0101	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.369093	0.853416	-3.515677	23393.376583
HLA B*4601	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.355788	0.839877	-3.515911	22687.559352
HLA A*6802	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.314608	0.798696	-3.515912	20635.184434
HLA B*1501	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.299442	0.783381	-3.516061	19927.023327
HLA B*1502	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.585838	1.069720	-3.516118	38533.424113
HLA A*0301	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.248179	0.732039	-3.516140	17708.387466
HLA B*5301	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.280625	0.764421	-3.516205	19082.066448
HLA B*4403	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.545405	1.029142	-3.516264	35107.937384
HLA B*2705	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.389555	0.873256	-3.516298	24521.925969
HLA B*5401	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.432818	0.916314	-3.516504	27090.560699
HLA B*4002	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.586289	1.069720	-3.516569	38573.469526
HLA B*5801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.346000	0.829345	-3.516655	22181.955209
HLA B*1801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.414057	0.897363	-3.516695	25945.219908
HLA B*3801	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.500760	0.984065	-3.516695	31678.193049
HLA A*0202	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.214595	0.697848	-3.516747	16390.623608
HLA B*4001	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.405141	0.888375	-3.516766	25417.981571
HLA A*8001	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.376987	0.860149	-3.516839	23822.491557
HLA A*2601	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.389973	0.873123	-3.516850	24545.550983
HLA B*4001	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.386848	0.869990	-3.516858	24369.575842
HLA A*2402	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.499210	0.982334	-3.516876	31565.286898
HLA A*6901	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.356760	0.839877	-3.516883	22738.429491
HLA B*4601	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.405416	0.888375	-3.517041	25434.075154
HLA A*0206	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.240019	0.722962	-3.517058	17378.778762
HLA B*4801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.414422	0.897363	-3.517059	25966.984950
HLA B*4801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.422288	0.905205	-3.517083	26441.592143
HLA A*0219	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.303984	0.786863	-3.517121	20136.499874
HLA B*4403	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-3.657645	0.140490	-3.517155	4546.166722
HLA A*0101	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.332516	0.815296	-3.517220	21503.845425
HLA A*3001	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.291743	0.774481	-3.517262	19576.865941
HLA B*5401	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.548514	1.031103	-3.517410	35360.116220
HLA A*3301	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.602827	1.085412	-3.517415	40070.681484
HLA B*0802	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.472198	0.954621	-3.517576	29661.814320
HLA A*1101	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.437752	0.920120	-3.517632	27400.085141
HLA B*5401	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.357522	0.839877	-3.517645	22778.320453
HLA B*1501	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.282780	0.765110	-3.517669	19176.965263
HLA B*5801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.141085	0.623337	-3.517748	13838.365294
HLA B*3501	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.387875	0.869990	-3.517885	24427.256637
HLA A*6901	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.365587	0.847664	-3.517924	23205.315660

HLA B*5401	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.532939	1.014994	-3.517945	34114.495073
HLA A*6801	1:196-204	9	RSDVYSLGC	1.035170	0.119769	-4.673011	1.154939	-3.518071	47098.876173
HLA B*4403	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.585405	1.067242	-3.518164	38495.086272
HLA A*6801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.514188	0.995952	-3.518236	32672.901831
HLA A*0211	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.502304	0.984065	-3.518239	31790.987094
HLA A*6802	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.347823	0.829510	-3.518314	22275.272437
HLA B*5801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.311690	0.793337	-3.518353	20496.999689
HLA B*1801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.383573	0.865145	-3.518427	24186.486717
HLA A*2603	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.601109	1.082637	-3.518472	39912.529728
HLA B*7301	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.413078	0.894591	-3.518487	25886.755440
HLA A*2301	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.479791	0.961256	-3.518535	30185.004675
HLA A*2601	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.381550	0.862842	-3.518708	24074.090099
HLA A*2603	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.479636	0.960920	-3.518716	30174.228962
HLA A*2301	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.513100	0.994371	-3.518729	32591.165852
HLA B*1501	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.233676	0.714935	-3.518740	17126.777079
HLA B*1509	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.463028	0.944277	-3.518750	29042.076961
HLA A*6802	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.433645	0.914880	-3.518765	27142.197888
HLA B*5701	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.372208	0.853416	-3.518792	23561.792620
HLA A*2501	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.480073	0.961256	-3.518817	30204.606741
HLA B*0801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.293360	0.774481	-3.518878	19649.866879
HLA A*0201	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.216870	0.697848	-3.519021	16476.682717
HLA B*1501	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.389059	0.869990	-3.519069	24493.950489
HLA B*4001	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.381945	0.862842	-3.519103	24095.980056
HLA B*1517	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.480834	0.961636	-3.519199	30257.595925
HLA B*4801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.427367	0.908065	-3.519302	26752.673458
HLA B*0702	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.441168	0.921765	-3.519404	27616.463528
HLA B*3801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.468556	0.949124	-3.519432	29414.130180
HLA B*5101	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.501811	0.982334	-3.519477	31754.890602
HLA B*0803	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.411663	0.892112	-3.519551	25802.585799
HLA B*5801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.252650	0.733042	-3.519608	17891.637314
HLA B*1801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.438039	0.918327	-3.519712	27418.175343
HLA B*1503	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.317200	0.797462	-3.519738	20758.684907
HLA A*6801	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.530399	1.010656	-3.519743	33915.572655
HLA B*5301	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.514244	0.994371	-3.519873	32677.144269
HLA B*3501	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.424574	0.904590	-3.519984	26581.142944
HLA B*0802	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.440108	0.920120	-3.519988	27549.165356
HLA B*5701	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.417389	0.897363	-3.520026	26145.016834
HLA B*1502	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.526609	1.006578	-3.520031	33620.907755
HLA B*0702	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.335354	0.815296	-3.520058	21644.836393
HLA A*2402	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.250827	0.730675	-3.520152	17816.684336
HLA B*4002	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.485470	0.965301	-3.520169	30582.286512
HLA A*0201	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.383051	0.862842	-3.520209	24157.456294
HLA A*2902	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.425142	0.904921	-3.520221	26615.965585
HLA A*0101	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.393372	0.873123	-3.520250	24738.450279
HLA B*4002	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.307278	0.786863	-3.520415	20289.809136
HLA B*1509	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.125935	0.605498	-3.520437	13363.964437
HLA B*5801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.351265	0.830662	-3.520603	22452.516277
HLA B*4403	1:221-229	9	PVSVAYQHV	1.134938	0.008312	-4.663906	1.143250	-3.520656	46121.804456
HLA B*5301	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.589839	1.069099	-3.520740	38890.074533
HLA A*2501	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.437040	0.916286	-3.520754	27355.207811
HLA B*4402	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.408736	0.887960	-3.520776	25629.242630
HLA A*0101	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.368654	0.847787	-3.520867	23369.722658
HLA A*3301	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.643562	1.122659	-3.520903	44011.087455
HLA A*3001	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.285334	0.764363	-3.520971	19290.068585
HLA B*5801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.304729	0.783751	-3.520978	20171.062287
HLA B*3801	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.557665	1.036678	-3.520987	36113.113086
HLA B*4002	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.634096	1.112976	-3.521120	43062.181238
HLA A*0301	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.368928	0.847664	-3.521265	23384.519370
HLA B*4601	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.254252	0.732827	-3.521425	17957.771231
HLA A*1101	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.490254	0.968816	-3.521438	30920.998106
HLA A*2602	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.045672	0.524138	-3.521534	11108.929346
HLA B*3901	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.416167	0.894591	-3.521576	26071.570536
HLA A*2902	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.430760	0.909118	-3.521641	26962.480558
HLA A*0212	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.391650	0.869990	-3.521661	24640.545469
HLA B*5701	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.410286	0.888375	-3.521911	25720.916092

HLA A*2403	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.317761	0.795837	-3.521925	20785.542488
HLA B*4801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.426785	0.904590	-3.522195	26716.804734
HLA A*2301	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.532901	1.010656	-3.522245	34111.542310
HLA A*0301	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.337666	0.815296	-3.522370	21760.366249
HLA A*0301	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.354197	0.831818	-3.522380	22604.618259
HLA B*1517	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.414609	0.892112	-3.522497	25978.225663
HLA B*1517	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.114592	0.592081	-3.522511	13019.430802
HLA A*2602	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.416607	0.894030	-3.522576	26097.959167
HLA B*1801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.478685	0.956046	-3.522639	30108.189445
HLA A*2602	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.626996	1.104337	-3.522659	42363.894788
HLA A*0250	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.277125	0.754459	-3.522666	18928.869241
HLA A*0101	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.273093	0.750403	-3.522690	18753.958684
HLA A*0201	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.342055	0.819348	-3.522707	21981.384280
HLA A*3301	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.625617	1.102823	-3.522794	42229.577177
HLA B*4001	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.397872	0.875034	-3.522838	24996.071247
HLA A*2402	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.497154	0.974301	-3.522853	31416.220875
HLA B*1801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.430130	0.907250	-3.522880	26923.417322
HLA B*4601	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.220808	0.697848	-3.522959	16626.755700
HLA B*0802	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.452145	0.929186	-3.522959	28323.365544
HLA A*0212	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.385847	0.862842	-3.523005	24313.478073
HLA B*1503	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.103033	0.579907	-3.523126	12677.468248
HLA B*1517	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.396441	0.873256	-3.523185	24913.854140
HLA A*3301	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.507323	0.984065	-3.523258	32160.479309
HLA B*0801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.428678	0.905205	-3.523473	26833.554255
HLA A*0203	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.438400	0.914880	-3.523521	27441.027572
HLA A*3002	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.497826	0.974301	-3.523525	31464.866564
HLA A*0250	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.560282	1.036678	-3.523604	36331.410104
HLA B*1517	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.278072	0.754459	-3.523612	18970.182703
HLA A*3301	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.597385	1.073598	-3.523787	39571.755886
HLA B*2705	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.468208	0.944277	-3.523931	29390.588782
HLA B*1503	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.428589	0.904590	-3.523999	26828.038493
HLA B*0801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.397129	0.873123	-3.524007	24953.376344
HLA B*5801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.350621	0.826538	-3.524083	22419.259350
HLA A*2501	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.444239	0.920120	-3.524119	27812.423925
HLA A*0216	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.439162	0.914880	-3.524282	27489.168496
HLA B*5101	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.453592	0.929186	-3.524407	28417.910372
HLA B*1502	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.566774	1.042359	-3.524415	36878.553752
HLA A*0301	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.305889	0.781429	-3.524460	20225.041250
HLA A*0219	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.387391	0.862842	-3.524549	24400.049157
HLA B*0801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.356389	0.831818	-3.524572	22719.001838
HLA B*4001	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.397834	0.873256	-3.524578	24993.907725
HLA A*2602	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.593802	1.069099	-3.524703	39246.628704
HLA B*4601	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.394827	0.869990	-3.524837	24821.431319
HLA B*0702	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.469115	0.944277	-3.524838	29452.026841
HLA B*1517	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.469174	0.944277	-3.524897	29456.010416
HLA A*3002	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.510311	0.985326	-3.524985	32382.550959
HLA B*1503	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.299475	0.774481	-3.524994	19928.532626
HLA B*4801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.412965	0.887960	-3.525005	25880.034178
HLA B*4402	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.418832	0.893801	-3.525031	26232.006398
HLA A*2403	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.369257	0.844164	-3.525093	23402.237151
HLA B*0802	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.441429	0.916314	-3.525114	27633.052131
HLA A*2603	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.647974	1.122659	-3.525316	44460.509206
HLA A*2403	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.422722	0.897363	-3.525360	26468.068915
HLA B*0803	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.480068	0.954621	-3.525447	30204.279935
HLA B*5101	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.443673	0.918162	-3.525511	27776.186180
HLA B*3501	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.413926	0.888375	-3.525551	25937.360896
HLA A*2902	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.257690	0.732039	-3.525651	18100.464967
HLA B*3501	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.238680	0.712902	-3.525778	17325.271461
HLA A*6901	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.373573	0.847787	-3.525786	23635.967274
HLA B*4402	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.419886	0.894030	-3.525856	26295.802447
HLA A*2603	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.611283	1.085412	-3.525871	40858.510005
HLA B*0702	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.399451	0.873492	-3.525959	25087.108482
HLA A*3101	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.388864	0.862842	-3.526022	24482.954664
HLA B*4403	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.654750	1.128536	-3.526214	45159.627097
HLA B*4801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.420067	0.893801	-3.526267	26306.758547

HLA A*2603	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.455462	0.929186	-3.526277	28540.549486
HLA A*1101	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.418521	0.892112	-3.526409	26213.280668
HLA B*3901	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.482524	0.956046	-3.526478	30375.518401
HLA B*1517	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.048318	0.521798	-3.526520	11176.806308
HLA B*4801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.420619	0.894030	-3.526589	26340.224227
HLA B*5101	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.386770	0.860149	-3.526622	24365.225619
HLA B*1509	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.421266	0.894591	-3.526675	26379.440257
HLA B*3801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.488320	0.961636	-3.526684	30783.633372
HLA B*1517	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.059764	0.532852	-3.526913	11475.309711
HLA A*2603	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.630071	1.103143	-3.526928	42664.961360
HLA B*0702	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.443412	0.916286	-3.527126	27759.511651
HLA A*2602	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.292307	0.765110	-3.527197	19602.300531
HLA B*0801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.356786	0.829510	-3.527277	22739.782667
HLA A*3201	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.051480	0.524138	-3.527342	11258.489615
HLA B*3501	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.471624	0.944277	-3.527347	29622.686171
HLA A*2402	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.569762	1.042359	-3.527403	37133.204225
HLA B*5301	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.421456	0.894030	-3.527426	26391.002288
HLA A*2603	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.614184	1.086732	-3.527452	41132.408385
HLA B*2705	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-3.884117	0.356622	-3.527495	7658.027418
HLA B*4402	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.392646	0.865145	-3.527501	24697.130652
HLA B*1517	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.435642	0.908065	-3.527577	27267.296134
HLA B*0802	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.401076	0.873492	-3.527585	25181.201683
HLA A*8001	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.432557	0.904921	-3.527636	27074.297763
HLA A*6802	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.311589	0.783751	-3.527838	20492.232124
HLA B*5801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.357378	0.829510	-3.527869	22770.804774
HLA B*0801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.301686	0.773768	-3.527918	20030.241586
HLA A*0219	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.249976	0.722004	-3.527972	17781.826644
HLA A*3101	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.319110	0.790996	-3.528114	20850.187660
HLA B*3901	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.449584	0.921444	-3.528140	28156.840376
HLA B*5801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.360024	0.831818	-3.528206	22909.937267
HLA A*1101	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.319218	0.790996	-3.528222	20855.376977
HLA A*2301	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.502574	0.974301	-3.528273	31810.771605
HLA B*4402	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.436352	0.908065	-3.528287	27311.881486
HLA B*1801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.482662	0.954333	-3.528329	30385.215311
HLA B*0802	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.443851	0.915512	-3.528339	27787.608750
HLA B*4403	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.641436	1.112976	-3.528460	43796.138006
HLA A*0202	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.502800	0.974301	-3.528499	31827.296799
HLA B*4501	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.559831	1.031103	-3.528728	36293.692307
HLA A*6801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.422837	0.894030	-3.528807	26475.086122
HLA B*4001	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.312668	0.783751	-3.528917	20543.180417
HLA B*3501	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.283379	0.754459	-3.528920	19203.438559
HLA A*6901	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.324770	0.795837	-3.528933	21123.694481
HLA B*5301	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.512999	0.984065	-3.528934	32583.585206
HLA A*2603	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.598727	1.069720	-3.529007	39694.183884
HLA B*4402	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.348373	0.819348	-3.529025	22303.488874
HLA B*1502	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.427078	0.898050	-3.529028	26734.877713
HLA A*2403	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.325216	0.796188	-3.529029	21145.418245
HLA A*0101	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.373242	0.844164	-3.529078	23617.944766
HLA A*0206	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.490040	0.960920	-3.529120	30905.779448
HLA B*3501	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.445484	0.916286	-3.529199	27892.283287
HLA B*7301	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.195748	0.666540	-3.529208	15694.515332
HLA B*1503	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.961532	0.432298	-3.529235	9152.346373
HLA B*4801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.423878	0.894591	-3.529288	26538.611899
HLA B*0803	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.490286	0.960920	-3.529367	30923.340103
HLA A*3001	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.218745	0.689311	-3.529434	16547.967826
HLA B*4801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.428396	0.898882	-3.529514	26816.139922
HLA B*5801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.362731	0.833148	-3.529583	23053.162240
HLA A*2403	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.083856	0.554273	-3.529583	12129.866885
HLA B*2705	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.451036	0.921444	-3.529592	28251.135004
HLA A*0250	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.392508	0.862842	-3.529666	24689.248994
HLA A*3101	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.311150	0.781429	-3.529721	20471.511655
HLA B*3801	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.544710	1.014988	-3.529722	35051.763078
HLA A*0216	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.212674	0.682948	-3.529726	16318.250610
HLA B*3801	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.530792	1.001026	-3.529765	33946.227575
HLA B*4001	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.435024	0.905205	-3.529819	27228.527788

HLA B*5101	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.424480	0.894591	-3.529889	26575.391525
HLA A*3201	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.603508	1.073598	-3.529910	40133.596428
HLA B*3901	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.448252	0.918327	-3.529925	28070.604211
HLA A*1101	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.474434	0.944464	-3.529970	29814.973086
HLA B*4002	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.629644	1.099547	-3.530096	42622.974120
HLA B*5301	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.552992	1.022881	-3.530111	35726.609427
HLA A*2501	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.474441	0.944277	-3.530164	29815.456977
HLA A*2603	1:115-123	9	AIEVIADAC	1.009676	0.118860	-4.658822	1.128536	-3.530286	45585.004774
HLA A*0250	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.424893	0.894591	-3.530302	26600.707081
HLA B*5801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.349710	0.819348	-3.530362	22372.249850
HLA B*0803	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.479495	0.949124	-3.530371	30164.436197
HLA B*1509	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.446809	0.916314	-3.530495	27977.517560
HLA A*0301	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.361166	0.830662	-3.530504	22970.251469
HLA A*0250	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.561685	1.031103	-3.530582	36448.939489
HLA B*5801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.354303	0.823629	-3.530674	22610.121910
HLA B*1801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.220027	0.689311	-3.530716	16596.919466
HLA A*3201	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.565684	1.034768	-3.530915	36786.097718
HLA A*0212	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.436121	0.905205	-3.530916	27297.405407
HLA B*4001	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.391209	0.860149	-3.531060	24615.497316
HLA A*2602	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.562164	1.031103	-3.531061	36489.187377
HLA A*3001	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.301193	0.770046	-3.531147	20007.498616
HLA A*0211	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.904529	0.373369	-3.531160	8026.556047
HLA A*0202	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.451283	0.920120	-3.531162	28267.187291
HLA B*3901	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.263540	0.732333	-3.531207	18345.939158
HLA A*2403	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.361894	0.830662	-3.531232	23008.806409
HLA B*2705	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.371318	0.839877	-3.531441	23513.532238
HLA B*2705	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.453287	0.921765	-3.531522	28397.931492
HLA B*1801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.446436	0.914880	-3.531556	27953.462419
HLA A*0203	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-3.794982	0.263371	-3.531611	6237.092068
HLA A*0101	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.379278	0.847664	-3.531614	23948.478646
HLA B*5401	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.264513	0.732827	-3.531686	18387.074498
HLA A*6802	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.296818	0.765110	-3.531708	19806.970486
HLA A*6801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-3.801518	0.269799	-3.531720	6331.672192
HLA A*0301	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.296931	0.765110	-3.531820	19812.114523
HLA B*4601	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.405059	0.873123	-3.531936	25413.169230
HLA B*4001	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.385398	0.853416	-3.531982	24288.368203
HLA A*0211	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-3.950495	0.418508	-3.531987	8922.664577
HLA A*3101	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.296400	0.764363	-3.532037	19787.906341
HLA B*0802	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.476347	0.944277	-3.532069	29946.557298
HLA A*0202	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.351535	0.819348	-3.532187	22466.489169
HLA A*0216	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.287425	0.755176	-3.532248	19383.170387
HLA B*4402	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.436859	0.904590	-3.532269	27343.815058
HLA B*1801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.441389	0.909118	-3.532271	27630.510888
HLA B*5701	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.392611	0.860149	-3.532463	24695.126602
HLA B*2705	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.450796	0.918327	-3.532469	28235.550082
HLA B*5701	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.406013	0.873492	-3.532521	25469.048441
HLA A*3301	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.635696	1.103143	-3.532553	43221.120703
HLA A*1101	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.488684	0.956046	-3.532638	30809.457284
HLA B*1503	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.454417	0.921765	-3.532652	28471.923587
HLA A*6801	1:83-91	9	PAGPLPYIV	1.230037	-0.117061	-4.645670	1.112976	-3.532694	44225.177798
HLA A*2402	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.555597	1.022881	-3.532716	35941.597890
HLA A*0206	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.395776	0.862842	-3.532934	24875.740247
HLA A*3101	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.406142	0.873123	-3.533019	25476.627728
HLA A*2603	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.420991	0.887960	-3.533031	26362.748488
HLA A*0250	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.482183	0.949124	-3.533059	30351.700157
HLA B*4402	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.427666	0.894591	-3.533075	26771.060356
HLA A*6901	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.298237	0.765110	-3.533127	19871.797064
HLA B*1509	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.349815	0.816673	-3.533142	22377.696926
HLA B*5801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.348589	0.815296	-3.533293	22314.592302
HLA A*0206	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.454769	0.921444	-3.533325	28495.037456
HLA A*3001	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.255453	0.722004	-3.533449	18007.483334
HLA A*0301	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.324535	0.790996	-3.533539	21112.269887
HLA B*4001	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.381407	0.847787	-3.533620	24066.146882
HLA B*5401	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.556577	1.022881	-3.533696	36022.770921
HLA B*5701	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.403717	0.869990	-3.533728	25334.787888

HLA A*2501	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.396575	0.862842	-3.533733	24921.537853
HLA A*8001	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.438945	0.905205	-3.533740	27475.490271
HLA B*1503	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-3.776464	0.242669	-3.533794	5976.728310
HLA A*3002	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.266695	0.732827	-3.533868	18479.716623
HLA B*4403	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.570557	1.036678	-3.533879	37201.165985
HLA A*0219	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.439244	0.905205	-3.534039	27494.373956
HLA A*3101	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.367204	0.833148	-3.534056	23291.846866
HLA A*2602	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.619637	1.085412	-3.534226	41652.137534
HLA B*0803	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.454506	0.920120	-3.534386	28477.777326
HLA B*4403	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.637223	1.102823	-3.534401	43373.372193
HLA B*1503	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.247305	0.712902	-3.534403	17672.785549
HLA B*4403	1:511-519	9	NLNVYGFTK	0.868901	0.230646	-4.633950	1.099547	-3.534403	43047.740039
HLA A*2403	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.366227	0.831818	-3.534409	23239.487182
HLA A*0301	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.363785	0.829345	-3.534440	23109.227364
HLA B*4601	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.397327	0.862842	-3.534485	24964.718501
HLA B*5301	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.490178	0.955683	-3.534495	30915.645636
HLA B*7301	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.528874	0.994371	-3.534504	33796.703265
HLA A*0219	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.433427	0.898882	-3.534544	27128.545549
HLA B*3901	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.479016	0.944464	-3.534552	30131.164564
HLA A*6901	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.363903	0.829345	-3.534558	23115.479127
HLA B*7301	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.557862	1.022974	-3.534889	36129.527722
HLA B*3501	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.440172	0.905205	-3.534967	27553.189674
HLA B*5101	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.451278	0.916286	-3.534992	28266.881448
HLA B*1501	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.281774	0.746693	-3.535082	19132.613660
HLA B*4403	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.632947	1.097819	-3.535128	42948.413551
HLA A*2601	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.364657	0.829510	-3.535148	23155.655751
HLA B*1517	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-3.957275	0.421976	-3.535299	9063.066798
HLA A*2403	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.440506	0.905205	-3.535300	27574.364283
HLA A*3301	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.639676	1.104337	-3.535339	43619.034804
HLA B*1503	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.201922	0.666540	-3.535382	15919.240915
HLA A*2603	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.558288	1.022881	-3.535406	36164.922718
HLA A*8001	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.408926	0.873492	-3.535434	25640.475851
HLA B*0803	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.496698	0.961256	-3.535442	31383.266266
HLA A*3001	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.299901	0.764421	-3.535480	19948.056002
HLA A*3201	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.622233	1.086732	-3.535502	41901.876711
HLA B*3801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.457060	0.921444	-3.535616	28645.735665
HLA A*0212	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.383575	0.847787	-3.535788	24186.617564
HLA A*2501	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.482138	0.946270	-3.535869	30348.580530
HLA A*0216	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.367711	0.831818	-3.535894	23319.080138
HLA A*0212	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.367718	0.831818	-3.535901	23319.458602
HLA B*2705	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.440675	0.904590	-3.536085	27585.106922
HLA A*0203	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.355553	0.819348	-3.536205	22675.288953
HLA B*1801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.428361	0.892112	-3.536249	26813.963925
HLA B*3501	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.323118	0.786863	-3.536255	21043.510432
HLA A*0101	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.333235	0.796898	-3.536337	21539.472933
HLA A*0219	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.434402	0.898050	-3.536351	27189.520377
HLA A*0211	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.409854	0.873492	-3.536362	25695.325727
HLA B*4402	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.323240	0.786863	-3.536377	21049.431104
HLA B*4501	1:537-545	9	TNPPAGTTV	1.062324	0.040499	-4.639267	1.102823	-3.536445	43577.994622
HLA B*4601	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.320315	0.783751	-3.536564	20908.132996
HLA B*0803	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.492258	0.955683	-3.536574	31064.016976
HLA A*3001	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.269660	0.733042	-3.536619	18606.314492
HLA B*5101	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.454948	0.918327	-3.536621	28506.755644
HLA B*1517	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.344600	0.807959	-3.536641	22110.549244
HLA A*8001	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.434712	0.898050	-3.536661	27208.943493
HLA B*2705	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.320414	0.783751	-3.536663	20912.884184
HLA B*1503	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.131720	0.594934	-3.536785	13543.151707
HLA B*0803	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.481112	0.944277	-3.536834	30276.917540
HLA B*1502	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.363402	0.826538	-3.536864	23088.858353
HLA A*0216	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.435010	0.898050	-3.536960	27227.643982
HLA B*4403	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.486097	0.949124	-3.536973	30626.492721
HLA A*0201	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.302191	0.765110	-3.537081	20053.552838
HLA B*5801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.334069	0.796898	-3.537171	21580.879468
HLA A*0211	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.498897	0.961636	-3.537262	31542.583361
HLA B*1509	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.493338	0.956046	-3.537292	31141.417572

HLA B*2705	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.397550	0.860149	-3.537401	24977.552152
HLA A*8001	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.336247	0.798791	-3.537456	21689.378704
HLA A*0202	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.481767	0.944277	-3.537490	30322.650785
HLA B*4402	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.390915	0.853416	-3.537499	24598.857054
HLA B*1509	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.425481	0.887960	-3.537521	26636.708140
HLA A*2402	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.521633	0.984065	-3.537568	33237.873136
HLA A*6802	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.442850	0.905205	-3.537645	27723.642809
HLA A*2602	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.369478	0.831818	-3.537661	23414.140907
HLA B*1509	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.319324	0.781429	-3.537895	20860.454733
HLA A*2601	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.385817	0.847787	-3.538030	24311.768201
HLA B*4501	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.329563	0.791452	-3.538111	21358.110394
HLA B*3901	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.403318	0.865145	-3.538172	25311.498672
HLA A*3301	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.493937	0.955683	-3.538254	31184.407481
HLA B*1517	1:159-167	9	IARAIADSG	0.805700	-0.564762	-3.779377	0.240938	-3.538439	6016.956552
HLA B*1517	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.456654	0.918162	-3.538492	28618.938353
HLA A*0211	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.494201	0.955683	-3.538517	31203.308075
HLA B*3901	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.413564	0.875034	-3.538530	25915.760885
HLA A*0301	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.368080	0.829510	-3.538571	23338.894672
HLA B*1501	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.335599	0.796898	-3.538700	21657.017821
HLA A*6802	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.436770	0.898050	-3.538720	27338.194410
HLA B*4501	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.458923	0.920120	-3.538803	28768.891059
HLA B*4801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.413865	0.875034	-3.538831	25933.712878
HLA A*0203	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.294055	0.755176	-3.538879	19681.357952
HLA B*4801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.386888	0.847787	-3.539101	24371.817169
HLA B*2705	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.432959	0.893801	-3.539158	27099.355542
HLA B*4001	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.370998	0.831818	-3.539181	23496.238638
HLA B*5801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.355910	0.816673	-3.539237	22693.942583
HLA A*2501	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.438149	0.898882	-3.539267	27425.147706
HLA B*4801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.392684	0.853416	-3.539268	24699.268484
HLA A*1101	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.483562	0.944277	-3.539285	30448.238368
HLA A*0211	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.293783	0.754459	-3.539323	19669.010847
HLA B*0801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.335531	0.796188	-3.539343	21653.620388
HLA A*0211	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.254285	0.714935	-3.539350	17959.131377
HLA B*4601	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.387182	0.847787	-3.539395	24388.303846
HLA A*2602	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.483952	0.944464	-3.539488	30475.594434
HLA B*0801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.383723	0.844164	-3.539559	24194.862325
HLA B*2705	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.444946	0.905205	-3.539741	27857.749920
HLA A*3002	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.409737	0.869990	-3.539747	25688.376224
HLA A*0201	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.387562	0.847787	-3.539775	24409.687174
HLA B*5101	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.488975	0.949124	-3.539851	30830.132011
HLA A*6901	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.366431	0.826538	-3.539893	23250.427662
HLA B*7301	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.568809	1.028753	-3.540055	37051.733803
HLA A*0250	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-3.782173	0.242067	-3.540106	6055.817277
HLA A*0216	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.437470	0.897363	-3.540107	27382.303142
HLA B*1502	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.458507	0.918327	-3.540180	28741.356581
HLA A*6901	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.370904	0.830662	-3.540243	23491.154707
HLA B*5101	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.413764	0.873492	-3.540272	25927.680743
HLA A*0201	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.393755	0.853416	-3.540340	24760.274561
HLA A*0202	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.438403	0.898050	-3.540353	27441.176025
HLA A*0301	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.366898	0.826538	-3.540360	23275.471805
HLA A*2301	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.536355	0.995952	-3.540403	34383.897135
HLA B*2705	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.437773	0.897363	-3.540410	27401.419256
HLA A*0206	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.132495	0.592081	-3.540414	13567.351395
HLA A*0203	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.331884	0.791452	-3.540432	21472.574495
HLA B*3801	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.536416	0.995952	-3.540464	34388.733815
HLA B*3801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.445768	0.905205	-3.540563	27910.547458
HLA A*8001	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.413860	0.873256	-3.540604	25933.432282
HLA B*5401	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.413909	0.873256	-3.540653	25936.378687
HLA A*2601	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.380601	0.839877	-3.540724	24021.531340
HLA A*3201	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.501644	0.960920	-3.540724	31742.695823
HLA A*2403	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.434561	0.893801	-3.540761	27199.524492
HLA B*2705	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.487079	0.946270	-3.540810	30695.827805
HLA A*2601	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.305951	0.765110	-3.540840	20227.886246
HLA B*1801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.495483	0.954621	-3.540862	31295.612647
HLA A*1101	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.490070	0.949124	-3.540946	30907.953083

HLA B*1517	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.459320	0.918327	-3.540993	28795.205657
HLA A*0202	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-3.757550	0.216497	-3.541053	5722.030388
HLA B*0702	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.487399	0.946270	-3.541129	30718.420415
HLA B*4001	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.338028	0.796898	-3.541130	21778.502863
HLA B*4402	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.388845	0.847664	-3.541181	24481.895087
HLA B*4402	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.440083	0.898882	-3.541201	27547.525987
HLA A*0206	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.370578	0.829345	-3.541233	23473.496595
HLA B*5301	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.577988	1.036678	-3.541310	37843.210468
HLA B*4801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.414910	0.873492	-3.541418	25996.220926
HLA A*2501	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.436081	0.894591	-3.541491	27294.895032
HLA B*3801	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.502452	0.960920	-3.541532	31801.824041
HLA B*0702	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.404394	0.862842	-3.541552	25374.291472
HLA B*3501	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.439714	0.898050	-3.541664	27524.138358
HLA A*6801	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.506972	0.965301	-3.541671	32134.566045
HLA B*2705	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.457969	0.916286	-3.541684	28705.771978
HLA B*0801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.314409	0.772678	-3.541731	20625.697720
HLA B*5101	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.463232	0.921444	-3.541788	29055.749133
HLA B*4402	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.404805	0.862842	-3.541963	25398.325465
HLA B*1501	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.389632	0.847664	-3.541968	24526.304170
HLA A*2403	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.415310	0.873123	-3.542187	26020.140158
HLA B*0802	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.460462	0.918162	-3.542300	28871.013802
HLA B*5401	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.536691	0.994371	-3.542320	34410.507295
HLA A*0101	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.374142	0.831818	-3.542324	23666.931586
HLA B*4403	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.612048	1.069720	-3.542329	40930.632628
HLA A*2301	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.486877	0.944464	-3.542413	30681.549879
HLA A*6801	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.584773	1.042359	-3.542414	38439.106648
HLA A*0301	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.329311	0.786863	-3.542448	21345.750656
HLA B*4402	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.085252	0.542619	-3.542632	12168.908595
HLA B*5301	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.557728	1.014994	-3.542735	36118.388405
HLA A*2501	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.464538	0.921765	-3.542774	29143.277445
HLA A*2501	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.412857	0.869990	-3.542867	25873.594606
HLA B*3901	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.430833	0.887960	-3.542873	26967.002722
HLA B*5401	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.264891	0.722004	-3.542886	18403.096472
HLA A*0202	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.416383	0.873492	-3.542891	26084.549842
HLA A*2501	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.461399	0.918327	-3.543072	28933.400514
HLA A*2301	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.498888	0.955683	-3.543204	31541.900801
HLA B*1503	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.362599	0.819348	-3.543251	23046.179255
HLA A*0211	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.487547	0.944277	-3.543269	30728.891744
HLA A*3301	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.155294	0.612002	-3.543293	14298.631568
HLA A*0250	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.448217	0.904921	-3.543295	28068.326420
HLA B*4002	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.641123	1.097819	-3.543304	43764.637350
HLA B*4402	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.431690	0.888375	-3.543315	27020.304630
HLA A*8001	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.416477	0.873123	-3.543355	26090.195033
HLA B*5101	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.504339	0.960920	-3.543419	31940.276158
HLA A*2902	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.416952	0.873492	-3.543460	26118.721920
HLA A*3201	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.416726	0.873256	-3.543470	26105.160701
HLA B*1801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.463617	0.920120	-3.543497	29081.539466
HLA A*6901	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.342358	0.798696	-3.543662	21996.729908
HLA A*0206	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.258674	0.714935	-3.543739	18141.540616
HLA A*2603	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.550351	1.006578	-3.543773	35510.025244
HLA A*0201	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.258756	0.714935	-3.543821	18144.975971
HLA B*7301	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.343902	0.799991	-3.543910	22075.051930
HLA A*3301	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.526273	0.982334	-3.543940	33594.908203
HLA B*1801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.460229	0.916286	-3.543944	28855.555232
HLA B*4001	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.383824	0.839877	-3.543947	24200.491315
HLA A*3101	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-3.953056	0.409024	-3.544031	8975.434995
HLA A*0219	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.459059	0.914880	-3.544180	28777.919393
HLA B*4501	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.620020	1.075727	-3.544293	41688.883085
HLA A*0219	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.299710	0.755176	-3.544534	19939.316658
HLA A*0206	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.277585	0.733042	-3.544543	18948.950890
HLA A*2501	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.436784	0.892112	-3.544672	27339.081804
HLA A*0201	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.392343	0.847664	-3.544680	24679.901138
HLA A*6801	1:447-455	9	AGFGRFKQA	1.254222	-0.168810	-4.630147	1.085412	-3.544735	42672.348006
HLA B*5701	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.384733	0.839877	-3.544856	24251.211195
HLA B*0803	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.460399	0.915512	-3.544887	28866.797007

HLA A*0211	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.207481	0.662443	-3.545039	16124.313623
HLA B*0803	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.463310	0.918162	-3.545148	29060.936812
HLA A*1101	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.466658	0.921444	-3.545213	29285.836019
HLA B*3901	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.460112	0.914880	-3.545232	28847.751020
HLA B*0802	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.437350	0.892112	-3.545238	27374.749288
HLA B*0803	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.510553	0.965301	-3.545252	32400.600147
HLA A*0301	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.368903	0.823629	-3.545273	23383.127828
HLA B*5801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.299804	0.754459	-3.545345	19943.631905
HLA A*2902	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.338839	0.793337	-3.545502	21819.188473
HLA B*2705	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.444389	0.898882	-3.545507	27822.055168
HLA B*7301	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.587872	1.042359	-3.545513	38714.375362
HLA B*5801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.309888	0.764363	-3.545526	20412.125955
HLA B*4002	1:168-176	9	NSVTQTAAV	0.877619	0.189623	-4.612937	1.067242	-3.545695	41014.418878
HLA B*5701	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.419038	0.873123	-3.545916	26244.497649
HLA A*0216	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.451137	0.905205	-3.545932	28257.707695
HLA B*5801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.344823	0.798791	-3.546032	22121.915649
HLA B*3501	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.393711	0.847664	-3.546047	24757.729635
HLA A*0203	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.278563	0.732333	-3.546229	18991.643790
HLA A*0301	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.354192	0.807959	-3.546234	22604.373683
HLA B*4403	1:17-25	9	LGFGGMSEV	1.001633	0.074094	-4.621963	1.075727	-3.546236	41875.816100
HLA B*1501	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.343808	0.797462	-3.546346	22070.275503
HLA A*0211	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.467851	0.921444	-3.546407	29366.430743
HLA B*5401	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.502198	0.955683	-3.546515	31783.248679
HLA A*0203	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.321067	0.774481	-3.546586	20944.359762
HLA A*2603	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.495770	0.949124	-3.546646	31316.274772
HLA A*8001	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.386552	0.839877	-3.546675	24352.970077
HLA B*0802	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.409586	0.862842	-3.546744	25679.483602
HLA A*2602	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.489001	0.942253	-3.546748	30831.966729
HLA B*5101	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.454017	0.907250	-3.546767	28445.750532
HLA A*6801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.378712	0.831818	-3.546894	23917.275365
HLA A*2402	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.564485	1.017549	-3.546937	36684.743160
HLA B*2705	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.394761	0.847787	-3.546974	24817.671730
HLA A*3301	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.444356	0.897363	-3.546994	27819.948049
HLA A*0202	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.503070	0.956046	-3.547024	31847.103907
HLA B*0702	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.391242	0.844164	-3.547077	24617.361727
HLA B*3901	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.467330	0.920120	-3.547209	29331.182965
HLA A*0211	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.071380	0.524138	-3.547242	11786.375403
HLA A*3001	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.237825	0.690572	-3.547253	17291.188112
HLA A*3002	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.501942	0.954621	-3.547321	31764.512323
HLA B*2705	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.435708	0.888375	-3.547333	27271.426812
HLA A*0301	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.366774	0.819348	-3.547426	23268.799122
HLA B*4002	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.204803	0.657361	-3.547441	16025.176586
HLA A*3301	1:164-172	9	ADSGNSVTQ	1.198468	-0.115831	-4.630168	1.082637	-3.547530	42674.425731
HLA B*0801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.364234	0.816673	-3.547561	23133.118211
HLA B*1503	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.371217	0.823629	-3.547588	23508.063033
HLA B*4601	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.395290	0.847664	-3.547626	24847.898815
HLA A*8001	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.367014	0.819348	-3.547666	23281.642591
HLA A*1101	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.463965	0.916286	-3.547680	29104.833320
HLA B*5401	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.548772	1.001026	-3.547746	35381.164857
HLA A*0201	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.377095	0.829345	-3.547750	23828.420638
HLA A*0211	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.141141	0.593391	-3.547750	13840.162147
HLA A*6901	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.391942	0.844164	-3.547778	24657.080539
HLA B*0802	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.442425	0.894591	-3.547834	27696.509383
HLA B*4601	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.379668	0.831818	-3.547850	23969.995036
HLA A*0219	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.417920	0.869990	-3.547930	26177.002195
HLA B*4002	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.543890	0.995952	-3.547938	34985.645987
HLA A*8001	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.445381	0.897363	-3.548018	27885.644734
HLA A*0203	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.377495	0.829345	-3.548149	23850.345268
HLA B*4002	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.634890	1.086732	-3.548158	43140.994302
HLA A*2603	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.609856	1.061692	-3.548164	40724.558774
HLA A*1101	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.442232	0.894030	-3.548202	27684.225634
HLA A*2602	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.464555	0.916314	-3.548240	29144.381099
HLA A*6802	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.347069	0.798791	-3.548278	22236.623337
HLA A*0212	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.313431	0.765110	-3.548321	20579.331495
HLA B*2705	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.442935	0.894591	-3.548344	27729.042681

HLA A*0212	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.270372	0.722004	-3.548368	18636.838907
HLA A*3301	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.509388	0.960920	-3.548468	32313.775994
HLA A*2301	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.530827	0.982334	-3.548493	33948.982366
HLA A*3101	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.367890	0.819348	-3.548542	23328.669785
HLA B*0801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.378000	0.829345	-3.548655	23878.102368
HLA B*0802	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.453585	0.904921	-3.548664	28417.449163
HLA B*4801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.281528	0.732827	-3.548701	19121.748687
HLA A*2601	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.392884	0.844164	-3.548720	24710.628822
HLA A*8001	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.402644	0.853416	-3.549228	25272.229566
HLA A*2501	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.470718	0.921444	-3.549273	29560.892110
HLA B*4501	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.471096	0.921765	-3.549331	29586.650631
HLA A*2402	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.545332	0.995952	-3.549381	35102.050046
HLA A*0206	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-3.929739	0.380356	-3.549383	8506.271038
HLA B*4402	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.409636	0.860149	-3.549487	25682.401154
HLA B*4501	1:456-464	9	NSPSTPELV	0.868149	0.229670	-4.647366	1.097819	-3.549547	44398.256485
HLA B*3901	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.340547	0.790996	-3.549551	21905.172086
HLA A*1101	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.454163	0.904590	-3.549573	28455.293211
HLA A*2402	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.510896	0.961256	-3.549640	32426.201669
HLA B*4801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.409812	0.860149	-3.549663	25692.823689
HLA B*0802	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.464543	0.914880	-3.549663	29143.592771
HLA B*4601	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.379311	0.829510	-3.549801	23950.292535
HLA B*4501	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.636577	1.086732	-3.549845	43308.892757
HLA B*1502	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.576585	1.026649	-3.549937	37721.185266
HLA A*0219	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.381865	0.831818	-3.550047	24091.548340
HLA B*5701	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.412979	0.862842	-3.550137	25880.874240
HLA A*2602	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.248073	0.697848	-3.550225	17704.076972
HLA A*0301	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.366983	0.816673	-3.550310	23280.005284
HLA B*2705	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.283219	0.732827	-3.550392	19196.375442
HLA A*0203	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.283480	0.733042	-3.550438	19207.906283
HLA B*1503	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.381118	0.830662	-3.550456	24050.138201
HLA A*2601	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.398140	0.847664	-3.550476	25011.491763
HLA A*2902	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.420486	0.869990	-3.550496	26332.103111
HLA B*4801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.438906	0.888375	-3.550530	27472.963518
HLA A*8001	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.305131	0.754459	-3.550671	20189.730990
HLA A*2603	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.358631	0.807959	-3.550672	22836.558481
HLA A*2403	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.423949	0.873256	-3.550692	26542.919377
HLA B*1501	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.342175	0.791452	-3.550723	21987.449876
HLA A*2902	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.370084	0.819348	-3.550736	23446.844045
HLA A*2902	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.263773	0.712902	-3.550870	18355.767490
HLA B*1503	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-3.811034	0.260101	-3.550933	6471.930374
HLA A*8001	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.347969	0.796898	-3.551070	22282.745109
HLA B*0702	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.449133	0.898050	-3.551083	28127.609086
HLA A*3101	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.338040	0.786863	-3.551176	21779.091967
HLA A*2402	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.507374	0.956046	-3.551328	32164.307199
HLA B*0803	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.458608	0.907250	-3.551358	28748.043324
HLA A*2301	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.513123	0.961636	-3.551488	32592.929045
HLA A*0211	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.383326	0.831818	-3.551508	24172.751766
HLA B*4801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.421771	0.869990	-3.551781	26410.140725
HLA A*0101	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.382447	0.830662	-3.551786	24123.892518
HLA A*3301	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.578855	1.026649	-3.552206	37918.830396
HLA A*3001	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-3.912785	0.360485	-3.552300	8180.603298
HLA A*3201	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.622114	1.069720	-3.552394	41890.317395
HLA A*0250	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.594803	1.042359	-3.552444	39337.181290
HLA B*4402	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-3.795123	0.242669	-3.552454	6239.116916
HLA B*5801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.349947	0.797462	-3.552485	22384.477361
HLA B*0803	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.457098	0.904590	-3.552508	28648.215297
HLA B*5701	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.379158	0.826538	-3.552620	23941.872068
HLA A*3201	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.575577	1.022881	-3.552696	37633.741848
HLA B*1501	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.351733	0.798791	-3.552941	22476.700952
HLA B*0803	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.446793	0.893801	-3.552992	27976.458093
HLA A*3301	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.474768	0.921765	-3.553004	29837.885875
HLA A*1101	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.406429	0.853416	-3.553013	25493.448018
HLA A*3201	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.074872	0.521798	-3.553073	11881.509080
HLA B*1503	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.469364	0.916286	-3.553079	29468.920898
HLA A*6802	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.397273	0.844164	-3.553109	24961.612398

HLA A*2501	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.458383	0.905205	-3.553178	28733.116922
HLA A*6801	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.584282	1.031103	-3.553179	38395.669386
HLA B*3501	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.326976	0.773768	-3.553208	21231.273452
HLA A*2402	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.547640	0.994371	-3.553269	35289.026295
HLA B*1502	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.473405	0.920120	-3.553285	29744.409205
HLA B*1502	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.518619	0.965301	-3.553318	33007.971572
HLA A*2402	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.584545	1.031103	-3.553442	38418.940663
HLA B*5401	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.471801	0.918327	-3.553474	29634.707768
HLA B*3801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.497854	0.944277	-3.553577	31466.909287
HLA A*0203	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.228838	0.675193	-3.553645	16937.061145
HLA B*5801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.335129	0.781429	-3.553700	21633.598080
HLA B*3501	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.401492	0.847787	-3.553705	25205.325501
HLA B*0803	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.509775	0.956046	-3.553729	32342.633172
HLA A*2402	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.560386	1.006578	-3.553808	36340.059285
HLA A*2902	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.451339	0.897363	-3.553976	28270.857666
HLA B*4002	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.401861	0.847787	-3.554074	25226.742803
HLA A*0101	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.383425	0.829345	-3.554080	24178.244811
HLA A*6802	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.327028	0.772678	-3.554350	21233.800497
HLA A*2902	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.245216	0.690866	-3.554350	17587.994266
HLA A*2603	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.596765	1.042359	-3.554406	39515.279419
HLA B*5701	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.383841	0.829345	-3.554495	24201.407786
HLA B*0802	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.472849	0.918327	-3.554522	29706.297035
HLA B*1509	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.474655	0.920120	-3.554535	29830.138738
HLA A*8001	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.424543	0.869990	-3.554554	26579.273596
HLA A*1101	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.459546	0.904921	-3.554625	28810.164312
HLA B*3901	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.476490	0.921765	-3.554726	29956.441390
HLA B*0802	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.459978	0.905205	-3.554773	28838.856793
HLA B*1801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.476580	0.921765	-3.554815	29962.600342
HLA B*3901	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.428598	0.873492	-3.555106	26828.619046
HLA A*6801	1:279-287	9	GEPPEAPKV	1.069255	0.053404	-4.677858	1.122659	-3.555199	47627.472190
HLA A*6801	1:108-116	9	GPMTPKRAI	1.142169	-0.023529	-4.673868	1.118640	-3.555228	47191.969945
HLA A*3001	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.270175	0.714935	-3.555240	18628.371679
HLA B*4601	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.388476	0.833148	-3.555329	24461.110154
HLA B*3501	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.395261	0.839877	-3.555384	24846.285775
HLA B*1502	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.470299	0.914880	-3.555420	29532.439847
HLA B*4801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.342306	0.786863	-3.555443	21994.112066
HLA B*1502	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.370742	0.815296	-3.555446	23482.387510
HLA B*1503	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.470346	0.914880	-3.555467	29535.635364
HLA B*1502	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.336964	0.781429	-3.555535	21725.196072
HLA B*1501	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.384891	0.829345	-3.555546	24260.002945
HLA B*0803	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.471873	0.916286	-3.555588	29639.678120
HLA B*1801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.499889	0.944277	-3.555611	31614.676496
HLA B*1501	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.374988	0.819348	-3.555640	23713.069271
HLA A*2402	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.497910	0.942253	-3.555657	31470.995132
HLA A*0250	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.472007	0.916314	-3.555693	29648.819330
HLA A*0101	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.375173	0.819348	-3.555825	23723.205957
HLA B*5301	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.566487	1.010656	-3.555831	36854.221698
HLA B*1517	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-3.703977	0.148101	-3.555876	5057.981107
HLA B*1501	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.385405	0.829510	-3.555896	24288.762398
HLA A*2301	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.521424	0.965301	-3.556123	33221.873612
HLA B*4001	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.347760	0.791452	-3.556308	22272.018992
HLA A*2902	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.404218	0.847787	-3.556431	25363.998152
HLA B*0801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.356429	0.799991	-3.556438	22721.091358
HLA A*2301	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.477930	0.921444	-3.556486	30055.949706
HLA B*1801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.517759	0.961256	-3.556503	32942.679808
HLA A*2501	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.464691	0.908065	-3.556626	29153.527271
HLA B*5301	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.587738	1.031103	-3.556635	38702.439095
HLA B*3901	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-3.989097	0.432298	-3.556799	9752.065415
HLA A*0203	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.387499	0.830662	-3.556837	24406.121985
HLA B*0802	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.444869	0.887960	-3.556909	27852.777021
HLA B*7301	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.591768	1.034768	-3.556999	39063.189699
HLA B*1501	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.419875	0.862842	-3.557033	26295.091170
HLA A*0101	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.383624	0.826538	-3.557086	24189.365505
HLA B*7301	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.588215	1.031103	-3.557112	38744.965751
HLA B*1801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.383728	0.826538	-3.557190	24195.124109

HLA B*1801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.450996	0.893801	-3.557195	28248.536920
HLA A*0212	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.404981	0.847664	-3.557317	25408.632715
HLA B*1502	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.930829	0.373369	-3.557460	8527.650204
HLA B*4501	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.607183	1.049687	-3.557495	40474.610096
HLA A*6801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.341308	0.783751	-3.557557	21943.601230
HLA A*0201	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.388239	0.830662	-3.557577	24447.748283
HLA B*0702	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.290446	0.732827	-3.557619	19518.491556
HLA A*6802	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.279625	0.722004	-3.557620	19038.140309
HLA A*2902	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.455704	0.898050	-3.557654	28556.457242
HLA B*3901	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.967430	0.409720	-3.557710	9277.472060
HLA A*0201	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.389564	0.831818	-3.557746	24522.456618
HLA A*0206	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.479528	0.921765	-3.557764	30166.720892
HLA A*2601	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.391000	0.833148	-3.557852	24603.648296
HLA A*3201	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.322996	0.765110	-3.557886	21037.591425
HLA B*0803	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.476377	0.918327	-3.558050	29948.663470
HLA A*6901	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.391227	0.833148	-3.558080	24616.562676
HLA B*3901	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.255486	0.697387	-3.558099	18008.847244
HLA B*4501	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.290449	0.732333	-3.558116	19518.597149
HLA A*2402	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.523445	0.965301	-3.558144	33376.798650
HLA B*1509	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.384776	0.826538	-3.558238	24253.572845
HLA B*4501	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.573249	1.014994	-3.558255	37432.519704
HLA A*0101	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.312809	0.754459	-3.558350	20549.849679
HLA A*0212	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.375049	0.816673	-3.558376	23716.404917
HLA A*2501	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.456428	0.898050	-3.558378	28604.078985
HLA A*1101	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.467513	0.909118	-3.558394	29343.562496
HLA B*1502	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.542480	0.984065	-3.558415	34872.269014
HLA B*4501	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.477146	0.918327	-3.558819	30001.690556
HLA B*4001	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.391996	0.833148	-3.558848	24660.148748
HLA A*0101	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.392010	0.833148	-3.558862	24660.949213
HLA B*5801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.355057	0.796188	-3.558869	22649.420182
HLA B*4002	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.587633	1.028753	-3.558879	38693.018326
HLA A*0216	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.406680	0.847787	-3.558893	25508.209379
HLA A*2601	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.355959	0.796898	-3.559061	22696.520936
HLA A*3201	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.527878	0.968816	-3.559062	33719.269466
HLA B*3901	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.467252	0.908065	-3.559187	29325.947044
HLA B*0802	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.456567	0.897363	-3.559204	28613.210391
HLA A*0206	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.350671	0.791452	-3.559219	22421.806495
HLA A*3201	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.388641	0.829345	-3.559295	24470.375141
HLA A*0203	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.323760	0.764421	-3.559339	21074.612549
HLA A*6901	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.343183	0.783751	-3.559432	22038.538544
HLA B*4501	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.528395	0.968816	-3.559579	33759.425210
HLA B*4601	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.403788	0.844164	-3.559624	25338.899973
HLA A*3301	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.629554	1.069720	-3.559835	42614.212770
HLA A*6802	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.173418	0.613540	-3.559879	14907.966328
HLA A*0203	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.285879	0.725976	-3.559903	19314.294640
HLA A*0250	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.457314	0.897363	-3.559951	28662.477343
HLA A*3001	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.283003	0.722962	-3.560042	19186.823595
HLA B*1502	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.582943	1.022881	-3.560062	38277.453448
HLA A*1101	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.273034	0.712902	-3.560132	18751.422435
HLA B*3901	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.407923	0.847787	-3.560136	25581.314130
HLA B*4001	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.375580	0.815296	-3.560284	23745.419156
HLA B*4501	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-3.877797	0.317460	-3.560336	7547.390177
HLA B*3901	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.454144	0.893801	-3.560344	28454.061717
HLA B*3901	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.324784	0.764421	-3.560363	21124.380154
HLA A*1101	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.433622	0.873256	-3.560365	27140.729565
HLA B*0802	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.465119	0.904590	-3.560529	29182.245964
HLA B*5101	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.458580	0.898050	-3.560530	28746.177100
HLA B*4801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.433739	0.873123	-3.560616	27148.071975
HLA B*3801	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.516443	0.955683	-3.560760	32843.029734
HLA A*6802	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.145300	0.584529	-3.560771	13973.325206
HLA A*2603	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.642686	1.081848	-3.560838	43922.367525
HLA B*4002	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.610564	1.049687	-3.560876	40790.927716
HLA A*0203	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.360973	0.799991	-3.560982	22960.063874
HLA B*5301	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.603358	1.042359	-3.560998	40119.703261
HLA B*4002	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.642918	1.081848	-3.561071	43945.897724

HLA B*7301	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.567678	1.006578	-3.561100	36955.444720
HLA B*5701	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.408888	0.847787	-3.561102	25638.256553
HLA B*3901	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.505546	0.944277	-3.561269	32029.215540
HLA B*5301	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.557237	0.995952	-3.561285	36077.573620
HLA A*2402	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.342720	0.781429	-3.561291	22015.063524
HLA A*0206	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.507626	0.946270	-3.561356	32182.931160
HLA A*0250	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-3.934734	0.373369	-3.561365	8604.670051
HLA B*4402	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.391000	0.829510	-3.561490	24603.648296
HLA B*1502	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.523198	0.961636	-3.561562	33357.844731
HLA B*1801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.469637	0.908065	-3.561572	29487.419839
HLA B*3801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.515908	0.954333	-3.561574	32802.544317
HLA A*0101	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.369560	0.807959	-3.561602	23418.574704
HLA B*3801	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.503897	0.942253	-3.561644	31907.807521
HLA B*1502	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.522954	0.961256	-3.561697	33339.081937
HLA A*2501	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.455883	0.894030	-3.561853	28568.200689
HLA B*3801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.568440	1.006578	-3.561862	37020.277178
HLA A*0211	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-3.803995	0.242067	-3.561928	6367.878661
HLA A*0201	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.343411	0.781429	-3.561982	22050.106506
HLA B*5101	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.506481	0.944464	-3.562017	32098.253090
HLA A*0203	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.409713	0.847664	-3.562049	25686.986549
HLA B*0801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.357914	0.795837	-3.562077	22798.908859
HLA A*2403	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.450597	0.888375	-3.562221	28222.569216
HLA B*0801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.432212	0.869990	-3.562222	27052.775386
HLA B*5701	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.406426	0.844164	-3.562262	25493.310101
HLA A*2402	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.516598	0.954333	-3.562265	32854.758519
HLA B*3801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.531085	0.968816	-3.562269	33969.191004
HLA A*6901	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.378996	0.816673	-3.562323	23932.936657
HLA A*6802	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.295434	0.733042	-3.562392	19743.957513
HLA A*0301	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.361093	0.798696	-3.562397	22966.399530
HLA B*4402	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.435835	0.873256	-3.562579	27279.394887
HLA B*0702	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.402472	0.839877	-3.562595	25262.250979
HLA A*2603	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.589247	1.026649	-3.562598	38837.092126
HLA B*5701	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.410265	0.847664	-3.562601	25719.663797
HLA B*5401	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.456466	0.893801	-3.562665	28606.555010
HLA A*0212	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.392264	0.829345	-3.562918	24675.362027
HLA A*2602	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.578000	1.014988	-3.563012	37844.234120
HLA B*1502	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.592367	1.029142	-3.563225	39117.115406
HLA B*5301	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.597996	1.034768	-3.563228	39627.455541
HLA A*2403	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.403219	0.839877	-3.563342	25305.748164
HLA A*0250	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.519077	0.955683	-3.563394	33042.810992
HLA B*2705	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.295500	0.732039	-3.563461	19746.948493
HLA A*6901	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.285479	0.722004	-3.563475	19296.539813
HLA A*0219	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.411323	0.847787	-3.563536	25782.353312
HLA A*2601	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.394249	0.830662	-3.563587	24788.420117
HLA A*2301	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.294328	0.730675	-3.563653	19693.712808
HLA A*0219	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.347546	0.783751	-3.563795	22261.057178
HLA B*5801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.359681	0.795837	-3.563844	22891.849139
HLA B*5101	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.480165	0.916314	-3.563850	30210.980152
HLA A*2902	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.437118	0.873256	-3.563861	27360.091872
HLA A*3001	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.221432	0.657361	-3.564071	16650.699333
HLA B*5801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.364112	0.799991	-3.564121	23126.611451
HLA A*3001	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.234019	0.669685	-3.564334	17140.309902
HLA B*5801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.363050	0.798696	-3.564354	23070.129729
HLA A*0206	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.259717	0.695361	-3.564356	18185.168805
HLA A*0101	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.363142	0.798696	-3.564446	23074.997709
HLA B*4501	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.157926	0.593391	-3.564535	14385.531061
HLA A*2601	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.379891	0.815296	-3.564595	23982.317328
HLA A*1101	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.462701	0.898050	-3.564651	29020.246266
HLA B*1801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.463573	0.898882	-3.564691	29078.550390
HLA A*3301	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.254008	0.689311	-3.564697	17947.670520
HLA B*5101	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.452671	0.887960	-3.564711	28357.709033
HLA A*3201	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.404601	0.839877	-3.564724	25386.374293
HLA B*4002	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.638327	1.073598	-3.564729	43483.795732
HLA B*0802	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.472896	0.908065	-3.564831	29709.511364
HLA A*3001	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.178719	0.613866	-3.564853	15091.028571

HLA A*2501	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.469815	0.904921	-3.564894	29499.546131
HLA B*0802	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.463843	0.898882	-3.564961	29096.646868
HLA B*4402	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.288017	0.722962	-3.565055	19409.613330
HLA B*1503	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.086863	0.521798	-3.565065	12214.153558
HLA A*3101	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.394585	0.829510	-3.565075	24807.604209
HLA A*3301	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.634176	1.069099	-3.565077	43070.102662
HLA A*2601	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.394439	0.829345	-3.565094	24799.284808
HLA A*2602	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.599932	1.034768	-3.565164	39804.499092
HLA A*2902	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.405066	0.839877	-3.565189	25413.581681
HLA B*1501	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.255770	0.690572	-3.565198	18020.639634
HLA B*4801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.428100	0.862842	-3.565258	26797.867035
HLA B*0802	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.435464	0.869990	-3.565474	27256.087446
HLA A*6802	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.358844	0.793337	-3.565508	22847.803684
HLA A*0219	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.347243	0.781690	-3.565553	22245.527147
HLA B*1517	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.440609	0.875034	-3.565575	27580.928732
HLA B*1509	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.511848	0.946270	-3.565578	32497.325531
HLA B*1501	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.382419	0.816673	-3.565746	24122.326478
HLA B*4801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.439004	0.873256	-3.565748	27479.206506
HLA B*0702	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.263608	0.697848	-3.565760	18348.817619
HLA A*0101	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.357228	0.791452	-3.565776	22762.922136
HLA A*2603	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.459762	0.893801	-3.565961	28824.506983
HLA B*4801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.395351	0.829345	-3.566006	24851.394095
HLA A*0211	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.487885	0.921765	-3.566121	30752.839616
HLA B*4601	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.392708	0.826538	-3.566169	24700.604724
HLA B*0802	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.460215	0.894030	-3.566185	28854.618615
HLA B*5101	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.470779	0.904590	-3.566189	29565.050352
HLA B*5101	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.454602	0.888375	-3.566227	28484.094553
HLA A*6801	1:438-446	9	AEAVKKLTA	1.345939	-0.242796	-4.669451	1.103143	-3.566308	46714.432229
HLA B*3901	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.482608	0.916286	-3.566323	30381.434791
HLA B*0803	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.512769	0.946270	-3.566499	32566.314973
HLA B*0802	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.487970	0.921444	-3.566525	30758.829500
HLA B*1509	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.473805	0.907250	-3.566555	29771.777160
HLA A*3301	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.628290	1.061692	-3.566599	42490.363556
HLA A*3101	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.393314	0.826538	-3.566776	24735.104698
HLA A*8001	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.429672	0.862842	-3.566830	26895.030021
HLA B*2705	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.340612	0.773768	-3.566844	21908.490464
HLA A*3101	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.365566	0.798696	-3.566870	23204.185844
HLA A*0211	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-3.708784	0.141914	-3.566870	5114.277030
HLA A*1101	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.382407	0.815296	-3.567111	24121.673991
HLA B*0802	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.364018	0.796898	-3.567120	23121.607496
HLA B*1517	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.299536	0.732333	-3.567203	19931.335913
HLA B*5801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.354077	0.786863	-3.567214	22598.382407
HLA A*0211	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.396582	0.829345	-3.567237	24921.942324
HLA A*2902	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.411419	0.844164	-3.567255	25788.072613
HLA A*2602	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.568310	1.001026	-3.567284	37009.263658
HLA B*5101	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.459426	0.892112	-3.567314	28802.216559
HLA B*0802	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.474578	0.907250	-3.567328	29824.813748
HLA A*0301	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.367347	0.799991	-3.567356	23299.534520
HLA B*0802	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.427590	0.860149	-3.567442	26766.426246
HLA B*1501	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.321953	0.754459	-3.567494	20987.119965
HLA A*0101	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.397082	0.829510	-3.567573	24950.676590
HLA A*2601	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.387109	0.819348	-3.567761	24384.214111
HLA A*2402	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.523515	0.955683	-3.567832	33382.216033
HLA B*3501	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.399681	0.831818	-3.567863	25100.412419
HLA B*7301	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.568910	1.001026	-3.567883	37060.353974
HLA B*0702	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.428079	0.860149	-3.567930	26796.562306
HLA A*2301	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.522690	0.954621	-3.568069	33318.887653
HLA A*0216	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.387421	0.819348	-3.568073	24401.765238
HLA A*2902	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.298761	0.730675	-3.568086	19895.784972
HLA A*3002	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.300598	0.732333	-3.568265	19980.133046
HLA B*1517	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.484584	0.916286	-3.568299	30519.976639
HLA B*5801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.351740	0.783381	-3.568358	22477.065744
HLA A*1101	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.467292	0.898882	-3.568410	29328.644220
HLA A*3001	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.277724	0.709300	-3.568424	18955.000047
HLA A*1101	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.416226	0.847787	-3.568439	26075.096882

HLA A*2403	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.385130	0.816673	-3.568457	24273.393519
HLA B*5301	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.595224	1.026649	-3.568575	39375.292692
HLA A*2402	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.579294	1.010656	-3.568638	37957.210363
HLA B*4501	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.650507	1.081848	-3.568659	44720.554229
HLA B*5301	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.575260	1.006578	-3.568682	37606.266643
HLA A*0301	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.364887	0.796188	-3.568700	23167.935420
HLA B*5401	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.514994	0.946270	-3.568724	32733.585690
HLA A*0301	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.366227	0.797462	-3.568765	23239.487182
HLA A*0211	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-3.982936	0.414162	-3.568774	9614.711474
HLA B*4403	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.579445	1.010656	-3.568788	37970.354674
HLA B*0802	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.442073	0.873256	-3.568816	27674.043243
HLA A*6901	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.302088	0.733042	-3.569046	20048.779957
HLA A*0206	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.474488	0.905205	-3.569283	29818.683118
HLA B*5401	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.551688	0.982334	-3.569354	35619.501570
HLA A*2402	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.530289	0.960920	-3.569369	33906.950215
HLA A*6801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.485705	0.916314	-3.569390	30598.835666
HLA A*0301	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.351105	0.781690	-3.569415	22444.258133
HLA A*0216	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.295467	0.725976	-3.569491	19745.452946
HLA A*8001	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.444547	0.875034	-3.569513	27832.141450
HLA A*0301	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.333921	0.764363	-3.569558	21573.525461
HLA A*0250	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.463613	0.894030	-3.569583	29081.224812
HLA A*6901	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.161709	0.592081	-3.569627	14511.375158
HLA A*8001	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.363062	0.793337	-3.569725	23070.753771
HLA A*3001	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.281692	0.711889	-3.569803	19128.991316
HLA B*4501	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.531492	0.961636	-3.569856	34000.998020
HLA B*1509	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.485369	0.915512	-3.569857	30575.173128
HLA B*0803	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.368564	0.798696	-3.569868	23364.918902
HLA B*1509	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.484814	0.914880	-3.569935	30536.161679
HLA A*2403	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.432839	0.862842	-3.569997	27091.879743
HLA B*3901	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.474597	0.904590	-3.570007	29826.104567
HLA A*6901	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.366217	0.796188	-3.570029	23238.984295
HLA B*0803	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.464654	0.894591	-3.570063	29151.003902
HLA A*0101	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.368863	0.798791	-3.570071	23380.977424
HLA A*2602	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.485009	0.914880	-3.570130	30549.876129
HLA B*0803	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.485094	0.914880	-3.570214	30555.826480
HLA B*4001	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.368943	0.798696	-3.570246	23385.278429
HLA A*2403	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.423674	0.853416	-3.570258	26526.124166
HLA A*0250	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.585307	1.014994	-3.570313	38486.340591
HLA A*0203	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.343171	0.772678	-3.570493	22037.942422
HLA B*1503	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-3.608762	0.038251	-3.570511	4062.206284
HLA A*3201	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.499731	0.929186	-3.570546	31603.219436
HLA B*1517	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.468737	0.898050	-3.570687	29426.385526
HLA A*0202	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.516969	0.946270	-3.570700	32882.853540
HLA B*4001	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.378686	0.807959	-3.570727	23915.852120
HLA B*1502	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.444034	0.873256	-3.570778	27799.336799
HLA A*1101	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.096712	0.525884	-3.570828	12494.314018
HLA B*5101	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.386134	0.815296	-3.570838	24329.530422
HLA A*2402	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.431018	0.860149	-3.570870	26978.530376
HLA B*0802	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.444032	0.873123	-3.570910	27799.186408
HLA B*3501	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.216912	0.645932	-3.570980	16478.287262
HLA B*0801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.362005	0.790996	-3.571009	23014.657482
HLA A*6901	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.394714	0.823629	-3.571085	24814.986659
HLA A*6801	1:230-238	9	REDPIPPSA	1.344593	-0.240256	-4.675534	1.104337	-3.571197	47373.327589
HLA A*3201	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.492979	0.921765	-3.571214	31115.652080
HLA A*6901	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.266611	0.695361	-3.571249	18476.117937
HLA A*3201	1:123-131	9	CQALNFSHQ	0.994986	0.041692	-4.607953	1.036678	-3.571275	40546.493768
HLA B*1502	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.582001	1.010656	-3.571345	38194.505664
HLA A*6802	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.419144	0.847664	-3.571480	26250.887519
HLA A*3201	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.613869	1.042359	-3.571510	41102.601273
HLA B*5701	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.404676	0.833148	-3.571528	25390.769472
HLA A*2601	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.362585	0.790996	-3.571589	23045.431204
HLA A*0203	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.364939	0.793337	-3.571602	23170.692975
HLA A*3101	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.403496	0.831818	-3.571679	25321.907674
HLA B*3501	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.401253	0.829510	-3.571743	25191.420820
HLA A*6801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.501049	0.929186	-3.571864	31699.279252

HLA B*1501	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.114522	0.542619	-3.571902	13017.317963
HLA B*1501	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.346467	0.774481	-3.571986	22205.848450
HLA B*4501	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.586975	1.014988	-3.571987	38634.451712
HLA A*0101	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.388664	0.816673	-3.571991	24471.698997
HLA B*0803	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.368982	0.796898	-3.572084	23387.429228
HLA B*5301	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.518391	0.946270	-3.572121	32990.654878
HLA A*2301	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.533181	0.960920	-3.572261	34133.509600
HLA B*4601	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.354014	0.781690	-3.572324	22595.081770
HLA B*0802	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.425772	0.853416	-3.572356	26654.582738
HLA B*4001	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.389033	0.816673	-3.572360	24492.492927
HLA B*7301	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.521535	0.949124	-3.572411	33230.321839
HLA A*0301	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.368278	0.795837	-3.572441	23349.502993
HLA A*3201	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.479843	0.907250	-3.572593	30188.597435
HLA B*1509	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.470774	0.898050	-3.572724	29564.730467
HLA A*0101	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.287672	0.714935	-3.572736	19394.183899
HLA B*5801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.346528	0.773768	-3.572760	22208.972080
HLA A*2601	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.396507	0.823629	-3.572877	24917.628299
HLA A*3201	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.481048	0.908065	-3.572983	30272.495404
HLA A*0203	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.363990	0.790996	-3.572994	23120.106521
HLA B*1501	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.285900	0.712902	-3.572998	19315.235056
HLA B*1801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.491273	0.918162	-3.573112	30993.682561
HLA B*4403	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.646715	1.073598	-3.573117	44331.773779
HLA A*2403	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.356923	0.783751	-3.573172	22746.918929
HLA A*6801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.527881	0.954621	-3.573259	33719.451884
HLA A*0216	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.402785	0.829345	-3.573439	25280.434095
HLA B*3801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.489866	0.916286	-3.573580	30893.409358
HLA B*1502	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.461743	0.887960	-3.573783	28956.262409
HLA A*0212	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.393135	0.819348	-3.573787	24724.936912
HLA A*0301	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.365266	0.791452	-3.573814	23188.123301
HLA B*1502	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.472825	0.898882	-3.573943	29704.690001
HLA A*0201	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.407101	0.833148	-3.573953	25532.922732
HLA B*4601	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.393403	0.819348	-3.574055	24740.190160
HLA A*3001	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.166539	0.592477	-3.574062	14673.682272
HLA B*4801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.421735	0.847664	-3.574072	26407.997673
HLA B*5701	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.405930	0.831818	-3.574113	25464.226432
HLA A*1101	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.414008	0.839877	-3.574131	25942.272499
HLA A*0219	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.328609	0.754459	-3.574150	21311.250601
HLA A*0101	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.370411	0.796188	-3.574223	23464.482107
HLA A*1101	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.367568	0.793337	-3.574231	23311.386035
HLA A*1101	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.471603	0.897363	-3.574241	29621.243907
HLA B*1801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.437157	0.862842	-3.574316	27362.608244
HLA B*5801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.365787	0.791452	-3.574335	23215.988860
HLA A*3101	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.405014	0.830662	-3.574353	25410.557198
HLA B*1501	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.370582	0.796188	-3.574395	23473.750575
HLA B*4501	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.597296	1.022881	-3.574415	39563.621727
HLA B*3801	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.518882	0.944464	-3.574418	33027.977413
HLA B*4501	1:96-104	9	DGVTLRDIV	1.137489	-0.063891	-4.648047	1.073598	-3.574449	44467.966150
HLA A*0212	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.405158	0.830662	-3.574496	25418.944148
HLA A*1101	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.418691	0.844164	-3.574526	26223.493045
HLA A*3002	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.489429	0.914880	-3.574549	30862.338828
HLA B*0802	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.462962	0.888375	-3.574587	29037.678091
HLA B*4403	1:132-140	9	NGIIHRDVK	0.974897	0.111835	-4.661345	1.086732	-3.574614	45850.634660
HLA A*2603	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.437470	0.862842	-3.574628	27382.303142
HLA B*4501	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.570615	0.995952	-3.574663	37206.197680
HLA B*1509	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.496498	0.921765	-3.574734	31368.838284
HLA A*2602	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.597634	1.022881	-3.574753	39594.454748
HLA A*0101	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.347435	0.772678	-3.574757	22255.397694
HLA A*2601	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.391472	0.816673	-3.574799	24630.416552
HLA A*0201	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.365813	0.790996	-3.574817	23217.370456
HLA B*4403	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.480047	0.905205	-3.574842	30202.809355
HLA A*2501	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.468657	0.893801	-3.574856	29420.973445
HLA A*3001	1:10-18	9	RYELGEILG	0.929933	-0.507247	-3.997616	0.422686	-3.574930	9945.253061
HLA B*2705	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.371128	0.796188	-3.574940	23503.230841
HLA B*0802	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.473022	0.898050	-3.574972	29718.191791
HLA B*5401	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.198328	0.623337	-3.574991	15788.019101

HLA B*4801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.307348	0.732333	-3.575015	20293.102371
HLA B*5101	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.496910	0.921765	-3.575145	31398.550186
HLA B*4001	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.394613	0.819348	-3.575265	24809.214738
HLA B*0702	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.146568	0.571232	-3.575337	14014.205726
HLA A*0201	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.401885	0.826538	-3.575346	25228.107579
HLA A*2501	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.407183	0.831818	-3.575365	25537.757750
HLA A*2403	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.445369	0.869990	-3.575379	27884.890453
HLA B*4403	1:493-501	9	ATKDIPDVA	1.268690	-0.242041	-4.602068	1.026649	-3.575419	40000.723348
HLA A*6802	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.448630	0.873123	-3.575508	28095.064137
HLA A*2601	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.402082	0.826538	-3.575544	25239.574611
HLA B*4501	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.617920	1.042359	-3.575561	41487.744057
HLA A*6901	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.367119	0.791452	-3.575668	23287.311081
HLA A*2403	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.449213	0.873492	-3.575721	28132.783248
HLA A*3002	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.391039	0.815296	-3.575743	24605.911151
HLA B*4002	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.610566	1.034768	-3.575797	40791.148391
HLA A*3301	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.429294	0.853416	-3.575878	26871.614859
HLA A*0101	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.371748	0.795837	-3.575911	23536.822390
HLA A*0206	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.406633	0.830662	-3.575971	25505.449597
HLA A*0219	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.258942	0.682948	-3.575994	18152.732451
HLA B*4001	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.366992	0.790996	-3.575997	23280.509059
HLA B*3801	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.530629	0.954621	-3.576008	33933.558412
HLA B*1501	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-3.985915	0.409720	-3.576196	9680.892622
HLA A*0250	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.561638	0.985326	-3.576312	36444.996008
HLA A*0219	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.423989	0.847664	-3.576325	26545.360592
HLA A*2902	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.400083	0.823629	-3.576453	25123.643330
HLA B*4801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.391857	0.815296	-3.576561	24652.278892
HLA B*1517	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.409795	0.833148	-3.576648	25691.850740
HLA A*2602	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.406274	0.829510	-3.576764	25484.347138
HLA B*3801	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.493139	0.916314	-3.576824	31127.100777
HLA A*3001	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.188840	0.612002	-3.576839	15446.867552
HLA A*8001	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.410007	0.833148	-3.576859	25704.362892
HLA A*3301	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.587527	1.010656	-3.576871	38683.599851
HLA B*1517	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.482136	0.905205	-3.576931	30348.416348
HLA A*2403	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.424809	0.847787	-3.577022	26595.526938
HLA B*1517	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.416917	0.839877	-3.577040	26116.602515
HLA B*0702	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.360865	0.783751	-3.577114	22954.350861
HLA A*2402	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.531783	0.954621	-3.577162	34023.814434
HLA B*5801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.342316	0.765110	-3.577205	21994.588014
HLA B*1503	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.437385	0.860149	-3.577237	27376.970794
HLA B*5101	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.485327	0.908065	-3.577262	30572.195923
HLA B*4403	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.521758	0.944277	-3.577480	33247.404603
HLA A*2403	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.364554	0.786863	-3.577690	23150.144548
HLA A*0219	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.407049	0.829345	-3.577704	25529.884047
HLA A*0201	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.268403	0.690572	-3.577832	18552.540266
HLA B*0802	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.404420	0.826538	-3.577882	25375.801510
HLA B*0802	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.471758	0.893801	-3.577958	29631.822140
HLA B*5101	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.476843	0.898882	-3.577961	29980.760410
HLA A*2902	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.385922	0.807959	-3.577964	24317.687500
HLA B*3501	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.369417	0.791452	-3.577965	23410.847773
HLA A*1101	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.483229	0.905205	-3.578024	30424.856883
HLA B*1503	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-3.845665	0.267585	-3.578080	7009.148243
HLA A*0201	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.394832	0.816673	-3.578158	24821.699883
HLA B*1509	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.507365	0.929186	-3.578179	32163.611185
HLA B*1501	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.301183	0.722962	-3.578222	20007.065668
HLA B*7301	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.507442	0.929186	-3.578257	32169.353750
HLA A*2403	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.359690	0.781429	-3.578261	22892.344514
HLA B*5801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.353032	0.774481	-3.578550	22544.044479
HLA B*0803	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.483900	0.905205	-3.578695	30471.967519
HLA A*3201	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.452316	0.873492	-3.578824	28334.553270
HLA A*3101	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.370315	0.791452	-3.578863	23459.278134
HLA A*0250	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.573280	0.994371	-3.578909	37435.152372
HLA A*0250	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.563001	0.984065	-3.578936	36559.530368
HLA B*5301	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.374776	0.795837	-3.578939	23701.526424
HLA B*7301	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.594063	1.014994	-3.579069	39270.203291
HLA A*2301	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.473798	0.894591	-3.579207	29771.293978

HLA A*0206	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.311615	0.732333	-3.579282	20493.451628
HLA B*1801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.452641	0.873256	-3.579384	28355.714746
HLA B*0803	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.500843	0.921444	-3.579398	31684.191760
HLA A*0202	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.563656	0.984065	-3.579591	36614.753492
HLA B*1509	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.354084	0.774481	-3.579603	22598.749174
HLA B*4403	1:110-118	9	MTPKRAIEV	0.972733	0.076954	-4.629294	1.049687	-3.579606	42588.630715
HLA B*1509	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.423775	0.844164	-3.579611	26532.295529
HLA A*0206	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.120057	0.540402	-3.579655	13184.294634
HLA A*2301	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.528794	0.949124	-3.579670	33790.487399
HLA B*0702	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.454781	0.875034	-3.579747	28495.808241
HLA B*3801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.526057	0.946270	-3.579787	33578.191849
HLA A*2402	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.444962	0.865145	-3.579817	27858.804891
HLA A*2902	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.427489	0.847664	-3.579826	26760.200424
HLA A*6801	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.501308	0.921444	-3.579864	31718.148720
HLA B*3901	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.312917	0.733042	-3.579875	20554.964246
HLA B*4601	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.363287	0.783381	-3.579906	23082.738664
HLA A*0201	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.403637	0.823629	-3.580008	25330.128331
HLA B*4501	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.488108	0.908065	-3.580044	30768.648776
HLA B*0801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.312910	0.732827	-3.580083	20554.630648
HLA B*1509	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.485101	0.904921	-3.580180	30556.322395
HLA A*2501	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.312261	0.732039	-3.580222	20523.962826
HLA B*1801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.420168	0.839877	-3.580291	26312.878874
HLA A*0211	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.275793	0.695361	-3.580431	18870.895652
HLA A*2402	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.542085	0.961636	-3.580450	34840.589354
HLA A*0101	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.404234	0.823629	-3.580605	25364.958685
HLA A*3002	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.489727	0.909118	-3.580609	30883.550266
HLA B*4001	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.407502	0.826538	-3.580964	25556.553939
HLA B*5801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.362676	0.781690	-3.580986	23050.293973
HLA A*0206	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.400538	0.819348	-3.581190	25150.024900
HLA B*5301	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.582231	1.001026	-3.581205	38214.760581
HLA B*2705	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.475374	0.894030	-3.581344	29879.561224
HLA A*0219	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.276730	0.695361	-3.581368	18911.673338
HLA B*5101	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.377328	0.795837	-3.581491	23841.186059
HLA A*3201	1:292-300	9	ERTSLLSSA	1.189960	-0.179304	-4.592162	1.010656	-3.581506	39098.708862
HLA A*0301	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.365049	0.783381	-3.581668	23176.585216
HLA B*4601	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.398353	0.816673	-3.581680	25023.807950
HLA B*0801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.378745	0.796898	-3.581846	23919.086891
HLA A*2602	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.503338	0.921444	-3.581893	31866.750945
HLA B*3801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.497408	0.915512	-3.581896	31434.581731
HLA A*2603	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.566067	0.984065	-3.582002	36818.550444
HLA A*0101	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.122425	0.540402	-3.582023	13256.387199
HLA B*5401	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.538174	0.956046	-3.582128	34528.173101
HLA B*1517	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.219713	0.637402	-3.582310	16584.892301
HLA B*5701	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.401683	0.819348	-3.582335	25216.372920
HLA B*4801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.399021	0.816673	-3.582348	25062.284291
HLA B*4403	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.365858	0.783381	-3.582477	23219.757043
HLA A*2601	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.369431	0.786863	-3.582568	23411.607686
HLA B*4402	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.406205	0.823629	-3.582576	25480.349295
HLA B*5301	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.491774	0.909118	-3.582655	31029.417364
HLA A*2501	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.487528	0.904590	-3.582938	30727.561854
HLA B*3901	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.488167	0.905205	-3.582962	30772.810432
HLA B*5101	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.456125	0.873123	-3.583002	28584.123857
HLA A*3101	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.355698	0.772678	-3.583021	22682.895819
HLA A*0203	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.306007	0.722962	-3.583045	20230.512751
HLA B*1801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.481114	0.898050	-3.583064	30277.081335
HLA B*4403	1:133-141	9	GIIHRDVKP	0.968634	0.113214	-4.665097	1.081848	-3.583250	46248.481624
HLA A*0212	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.374783	0.791452	-3.583332	23701.911095
HLA B*5701	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.412864	0.829510	-3.583354	25874.014529
HLA B*3901	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.480724	0.897363	-3.583361	30249.903462
HLA A*6801	1:152-160	9	VKVMDFGIA	1.152124	-0.082404	-4.653129	1.069720	-3.583409	44991.368415
HLA B*3901	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.315492	0.732039	-3.583453	20677.201560
HLA B*4601	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.414128	0.830662	-3.583466	25949.431073
HLA A*0301	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.330225	0.746693	-3.583533	21390.718954
HLA A*3101	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.407180	0.823629	-3.583551	25537.619594
HLA B*1801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.529892	0.946270	-3.583622	33875.964232

HLA B*5801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.353699	0.770046	-3.583653	22578.707963
HLA B*0702	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.380582	0.796898	-3.583684	24020.491732
HLA B*5701	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.380636	0.796898	-3.583738	24023.480726
HLA B*3901	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.482648	0.898882	-3.583766	30384.229043
HLA B*5701	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.391744	0.807959	-3.583786	24645.878151
HLA A*2603	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.598793	1.014988	-3.583805	39700.197091
HLA A*0212	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.358309	0.774481	-3.583827	22819.639326
HLA B*1502	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.505286	0.921444	-3.583841	32009.987844
HLA A*3001	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.309862	0.725976	-3.583886	20410.911290
HLA B*1502	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.584975	1.001026	-3.583949	38456.994621
HLA A*3301	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.491210	0.907250	-3.583960	30989.155737
HLA A*0101	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.383986	0.799991	-3.583995	24209.526618
HLA B*5301	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.481368	0.897363	-3.584005	30294.776434
HLA B*4601	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.407780	0.823629	-3.584150	25572.873606
HLA A*1101	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.416000	0.831818	-3.584183	26061.558313
HLA B*4501	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.545450	0.961256	-3.584194	35111.546240
HLA B*1801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.399512	0.815296	-3.584216	25090.637411
HLA A*2902	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.447103	0.862842	-3.584261	27996.443367
HLA B*5101	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.457593	0.873256	-3.584337	28680.935522
HLA A*0201	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.366039	0.781690	-3.584348	23229.431514
HLA A*0212	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.437782	0.853416	-3.584367	27402.012217
HLA A*2902	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.457492	0.873123	-3.584370	28674.264389
HLA B*4801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.415117	0.830662	-3.584455	26008.599900
HLA A*0206	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.432256	0.847787	-3.584469	27055.556227
HLA B*4001	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.414003	0.829510	-3.584494	25941.991811
HLA B*5401	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.545772	0.961256	-3.584516	35137.578978
HLA A*0216	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.417676	0.833148	-3.584528	26162.278410
HLA B*3901	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-3.854044	0.269402	-3.584642	7145.679100
HLA A*0202	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.489889	0.905205	-3.584684	30895.080702
HLA A*6802	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.380568	0.795837	-3.584731	24019.712055
HLA B*5701	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.415406	0.830662	-3.584744	26025.912207
HLA A*8001	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.415476	0.830662	-3.584815	26030.136469
HLA B*3501	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.317244	0.732333	-3.584911	20760.818758
HLA A*8001	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.358722	0.773768	-3.584954	22841.377176
HLA A*0203	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.411511	0.826538	-3.584972	25793.514101
HLA A*1101	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.473471	0.888375	-3.585096	29748.915137
HLA A*0202	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.506878	0.921765	-3.585114	32127.613020
HLA A*0212	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.366934	0.781690	-3.585244	23277.360647
HLA A*1101	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.369032	0.783751	-3.585281	23390.086370
HLA A*2403	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.376745	0.791452	-3.585293	23809.220920
HLA A*3002	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.477435	0.892112	-3.585322	30021.660816
HLA B*5101	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.460389	0.875034	-3.585355	28866.172349
HLA A*0211	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.366790	0.781429	-3.585361	23269.680310
HLA B*3901	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.483463	0.898050	-3.585413	30441.320847
HLA A*3001	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.280881	0.695361	-3.585520	19093.322039
HLA B*7301	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.483640	0.898050	-3.585590	30453.674666
HLA A*3301	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.616762	1.031103	-3.585658	41377.240544
HLA A*3002	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.417490	0.831818	-3.585672	26151.099532
HLA A*0211	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.490925	0.905205	-3.585720	30968.876980
HLA B*4601	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.307917	0.722004	-3.585913	20319.687361
HLA B*0702	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.415338	0.829345	-3.585993	26021.829406
HLA B*4501	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.495209	0.909118	-3.586090	31275.810137
HLA A*6801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.107938	0.521798	-3.586140	12821.482861
HLA A*6901	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.379513	0.793337	-3.586176	23961.438012
HLA A*0202	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.222213	0.635971	-3.586241	16680.632247
HLA B*3801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.547503	0.961256	-3.586247	35277.955268
HLA B*4402	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.402961	0.816673	-3.586288	25290.693502
HLA A*0212	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.319387	0.733042	-3.586345	20863.501980
HLA B*7301	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.582325	0.995952	-3.586373	38223.030980
HLA A*0101	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.383899	0.797462	-3.586437	24204.681181
HLA B*4002	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.628946	1.042359	-3.586587	42554.545196
HLA A*0216	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.440005	0.853416	-3.586589	27542.608467
HLA B*4601	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.416078	0.829345	-3.586733	26066.211403
HLA A*2301	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.505163	0.918327	-3.586836	32000.984245
HLA B*4402	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.416289	0.829345	-3.586944	26078.905871

HLA A*0211	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.533472	0.946270	-3.587202	34156.414937
HLA A*8001	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.402531	0.815296	-3.587235	25265.667860
HLA B*1509	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.402620	0.815296	-3.587324	25270.862403
HLA A*3001	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.009344	0.421976	-3.587369	10217.495792
HLA B*1801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.374325	0.786863	-3.587462	23676.920460
HLA A*2301	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.462504	0.875034	-3.587470	29007.061572
HLA A*0216	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.435198	0.847664	-3.587534	27239.430416
HLA A*0203	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.404215	0.816673	-3.587542	25363.860936
HLA B*0702	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-3.508321	-0.079239	-3.587560	3223.454095
HLA A*2602	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.495627	0.908065	-3.587562	31305.942005
HLA A*0212	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.386336	0.798696	-3.587640	24340.852381
HLA A*0216	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.386340	0.798696	-3.587644	24341.115745
HLA A*0101	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.374682	0.786863	-3.587819	23696.398074
HLA B*1509	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.460967	0.873123	-3.587845	28904.613970
HLA B*0803	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.476227	0.888375	-3.587852	29938.296053
HLA B*0801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.418590	0.830662	-3.587928	26217.393508
HLA A*3201	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.594524	1.006578	-3.587946	39311.865075
HLA A*2403	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.417462	0.829510	-3.587952	26149.401893
HLA A*2301	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.544144	0.956046	-3.588098	35006.092954
HLA B*4001	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.417558	0.829345	-3.588213	26155.202616
HLA A*6901	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.211682	0.623337	-3.588345	16281.038974
HLA B*5401	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.542682	0.954333	-3.588349	34888.497128
HLA A*2501	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.385358	0.796898	-3.588460	24286.134550
HLA A*2601	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.372119	0.783381	-3.588738	23556.949383
HLA B*3801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.507073	0.918327	-3.588746	32142.042226
HLA B*0803	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.517940	0.929186	-3.588754	32956.405318
HLA A*6802	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.054436	0.465424	-3.589012	11335.372169
HLA B*2705	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.459099	0.869990	-3.589110	28780.566166
HLA A*6801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.404537	0.815296	-3.589241	25382.666452
HLA B*5101	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.452143	0.862842	-3.589301	28323.212318
HLA B*1801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.449471	0.860149	-3.589322	28149.529707
HLA A*2601	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.385250	0.795837	-3.589413	24280.091578
HLA B*2705	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.422581	0.833148	-3.589434	26459.478950
HLA A*0206	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.437169	0.847664	-3.589505	27363.348397
HLA B*5801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.362209	0.772678	-3.589531	23025.492118
HLA B*3801	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.504423	0.914880	-3.589544	31946.497324
HLA A*2403	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.336245	0.746693	-3.589552	21689.261368
HLA B*2705	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.302741	0.712902	-3.589839	20078.954988
HLA A*0203	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.301761	0.711889	-3.589872	20033.709451
HLA B*0702	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.406548	0.816673	-3.589875	25500.482741
HLA B*5301	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.555304	0.965301	-3.590003	35917.301099
HLA B*0803	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.511768	0.921765	-3.590003	32491.348645
HLA B*5401	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.551157	0.960920	-3.590237	35575.978534
HLA A*2603	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.460239	0.869990	-3.590249	28856.179661
HLA A*3001	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.193713	0.603309	-3.590405	15621.159062
HLA A*0301	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.323273	0.732827	-3.590446	21051.025415
HLA A*3101	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.390530	0.799991	-3.590538	24577.042091
HLA A*0202	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-3.854086	0.263371	-3.590714	7146.374966
HLA B*2705	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.463855	0.873123	-3.590732	29097.433927
HLA B*0702	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.355910	0.765110	-3.590800	22693.942583
HLA A*0216	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.372284	0.781429	-3.590855	23565.871907
HLA B*4601	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.398823	0.807959	-3.590865	25050.897808
HLA B*4402	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.430797	0.839877	-3.590920	26964.814483
HLA A*2601	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.389649	0.798696	-3.590952	24527.232979
HLA B*3501	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.453860	0.862842	-3.591018	28435.441881
HLA A*6801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-3.939480	0.348457	-3.591023	8699.217344
HLA A*0203	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.374438	0.783381	-3.591057	23683.069555
HLA A*0216	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.387254	0.796188	-3.591067	24392.394268
HLA A*3101	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.389895	0.798791	-3.591104	24541.169346
HLA B*4002	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.506679	0.915512	-3.591167	32112.842836
HLA A*6901	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.374624	0.783381	-3.591242	23693.193418
HLA A*8001	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.439051	0.847787	-3.591264	27482.179856
HLA A*0101	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.324316	0.733042	-3.591275	21101.650560
HLA A*0201	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.389982	0.798696	-3.591286	24546.082143
HLA A*8001	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.304191	0.712902	-3.591289	20146.088544

HLA B*0803	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.479359	0.887960	-3.591399	30154.972879
HLA B*1501	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.382438	0.790996	-3.591442	24123.370494
HLA B*5301	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.486039	0.894591	-3.591448	30622.350853
HLA B*4801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.423467	0.831818	-3.591649	26513.498873
HLA B*1517	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.385095	0.793337	-3.591758	24271.423854
HLA A*0301	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.364523	0.772678	-3.591845	23148.516489
HLA A*2603	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.536310	0.944464	-3.591846	34380.363068
HLA A*6901	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.389327	0.797462	-3.591865	24509.061237
HLA A*3001	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.018108	0.426123	-3.591985	10425.767761
HLA A*0203	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.185443	0.593391	-3.592052	15326.502748
HLA B*4501	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.324951	0.732827	-3.592124	21132.495632
HLA B*4801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.411480	0.819348	-3.592132	25791.700144
HLA A*0202	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-3.544499	-0.047884	-3.592382	3503.473685
HLA B*1502	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.432367	0.839877	-3.592490	27062.436377
HLA B*2705	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.466068	0.873492	-3.592576	29246.096291
HLA A*0250	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.374290	0.781690	-3.592600	23674.999195
HLA B*7301	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.001417	0.408739	-3.592678	10032.687966
HLA A*3001	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.290075	0.697387	-3.592688	19501.815010
HLA B*3801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.501808	0.909118	-3.592690	31754.718812
HLA A*3301	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.507626	0.914880	-3.592746	32182.931160
HLA A*3201	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.412194	0.819348	-3.592846	25834.152235
HLA A*0201	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.389790	0.796898	-3.592891	24535.195648
HLA B*0803	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.466150	0.873256	-3.592894	29251.634451
HLA A*2602	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.491849	0.898882	-3.592967	31034.789532
HLA A*6802	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.423702	0.830662	-3.593040	26527.846262
HLA B*5301	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.513229	0.920120	-3.593109	32600.864597
HLA A*0216	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.255599	0.662443	-3.593156	18013.524293
HLA A*2601	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.390840	0.797462	-3.593378	24594.598956
HLA A*2601	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.393370	0.799991	-3.593379	24738.316447
HLA B*5301	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.419983	0.826538	-3.593445	26301.635646
HLA B*4601	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.374955	0.781429	-3.593526	23711.273347
HLA B*1503	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.392224	0.798696	-3.593527	24673.092785
HLA A*8001	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.420168	0.826538	-3.593630	26312.878874
HLA A*2403	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.392473	0.798791	-3.593681	24687.245584
HLA A*3101	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.186167	0.592477	-3.593690	15352.061758
HLA B*1501	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.187191	0.593391	-3.593800	15388.315584
HLA B*4601	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.392600	0.798791	-3.593808	24694.458622
HLA B*2705	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.423169	0.829345	-3.593823	26495.288873
HLA A*3002	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.423340	0.829510	-3.593831	26505.754509
HLA A*0101	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.289201	0.695361	-3.593840	19462.607487
HLA B*7301	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.515642	0.921765	-3.593878	32782.497677
HLA A*2601	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.392710	0.798791	-3.593919	24700.738352
HLA B*3901	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.289288	0.695361	-3.593926	19466.503627
HLA A*0206	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.391406	0.797462	-3.593944	24626.685896
HLA A*3001	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.284857	0.690866	-3.593991	19268.895715
HLA A*2902	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.425828	0.831818	-3.594011	26658.043723
HLA A*0101	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.387363	0.793337	-3.594026	24398.465190
HLA A*6901	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.375476	0.781429	-3.594047	23739.767585
HLA A*3101	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.390241	0.796188	-3.594053	24560.693564
HLA A*0301	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.368562	0.774481	-3.594080	23364.792501
HLA B*1503	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.402040	0.807959	-3.594081	25237.116951
HLA B*5401	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.512256	0.918162	-3.594095	32527.930338
HLA B*3801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.550292	0.956046	-3.594246	35505.222936
HLA A*8001	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.441969	0.847664	-3.594305	27667.456633
HLA A*0101	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.368851	0.774481	-3.594369	23380.344990
HLA A*0201	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.387743	0.793337	-3.594406	24419.857428
HLA B*4501	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.629268	1.034768	-3.594499	42586.096393
HLA B*1517	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.421087	0.826538	-3.594549	26368.596538
HLA B*1503	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.249062	0.654485	-3.594578	17744.445082
HLA B*5101	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.434470	0.839877	-3.594593	27193.786388
HLA B*5701	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.326652	0.732039	-3.594613	21215.428848
HLA B*0702	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.369173	0.774481	-3.594691	23397.679869
HLA B*7301	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.540972	0.946270	-3.594702	34751.362518
HLA A*0202	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.309684	0.714935	-3.594749	20402.521037
HLA B*4403	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.617645	1.022881	-3.594764	41461.492407

HLA B*5701	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.411485	0.816673	-3.594812	25791.979206
HLA B*4403	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.626016	1.031103	-3.594913	42268.432788
HLA B*1801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.392376	0.797462	-3.594914	24681.770426
HLA A*3301	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.637472	1.042359	-3.595113	43398.251711
HLA B*5701	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.386178	0.790996	-3.595183	24332.031332
HLA A*3301	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.624496	1.029142	-3.595354	42120.743514
HLA B*1501	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.395358	0.799991	-3.595367	24851.797428
HLA A*3101	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.443156	0.847664	-3.595492	27743.147305
HLA B*5401	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.494393	0.898882	-3.595511	31217.153274
HLA B*5701	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.395541	0.799991	-3.595550	24862.286387
HLA A*2301	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.541883	0.946270	-3.595614	34824.383523
HLA A*1101	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.424968	0.829345	-3.595623	26605.312500
HLA A*3001	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.058947	0.463212	-3.595734	11453.726141
HLA A*2603	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.626893	1.031103	-3.595789	42353.811893
HLA B*0702	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.426592	0.830662	-3.595930	26704.955496
HLA A*0201	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.271199	0.675193	-3.596006	18672.362497
HLA A*6801	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.552080	0.956046	-3.596034	35651.696602
HLA A*6801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.322042	0.725976	-3.596066	20991.434852
HLA B*5301	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.517839	0.921765	-3.596074	32948.739718
HLA A*3201	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.342844	0.746693	-3.596152	22021.376679
HLA B*1503	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.188248	0.592081	-3.596167	15425.823308
HLA B*3501	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.308284	0.711889	-3.596394	20336.843251
HLA A*2603	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.461592	0.865145	-3.596447	28946.238534
HLA B*5801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.351629	0.755176	-3.596453	22471.351344
HLA B*5701	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.378192	0.781690	-3.596502	23888.697305
HLA B*0702	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.469672	0.873123	-3.596550	29489.812791
HLA A*3001	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.276636	0.680074	-3.596562	18907.581379
HLA A*0219	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.450002	0.853416	-3.596586	28183.967353
HLA A*2601	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.380349	0.783751	-3.596598	24007.630305
HLA B*5401	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.369288	0.772678	-3.596610	23403.883055
HLA B*4801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.393553	0.796898	-3.596655	24748.757511
HLA A*2301	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.518433	0.921765	-3.596669	32993.867599
HLA B*1501	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.347097	0.750403	-3.596694	22238.066956
HLA B*5101	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.511580	0.914880	-3.596700	32477.289720
HLA A*2403	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.329615	0.732827	-3.596787	21360.652536
HLA B*0803	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.494234	0.897363	-3.596871	31205.671455
HLA A*0201	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.369565	0.772678	-3.596887	23418.828089
HLA A*0201	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.396899	0.799991	-3.596908	24940.150340
HLA B*3901	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.490949	0.894030	-3.596919	30970.552407
HLA B*1501	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-3.860340	0.263371	-3.596969	7250.035426
HLA A*3002	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.541247	0.944277	-3.596969	34773.365600
HLA B*4002	1:501-509	9	AGQTVDVAQ	1.125120	-0.094017	-4.628084	1.031103	-3.596980	42470.139973
HLA A*2301	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.470116	0.873123	-3.596994	29519.980632
HLA A*2602	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.626338	1.029142	-3.597196	42299.771853
HLA A*0201	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.393196	0.795837	-3.597359	24728.414894
HLA B*5801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.347818	0.750403	-3.597415	22275.031425
HLA A*8001	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.426970	0.829510	-3.597461	26728.225435
HLA A*0201	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.388923	0.791452	-3.597471	24486.266140
HLA B*0801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.445216	0.847664	-3.597552	27875.086656
HLA A*2902	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.427123	0.829510	-3.597613	26737.625876
HLA B*3501	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.295465	0.697848	-3.597616	19745.346126
HLA B*4601	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.391016	0.793337	-3.597679	24604.580035
HLA B*5301	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.542008	0.944277	-3.597731	34834.369946
HLA B*7301	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-3.623028	0.025261	-3.597767	4197.860927
HLA B*0803	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.502727	0.904921	-3.597806	31821.959600
HLA B*0803	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.470931	0.873123	-3.597809	29575.448517
HLA B*4001	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.371597	0.773768	-3.597829	23528.674578
HLA A*0202	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.391185	0.793337	-3.597848	24614.165681
HLA B*1501	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.138312	0.540402	-3.597910	13750.307114
HLA A*2301	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.516074	0.918162	-3.597913	32815.146264
HLA A*0301	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.367968	0.770046	-3.597922	23332.834939
HLA B*4001	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.370777	0.772678	-3.598100	23484.293144
HLA B*1501	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.307438	0.709300	-3.598137	20297.274571
HLA B*2705	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.352597	0.754459	-3.598138	22521.493021
HLA A*3101	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.395651	0.797462	-3.598190	24868.608795

HLA B*5401	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.505570	0.907250	-3.598320	32030.948332
HLA B*4801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.389449	0.790996	-3.598453	24515.956955
HLA A*3301	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.594855	0.995952	-3.598903	39341.863384
HLA B*4001	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.397750	0.798791	-3.598958	24989.040486
HLA A*2403	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.432108	0.833148	-3.598961	27046.336642
HLA B*1509	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.349414	0.750403	-3.599011	22357.005091
HLA A*0101	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.380721	0.781690	-3.599030	24028.159899
HLA B*2705	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.265617	0.666540	-3.599077	18433.885841
HLA A*0212	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.329755	0.730675	-3.599081	21367.587187
HLA A*2902	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.173339	0.574191	-3.599147	14905.224465
HLA A*0250	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.560834	0.961636	-3.599199	36377.628469
HLA B*5401	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-3.446662	-0.152648	-3.599309	2796.801252
HLA A*2402	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.515684	0.916314	-3.599370	32785.690126
HLA B*4402	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.431244	0.831818	-3.599426	26992.545297
HLA B*1509	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.473034	0.873492	-3.599542	29718.995662
HLA A*8001	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.443776	0.844164	-3.599612	27782.798674
HLA B*5701	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.414955	0.815296	-3.599659	25998.893160
HLA A*3301	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.634524	1.034768	-3.599755	43104.601134
HLA B*1801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.504365	0.904590	-3.599775	31942.176941
HLA A*2601	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.395976	0.796188	-3.599788	24887.181753
HLA A*0201	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.395987	0.796188	-3.599800	24887.854946
HLA B*0801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.381400	0.781429	-3.599971	24065.756300
HLA B*4403	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.634777	1.034768	-3.600009	43129.793133
HLA B*4402	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.433220	0.833148	-3.600072	27115.633529
HLA B*4801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.429602	0.829510	-3.600092	26890.665401
HLA B*3501	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.460338	0.860149	-3.600189	28862.736972
HLA B*1509	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.497626	0.897363	-3.600263	31450.401067
HLA A*6901	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.370315	0.770046	-3.600269	23459.278134
HLA A*0206	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.515153	0.914880	-3.600274	32745.629690
HLA B*5801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.364939	0.764421	-3.600518	23170.692975
HLA B*0803	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.499510	0.898882	-3.600628	31587.152349
HLA B*5401	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.544914	0.944277	-3.600637	35068.264436
HLA A*0202	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.470647	0.869990	-3.600657	29556.094865
HLA B*4801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.440562	0.839877	-3.600685	27577.944698
HLA A*2601	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.394084	0.793337	-3.600747	24779.034712
HLA B*1509	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.392256	0.791452	-3.600805	24674.961557
HLA B*3801	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.530063	0.929186	-3.600878	33889.345234
HLA A*0206	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.143524	0.542619	-3.600904	13916.292744
HLA A*3201	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.556988	0.956046	-3.600942	36056.890929
HLA A*2601	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.333033	0.732039	-3.600994	21529.454014
HLA A*2603	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.586340	0.985326	-3.601014	38578.060719
HLA A*0211	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.373792	0.772678	-3.601114	23647.861987
HLA B*5301	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.569946	0.968816	-3.601130	37148.876680
HLA A*0250	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.500128	0.898882	-3.601246	31632.126564
HLA B*5101	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.506465	0.905205	-3.601260	32097.037577
HLA A*0211	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.420610	0.819348	-3.601262	26339.654243
HLA B*5401	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.433102	0.831818	-3.601285	27108.299893
HLA A*6802	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.427872	0.826538	-3.601334	26783.808296
HLA A*6801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.461503	0.860149	-3.601354	28940.288500
HLA B*1501	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.397306	0.795837	-3.601469	24963.503023
HLA A*2301	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.506068	0.904590	-3.601478	32067.705589
HLA B*3501	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.365851	0.764363	-3.601488	23219.380197
HLA B*4601	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.392538	0.790996	-3.601543	24690.985415
HLA A*2602	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.557254	0.955683	-3.601570	36078.939875
HLA B*4403	1:398-406	9	HVIGTDPAA	1.258672	-0.241123	-4.619174	1.017549	-3.601626	41607.770492
HLA B*3901	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.490004	0.888375	-3.601629	30903.271597
HLA B*4402	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.409596	0.807959	-3.601637	25680.039301
HLA B*4402	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.371696	0.770046	-3.601650	23534.021261
HLA B*3901	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.461883	0.860149	-3.601735	28965.662945
HLA A*0212	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.316681	0.714935	-3.601745	20733.880954
HLA A*2301	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.531038	0.929186	-3.601853	33965.515812
HLA A*0219	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.327996	0.725976	-3.602020	21281.180753
HLA B*5701	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.356603	0.754459	-3.602144	22730.189154
HLA A*0201	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.399608	0.797462	-3.602146	25096.203268
HLA B*0702	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.472155	0.869990	-3.602166	29658.926052

HLA A*0250	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.517719	0.915512	-3.602207	32939.650271
HLA B*5701	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.401006	0.798791	-3.602215	25177.115190
HLA A*2902	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.214238	0.612002	-3.602237	16377.151086
HLA B*2705	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.455655	0.853416	-3.602239	28553.213194
HLA B*0702	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.395581	0.793337	-3.602244	24864.573030
HLA A*2602	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.507221	0.904921	-3.602300	32152.998840
HLA B*5401	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.477383	0.875034	-3.602349	30018.087924
HLA B*1801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.398222	0.795837	-3.602385	25016.228040
HLA B*0803	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.510480	0.908065	-3.602415	32395.166809
HLA B*4402	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.383859	0.781429	-3.602430	24202.455224
HLA B*0801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.426084	0.823629	-3.602455	26673.768018
HLA A*3301	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.490836	0.888375	-3.602461	30962.511183
HLA B*4601	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.375258	0.772678	-3.602580	23727.826644
HLA B*1501	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.426232	0.823629	-3.602603	26682.860601
HLA B*5701	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.426296	0.823629	-3.602667	26686.758372
HLA B*4501	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.558367	0.955683	-3.602684	36171.575369
HLA A*2403	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.335768	0.733042	-3.602726	21665.455133
HLA B*0801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.220667	0.617889	-3.602778	16621.359642
HLA B*0803	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.465683	0.862842	-3.602841	29220.160024
HLA B*3801	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.524629	0.921765	-3.602864	33467.927478
HLA B*4601	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.399841	0.796898	-3.602942	25109.647868
HLA B*4801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.436147	0.833148	-3.603000	27299.029891
HLA B*5401	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.547478	0.944464	-3.603014	35275.855983
HLA A*2501	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.476281	0.873256	-3.603025	29942.021430
HLA A*0212	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.399263	0.796188	-3.603075	25076.253353
HLA B*5101	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.456545	0.853416	-3.603130	28611.817276
HLA A*2301	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.495389	0.892112	-3.603277	31288.841148
HLA B*4001	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.386728	0.783381	-3.603347	24362.853097
HLA B*5801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.335718	0.732333	-3.603385	21662.993911
HLA A*3101	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.399232	0.795837	-3.603395	25074.489839
HLA A*0101	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.367831	0.764421	-3.603411	23325.514861
HLA B*1801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.451109	0.847664	-3.603445	28255.873302
HLA B*3901	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.476702	0.873256	-3.603445	29971.030434
HLA A*6801	1:606-614	9	QNPPAGTGV	0.988736	0.046032	-4.638424	1.034768	-3.603655	43493.441744
HLA A*2501	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.476833	0.873123	-3.603711	29980.111646
HLA A*3101	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.334391	0.730675	-3.603716	21596.880170
HLA A*0301	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.368212	0.764421	-3.603791	23345.966350
HLA A*6901	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.378279	0.774481	-3.603798	23893.479486
HLA A*0219	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.395334	0.791452	-3.603883	24850.453010
HLA A*0250	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.437089	0.833148	-3.603942	27358.315749
HLA A*0101	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.385570	0.781429	-3.604141	24297.962106
HLA B*7301	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.448310	0.844164	-3.604146	28074.400939
HLA B*4001	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.354622	0.750403	-3.604219	22626.763314
HLA A*8001	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.436044	0.831818	-3.604226	27292.532536
HLA B*0702	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.412208	0.807959	-3.604250	25834.990808
HLA A*1101	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.477766	0.873492	-3.604274	30044.569906
HLA B*1502	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.559002	0.954621	-3.604381	36224.448713
HLA B*3501	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.054036	0.449508	-3.604528	11324.952033
HLA A*3201	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.578843	0.974301	-3.604542	37917.804726
HLA B*7301	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.400731	0.796188	-3.604543	25161.184200
HLA A*2601	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.377246	0.772678	-3.604568	23836.672250
HLA B*5301	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.125672	0.521039	-3.604634	13355.869563
HLA B*4403	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.633391	1.028753	-3.604638	42992.349433
HLA B*3901	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.196768	0.592081	-3.604686	15731.407650
HLA A*3101	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.386472	0.781690	-3.604782	24348.491096
HLA B*0702	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.428533	0.823629	-3.604903	26824.555438
HLA B*7301	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.521347	0.916314	-3.605032	33215.943162
HLA A*2603	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.514157	0.909118	-3.605039	32670.604074
HLA B*3501	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.478187	0.873123	-3.605064	30073.678262
HLA B*4501	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.512325	0.907250	-3.605074	32533.033941
HLA A*0202	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.566717	0.961636	-3.605082	36873.765850
HLA A*6802	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.438243	0.833148	-3.605095	27431.083029
HLA B*4801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.428744	0.823629	-3.605115	26837.619227
HLA B*1517	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.259393	0.654207	-3.605186	18171.597467
HLA B*3901	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.317172	0.711889	-3.605283	20757.337324

HLA B*1801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.449624	0.844164	-3.605460	28159.430026
HLA A*2601	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.387151	0.781690	-3.605461	24386.588712
HLA B*4501	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.560122	0.954621	-3.605501	36318.047237
HLA A*0101	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.388887	0.783381	-3.605506	24484.279201
HLA A*0250	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.327535	0.722004	-3.605531	21258.627461
HLA A*6901	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.405543	0.799991	-3.605552	25441.506398
HLA B*2705	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.138420	0.532852	-3.605569	13753.729371
HLA A*0211	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.370707	0.765110	-3.605597	23480.482030
HLA A*2501	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.404305	0.798696	-3.605609	25369.075668
HLA A*3001	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.280806	0.675193	-3.605613	19090.016957
HLA B*2705	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.453296	0.847664	-3.605632	28398.546017
HLA B*4001	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.401854	0.796188	-3.605666	25226.333385
HLA A*2501	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.432226	0.826538	-3.605688	27053.653516
HLA B*0801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.370801	0.765110	-3.605691	23485.563652
HLA B*4601	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.338846	0.733042	-3.605804	21819.542594
HLA A*0101	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.389559	0.783751	-3.605808	24522.191292
HLA A*3201	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.600212	0.994371	-3.605841	39830.132556
HLA A*0219	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.425257	0.819348	-3.605909	26623.022002
HLA A*0202	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.435391	0.829345	-3.606045	27251.516805
HLA B*7301	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.399472	0.793337	-3.606135	25088.329978
HLA B*1517	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.469042	0.862842	-3.606201	29447.087957
HLA B*7301	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.561972	0.955683	-3.606288	36473.003965
HLA A*6801	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.612946	1.006578	-3.606368	41015.306421
HLA B*1509	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.454034	0.847664	-3.606370	28446.827771
HLA A*1101	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.360936	0.754459	-3.606476	22958.076578
HLA A*1101	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.469345	0.862842	-3.606504	29467.645537
HLA B*5301	1:598-606	9	SQHNRVVYQ	0.974360	0.007974	-4.588908	0.982334	-3.606575	38806.848879
HLA B*1801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.481694	0.875034	-3.606660	30317.565904
HLA A*0211	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.439864	0.833148	-3.606717	27533.669770
HLA B*1517	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.450968	0.844164	-3.606804	28246.703122
HLA B*5701	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.393711	0.786863	-3.606847	24757.729635
HLA B*7301	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.561480	0.954621	-3.606859	36431.788454
HLA A*3101	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.414842	0.807959	-3.606884	25992.142783
HLA B*4601	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.402726	0.795837	-3.606889	25277.015217
HLA A*2402	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.551460	0.944464	-3.606996	35600.814810
HLA B*5101	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.329166	0.722004	-3.607161	21338.592211
HLA B*1801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.501193	0.894030	-3.607163	31709.741843
HLA B*4002	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.622318	1.014988	-3.607330	41910.038148
HLA B*3501	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.406130	0.798696	-3.607434	25475.938609
HLA B*1517	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.388871	0.781429	-3.607442	24483.352018
HLA A*2301	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.472590	0.865145	-3.607445	29688.624439
HLA A*0212	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.434037	0.826538	-3.607499	27166.730628
HLA A*3301	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.561849	0.954333	-3.607516	36462.745033
HLA A*0201	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.382008	0.774481	-3.607527	24099.499940
HLA A*2601	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.362002	0.754459	-3.607543	23014.532975
HLA B*4601	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.358003	0.750403	-3.607600	22803.596245
HLA B*1503	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.390990	0.783381	-3.607609	24603.115890
HLA B*4501	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.148011	0.540402	-3.607609	14060.833718
HLA A*6801	1:8-16	9	SDRYELGEI	0.899282	0.162410	-4.669331	1.061692	-3.607639	46701.545292
HLA A*1101	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.480823	0.873123	-3.607700	30256.777485
HLA A*2403	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.372201	0.764421	-3.607781	23561.410223
HLA B*0702	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.407775	0.799991	-3.607784	25572.596915
HLA A*6802	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-3.956288	0.348457	-3.607831	9042.497497
HLA A*2403	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.381663	0.773768	-3.607894	24080.342342
HLA B*4601	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.407935	0.799991	-3.607943	25582.006099
HLA B*7301	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-3.748035	0.139887	-3.608147	5598.023865
HLA A*8001	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.437524	0.829345	-3.608179	27385.710464
HLA B*4402	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.405096	0.796898	-3.608198	25415.369044
HLA B*3901	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.440155	0.831818	-3.608338	27552.146275
HLA B*4402	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.423643	0.815296	-3.608347	26524.258687
HLA B*7301	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.529922	0.921444	-3.608478	33878.346763
HLA A*3201	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.569819	0.961256	-3.608563	37138.025815
HLA A*0301	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.321504	0.712902	-3.608602	20965.445408
HLA A*2602	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.577436	0.968816	-3.608620	37795.130058
HLA B*1502	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.462050	0.853416	-3.608634	28976.790855

HLA B*4402	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.399740	0.790996	-3.608744	25103.807410
HLA A*0219	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.441922	0.833148	-3.608775	27664.463237
HLA B*0801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.323736	0.714935	-3.608801	21073.472466
HLA A*0216	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.299722	0.690866	-3.608856	19939.856013
HLA A*0201	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.330928	0.722004	-3.608923	21425.347658
HLA A*2603	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.563259	0.954333	-3.608926	36581.292973
HLA B*7301	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.564991	0.956046	-3.608945	36727.436969
HLA A*8001	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.374064	0.765110	-3.608954	23662.706792
HLA B*0801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.407796	0.798791	-3.609005	25573.842049
HLA B*7301	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.594338	0.985326	-3.609012	39295.067511
HLA A*2603	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.610171	1.001026	-3.609145	40754.091734
HLA A*0101	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.374257	0.765110	-3.609147	23673.206156
HLA B*3901	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.417163	0.807959	-3.609205	26131.441962
HLA B*5701	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.392990	0.783751	-3.609239	24716.645234
HLA A*2403	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.402587	0.793337	-3.609250	25268.948500
HLA A*3001	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.160398	0.550986	-3.609412	14467.635458
HLA B*4403	1:61-69	9	QNAAALNHP	0.984550	0.057809	-4.651877	1.042359	-3.609518	44861.823972
HLA B*0702	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.396514	0.786863	-3.609650	24918.032708
HLA B*3901	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.482860	0.873123	-3.609737	30399.026423
HLA B*4801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.360167	0.750403	-3.609764	22917.498868
HLA B*4801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.405956	0.796188	-3.609769	25465.741822
HLA B*2705	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.400844	0.790996	-3.609848	25167.718771
HLA A*2301	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.483381	0.873492	-3.609889	30435.557446
HLA B*0803	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.470205	0.860149	-3.610057	29526.049849
HLA B*4402	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.410103	0.799991	-3.610112	25710.064892
HLA A*1101	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.383897	0.773768	-3.610129	24204.550237
HLA A*3002	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.365315	0.755176	-3.610138	23190.757799
HLA A*2902	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.439540	0.829345	-3.610195	27513.121776
HLA B*4601	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.383984	0.773768	-3.610216	24209.395647
HLA B*1503	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.333268	0.722962	-3.610306	21541.104361
HLA A*0206	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-3.885522	0.275124	-3.610398	7682.842125
HLA B*4402	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.285602	0.675193	-3.610409	19301.968967
HLA B*4601	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.409107	0.798696	-3.610411	25651.158910
HLA B*5401	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.559563	0.949124	-3.610439	36271.315895
HLA A*3101	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.427167	0.816673	-3.610494	26740.374321
HLA A*0101	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.365689	0.755176	-3.610512	23210.714430
HLA B*0801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.332582	0.722004	-3.610577	21507.103008
HLA A*3201	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.554984	0.944277	-3.610707	35890.884846
HLA A*0212	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.444030	0.833148	-3.610882	27799.036018
HLA A*0301	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.366086	0.755176	-3.610909	23231.945023
HLA A*3001	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.256851	0.645932	-3.610919	18065.540725
HLA B*3801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.402439	0.791452	-3.610987	25260.337728
HLA A*3201	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.553241	0.942253	-3.610988	35747.102664
HLA B*7301	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.555527	0.944464	-3.611063	35935.765162
HLA B*5401	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.509289	0.898050	-3.611239	32306.434642
HLA A*2902	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.444448	0.833148	-3.611300	27825.818279
HLA A*3002	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.474199	0.862842	-3.611358	29798.847879
HLA B*5401	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.533122	0.921765	-3.611358	34128.893450
HLA B*1503	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.333371	0.722004	-3.611367	21546.232511
HLA B*5401	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.532868	0.921444	-3.611424	34108.958853
HLA A*0101	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.333491	0.722004	-3.611487	21552.178030
HLA B*4001	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.375852	0.764363	-3.611490	23760.325202
HLA A*2601	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.402991	0.791452	-3.611540	25292.472223
HLA A*3201	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.343878	0.732333	-3.611545	22073.857726
HLA B*7301	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.527112	0.915512	-3.611600	33659.853767
HLA A*2501	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.205089	0.593391	-3.611698	16035.756797
HLA B*1509	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.500079	0.888375	-3.611704	31628.533115
HLA B*4402	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.403172	0.791452	-3.611720	25303.010287
HLA B*1501	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.120217	0.508438	-3.611779	13189.145665
HLA A*6801	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.580720	0.968816	-3.611905	38082.059231
HLA A*3002	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.403480	0.791452	-3.612028	25320.948771
HLA A*3201	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.420020	0.807959	-3.612062	26303.912368
HLA B*7301	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.517308	0.905205	-3.612103	32908.480054
HLA B*1517	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.334163	0.722004	-3.612159	21585.549980
HLA B*1503	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.444013	0.831818	-3.612196	27797.983310

HLA A*2603	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.327209	0.714935	-3.612273	21242.647523
HLA A*0203	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.343011	0.730675	-3.612336	22029.836761
HLA B*1509	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.487413	0.875034	-3.612379	30719.417531
HLA B*0702	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.395764	0.783381	-3.612383	24875.067382
HLA B*7301	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.441781	0.829345	-3.612436	27655.484994
HLA B*1503	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.500876	0.888375	-3.612500	31686.591562
HLA B*4801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.439054	0.826538	-3.612515	27482.328532
HLA A*2301	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.528050	0.915512	-3.612538	33732.588575
HLA B*1801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.460342	0.847787	-3.612555	28863.049262
HLA B*4001	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.405902	0.793337	-3.612565	25462.573382
HLA A*0219	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.394009	0.781429	-3.612580	24774.745424
HLA B*4501	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.517794	0.905205	-3.612589	32945.353160
HLA B*1509	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.486114	0.873256	-3.612858	30627.652544
HLA B*1801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.377297	0.764421	-3.612877	23839.509402
HLA B*3901	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.439540	0.826538	-3.613002	27513.121776
HLA B*0702	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.444826	0.831818	-3.613009	27850.064906
HLA B*1517	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.385760	0.772678	-3.613082	24308.611831
HLA A*0219	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.439690	0.826538	-3.613152	27522.649373
HLA A*8001	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.377518	0.764363	-3.613155	23851.635580
HLA A*3002	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.359970	0.746693	-3.613277	22907.086819
HLA A*0216	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.387762	0.774481	-3.613280	24420.914320
HLA A*0219	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.413308	0.799991	-3.613317	25900.483438
HLA B*4601	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.400238	0.786863	-3.613374	25132.615396
HLA B*1502	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.473584	0.860149	-3.613435	29756.641180
HLA B*0802	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.444119	0.830662	-3.613457	27804.751415
HLA A*3201	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.597554	0.984065	-3.613489	39587.172563
HLA B*4601	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.410982	0.797462	-3.613520	25762.136690
HLA A*0212	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.311573	0.697848	-3.613724	20491.456114
HLA A*0202	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.535171	0.921444	-3.613727	34290.274240
HLA A*1101	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.311615	0.697848	-3.613767	20493.451628
HLA A*6801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.512689	0.898882	-3.613807	32560.325399
HLA B*1509	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.231766	0.617889	-3.613877	17051.614817
HLA B*0803	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.388361	0.774481	-3.613880	24454.626750
HLA B*4601	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.410101	0.796188	-3.613913	25709.925804
HLA A*0216	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.395607	0.781690	-3.613917	24866.052735
HLA A*2603	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.643116	1.029142	-3.613974	43965.872627
HLA A*2501	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.458197	0.844164	-3.614033	28720.839551
HLA A*1101	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.461735	0.847664	-3.614072	28955.792463
HLA A*2601	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.378622	0.764421	-3.614202	23912.359058
HLA A*2402	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.563351	0.949124	-3.614227	36589.011917
HLA A*2601	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.395703	0.781429	-3.614274	24871.568772
HLA A*0250	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.405303	0.790996	-3.614308	25427.471426
HLA A*6901	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.327312	0.712902	-3.614410	21247.704621
HLA B*4601	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.378796	0.764363	-3.614434	23921.933852
HLA A*0101	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.384501	0.770046	-3.614455	24238.226233
HLA A*0219	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.445167	0.830662	-3.614505	27871.920012
HLA B*0803	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.488021	0.873492	-3.614530	30762.490558
HLA B*5701	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.387240	0.772678	-3.614562	24391.602520
HLA A*2602	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.575873	0.961256	-3.614617	37659.403484
HLA A*3201	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.369114	0.754459	-3.614655	23394.515611
HLA B*4601	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.406116	0.791452	-3.614664	25475.111690
HLA A*0203	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.410512	0.795837	-3.614675	25734.277703
HLA B*3801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.477583	0.862842	-3.614741	30031.894633
HLA A*6901	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.370075	0.755176	-3.614899	23446.336671
HLA A*2301	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.522277	0.907250	-3.615027	33287.178489
HLA B*2705	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.413888	0.798791	-3.615097	25935.115901
HLA A*2602	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.347955	0.732827	-3.615127	22282.021838
HLA A*0219	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.389653	0.774481	-3.615172	24527.498360
HLA B*3801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.535382	0.920120	-3.615262	34306.973897
HLA B*1502	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.571071	0.955683	-3.615388	37245.266771
HLA A*3301	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.638313	1.022881	-3.615432	43482.384299
HLA A*2403	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.434789	0.819348	-3.615441	27213.801440
HLA B*3501	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.348493	0.733042	-3.615451	22309.643352
HLA A*1101	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.396927	0.781429	-3.615498	24941.769474
HLA A*3001	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.034164	0.418508	-3.615657	10818.434677

HLA A*0201	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.370834	0.755176	-3.615657	23487.342480
HLA B*1801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.399429	0.783751	-3.615679	25085.887046
HLA B*4501	1:561-569	9	FVMPDLSGM	0.870850	0.157903	-4.644523	1.028753	-3.615770	44108.576167
HLA A*2601	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.348619	0.732827	-3.615792	22316.161710
HLA B*4601	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.386012	0.770046	-3.615966	24322.687142
HLA A*3101	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.399375	0.783381	-3.615994	25082.765867
HLA A*0250	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.537488	0.921444	-3.616043	34473.672432
HLA B*4501	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.639079	1.022974	-3.616106	43559.138533
HLA B*2705	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-3.983735	0.367626	-3.616109	9632.412686
HLA B*5101	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.370622	0.754459	-3.616163	23475.909511
HLA B*0702	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-3.738458	0.122274	-3.616184	5475.934500
HLA B*0702	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.463956	0.847664	-3.616292	29104.203511
HLA A*0201	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.399690	0.783381	-3.616309	25100.955587
HLA A*6802	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.413296	0.796898	-3.616398	25899.782853
HLA A*0203	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.440047	0.823629	-3.616418	27545.290642
HLA A*3001	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.208604	0.592081	-3.616523	16166.063880
HLA B*5801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.339503	0.722962	-3.616542	21852.619205
HLA A*6802	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.001850	0.385288	-3.616561	10042.679672
HLA A*2403	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.424560	0.807959	-3.616601	26580.280152
HLA A*6801	1:29-37	9	RDLRLHRDV	0.886328	0.182771	-4.685724	1.069099	-3.616624	48497.975289
HLA A*2402	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.521584	0.904921	-3.616663	33234.097273
HLA B*4001	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.416668	0.799991	-3.616676	26101.630289
HLA B*0802	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.491738	0.875034	-3.616704	31026.899481
HLA A*6802	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.412897	0.796188	-3.616709	25875.974261
HLA A*0211	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.407989	0.790996	-3.616993	25585.189401
HLA B*3501	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.367453	0.750403	-3.617050	23305.207366
HLA A*1101	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.487065	0.869990	-3.617076	30694.831455
HLA A*2603	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.533430	0.916314	-3.617116	34153.089015
HLA B*1501	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.329044	0.711889	-3.617154	21332.590206
HLA A*3301	1:197-205	9	SDVYSLGCV	0.890967	0.115611	-4.623735	1.006578	-3.617157	42046.978770
HLA A*0203	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.263115	0.645932	-3.617183	18327.983791
HLA A*0250	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.461392	0.844164	-3.617228	28932.930939
HLA B*5701	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.398675	0.781429	-3.617246	25042.361340
HLA A*3002	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.371741	0.754459	-3.617282	23536.440398
HLA A*2601	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.391866	0.774481	-3.617385	24652.812362
HLA B*1517	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.448242	0.830662	-3.617581	28069.996782
HLA A*6801	1:547-555	9	VDSVIELQV	1.065399	-0.036257	-4.646760	1.029142	-3.617618	44336.330783
HLA A*2601	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.387731	0.770046	-3.617685	24419.196893
HLA B*3901	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.433006	0.815296	-3.617710	27102.287791
HLA A*3101	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.106162	0.488312	-3.617850	12769.151671
HLA A*2902	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.280322	0.662443	-3.617880	19068.754183
HLA B*5801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.040156	0.421976	-3.618180	10968.711502
HLA A*0250	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.308756	0.690572	-3.618184	20358.969313
HLA A*3101	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.307499	0.689311	-3.618188	20300.129728
HLA A*0206	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.444777	0.826538	-3.618239	27846.901104
HLA B*3801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.516307	0.898050	-3.618257	32832.726076
HLA B*3501	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.417076	0.798791	-3.618285	26126.211862
HLA A*0250	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.450129	0.831818	-3.618311	28192.202052
HLA B*0702	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.437691	0.819348	-3.618343	27396.231395
HLA A*2601	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.392137	0.773768	-3.618368	24668.154567
HLA B*5801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.316295	0.697848	-3.618447	20715.493561
HLA B*4001	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.383831	0.765110	-3.618721	24200.884084
HLA A*0216	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.415639	0.796898	-3.618740	26039.854873
HLA B*4001	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.414671	0.795837	-3.618834	25981.879943
HLA A*0203	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.415733	0.796898	-3.618834	26045.490392
HLA B*4403	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.535206	0.916286	-3.618921	34293.056951
HLA A*0216	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.445463	0.826538	-3.618925	27890.925273
HLA A*3002	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.309585	0.690572	-3.619013	20397.885798
HLA B*5401	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.448583	0.829510	-3.619074	28092.024478
HLA B*7301	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.374506	0.755176	-3.619330	23686.785407
HLA B*7301	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.581134	0.961636	-3.619498	38118.335969
HLA B*1801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.524725	0.905205	-3.619520	33475.351670
HLA A*3301	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.489661	0.869990	-3.619672	30878.872476
HLA A*2501	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.494814	0.875034	-3.619780	31247.397675
HLA A*1101	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.406659	0.786863	-3.619795	25506.967440

HLA A*0211	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.517848	0.898050	-3.619798	32949.452722
HLA B*5701	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.417271	0.797462	-3.619809	26137.945708
HLA B*4501	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.620904	1.001026	-3.619877	41773.769511
HLA B*5301	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.524544	0.904590	-3.619955	33461.410033
HLA A*6801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.489995	0.869990	-3.620005	30902.602871
HLA B*0702	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.453183	0.833148	-3.620036	28391.172591
HLA B*2705	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.420037	0.799991	-3.620046	26304.908495
HLA B*0702	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.401497	0.781429	-3.620068	25205.598218
HLA B*5801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.350743	0.730675	-3.620069	22425.567094
HLA B*4402	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.446631	0.826538	-3.620092	27966.016924
HLA B*1509	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.518988	0.898882	-3.620106	33036.018888
HLA B*3501	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.449452	0.829345	-3.620107	28148.311446
HLA A*2902	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.450846	0.830662	-3.620184	28238.758040
HLA B*0802	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.435553	0.815296	-3.620257	27261.691214
HLA B*0803	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.460173	0.839877	-3.620296	28851.808947
HLA B*3501	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.171351	0.550986	-3.620365	14837.162608
HLA A*6802	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.437111	0.816673	-3.620437	27359.647830
HLA B*5101	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.468267	0.847787	-3.620480	29394.564047
HLA B*1801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.413966	0.793337	-3.620629	25939.746416
HLA A*2601	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.384994	0.764363	-3.620631	24265.778365
HLA A*0202	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.419520	0.798696	-3.620824	26273.619658
HLA B*5701	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.412345	0.791452	-3.620893	25843.098418
HLA A*0203	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.316267	0.695361	-3.620906	20714.148782
HLA A*6901	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.353445	0.732333	-3.621112	22565.519798
HLA A*8001	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.367852	0.746693	-3.621160	23326.650585
HLA B*5801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.336127	0.714935	-3.621192	21683.395336
HLA A*2602	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.605345	0.984065	-3.621280	40303.742595
HLA B*4001	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.403027	0.781690	-3.621336	25294.524748
HLA B*4801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.429329	0.807959	-3.621371	26873.795535
HLA B*0801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.031359	0.409720	-3.621640	10748.779206
HLA A*0201	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.386178	0.764421	-3.621758	24332.031332
HLA A*6901	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.352461	0.730675	-3.621786	22514.427480
HLA A*0219	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.420495	0.798696	-3.621799	26332.672932
HLA A*6802	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.445529	0.823629	-3.621899	27895.150423
HLA B*4801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.419405	0.797462	-3.621943	26266.655850
HLA B*0802	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.453881	0.831818	-3.622064	28436.826408
HLA A*2301	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.527037	0.904921	-3.622116	33654.027197
HLA B*5701	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.420817	0.798696	-3.622121	26352.196754
HLA A*2501	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.469963	0.847787	-3.622176	29509.601969
HLA B*5701	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.395948	0.773768	-3.622179	24885.566162
HLA B*4002	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.645174	1.022974	-3.622200	44174.724152
HLA A*0219	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.352905	0.730675	-3.622230	22537.459558
HLA A*6802	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.413724	0.791452	-3.622272	25925.296333
HLA B*0801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.311662	0.689311	-3.622351	20495.669094
HLA B*1502	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.312933	0.690572	-3.622361	20555.742661
HLA B*7301	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.576710	0.954333	-3.622376	37732.002390
HLA B*5401	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.404119	0.781690	-3.622429	25358.235717
HLA B*5401	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.538925	0.916286	-3.622640	34587.998819
HLA A*2403	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.421397	0.798696	-3.622701	26387.433219
HLA A*3001	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.239096	0.616392	-3.622704	17341.869226
HLA A*0201	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.392806	0.770046	-3.622760	24706.217718
HLA B*4601	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.397294	0.774481	-3.622812	24962.827783
HLA A*2603	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.588234	0.965301	-3.622933	38746.642635
HLA A*2902	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.378143	0.755176	-3.622967	23885.983520
HLA B*4402	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.419156	0.796188	-3.622968	26251.597600
HLA A*2902	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.420678	0.797462	-3.623216	26343.786911
HLA A*3001	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.306247	0.682948	-3.623299	20241.679205
HLA A*2402	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.545067	0.921765	-3.623302	35080.598107
HLA B*0802	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.373785	0.750403	-3.623382	23647.478193
HLA B*5801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.318755	0.695361	-3.623394	20833.162237
HLA A*8001	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.410324	0.786863	-3.623461	25723.142546
HLA B*0702	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.422363	0.798791	-3.623572	26446.170014
HLA B*4402	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.378756	0.755176	-3.623580	23919.733898
HLA A*2501	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.463538	0.839877	-3.623660	29076.190810
HLA A*3201	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.528609	0.904921	-3.623688	33776.049064

HLA A*2301	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.543942	0.920120	-3.623821	34989.810141
HLA A*0202	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-3.883022	0.259153	-3.623869	7638.745782
HLA B*3801	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.511977	0.887960	-3.624017	32506.996350
HLA A*3301	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.589336	0.965301	-3.624035	38845.076913
HLA A*2403	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.346138	0.722004	-3.624134	22189.036452
HLA B*0702	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.378634	0.754459	-3.624175	23913.005883
HLA B*2705	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.389308	0.765110	-3.624197	24508.000530
HLA A*3201	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.544362	0.920120	-3.624242	35023.709640
HLA B*4601	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.370977	0.746693	-3.624284	23495.094658
HLA A*2602	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.539842	0.915512	-3.624330	34661.051581
HLA A*8001	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.432320	0.807959	-3.624361	27059.508440
HLA B*3501	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.455049	0.830662	-3.624387	28513.387806
HLA A*2902	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.441159	0.816673	-3.624486	27615.865926
HLA A*2501	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.454003	0.829345	-3.624658	28444.827217
HLA A*0216	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.422128	0.797462	-3.624666	26431.866798
HLA A*0211	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.539658	0.914880	-3.624779	34646.428695
HLA B*3901	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.380107	0.755176	-3.624931	23994.256534
HLA A*0211	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.472820	0.847787	-3.625033	29704.368604
HLA A*0212	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.448668	0.823629	-3.625038	28097.496102
HLA B*4403	1:499-507	9	DVAGQTVDV	1.020621	0.002353	-4.648061	1.022974	-3.625088	44469.409574
HLA A*0202	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.454661	0.829510	-3.625152	28487.947209
HLA B*1502	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.389540	0.764363	-3.625178	24521.130017
HLA B*1509	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.418547	0.793337	-3.625210	26214.840635
HLA B*5701	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.421451	0.796188	-3.625264	26390.716744
HLA A*0203	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-3.841807	0.216497	-3.625310	6947.161436
HLA B*2705	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.398074	0.772678	-3.625396	25007.703387
HLA B*4801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.399921	0.774481	-3.625439	25114.266867
HLA B*3801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.517583	0.892112	-3.625470	32929.316301
HLA B*1501	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.395605	0.770046	-3.625559	24865.918212
HLA B*7301	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.545748	0.920120	-3.625628	35135.678125
HLA A*0250	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.569920	0.944277	-3.625642	37146.666062
HLA B*1503	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.399563	0.773768	-3.625795	25093.623815
HLA B*4402	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.358635	0.732827	-3.625808	22836.805569
HLA A*3001	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.280059	0.654207	-3.625852	19057.203780
HLA B*4501	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.357933	0.732039	-3.625894	22799.895597
HLA B*1517	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.499090	0.873123	-3.625967	31556.579099
HLA A*0250	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.496064	0.869990	-3.626074	31337.459131
HLA A*6801	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.544428	0.918327	-3.626101	35029.015324
HLA A*6801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.398804	0.772678	-3.626127	25049.813650
HLA A*2602	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.547891	0.921765	-3.626127	35309.459548
HLA B*1509	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.534259	0.908065	-3.626194	34218.373174
HLA B*3801	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.525078	0.898882	-3.626196	33502.527386
HLA A*2301	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.542642	0.916314	-3.626328	34885.288646
HLA B*0801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.358436	0.732039	-3.626397	22826.306693
HLA B*1503	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.150558	0.524138	-3.626419	14143.533195
HLA B*5301	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.587818	0.961256	-3.626562	38709.558531
HLA B*1517	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.474357	0.847787	-3.626570	29809.650803
HLA B*2705	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.456092	0.829510	-3.626582	28581.959022
HLA A*2902	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.377065	0.750403	-3.626662	23826.744879
HLA B*4002	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.546900	0.920120	-3.626779	35228.940944
HLA B*1801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.496834	0.869990	-3.626845	31393.115051
HLA B*3901	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.474535	0.847664	-3.626872	29821.909608
HLA A*3101	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.401384	0.774481	-3.626903	25199.053812
HLA B*4601	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.381383	0.754459	-3.626924	24064.844965
HLA A*3201	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.541867	0.914880	-3.626987	34823.064776
HLA B*4001	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.397078	0.770046	-3.627032	24950.406630
HLA A*2402	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.573334	0.946270	-3.627064	37439.810623
HLA A*0201	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.322442	0.695361	-3.627080	21010.749159
HLA A*0212	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.422988	0.795837	-3.627151	26484.254255
HLA A*3201	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.029870	0.402654	-3.627215	10711.975446
HLA A*0201	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.310184	0.682948	-3.627236	20426.044543
HLA B*4402	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.411015	0.783751	-3.627264	25764.087948
HLA B*3501	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.410667	0.783381	-3.627286	25743.467837
HLA B*4501	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.409008	0.781690	-3.627318	25645.331236
HLA B*5701	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.423183	0.795837	-3.627346	26496.148906

HLA B*0802	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.471662	0.844164	-3.627498	29625.250369
HLA B*5801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.340408	0.712902	-3.627506	21898.181433
HLA A*3301	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.621879	0.994371	-3.627508	41867.661327
HLA B*2705	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.458254	0.830662	-3.627592	28724.568830
HLA A*2403	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.451325	0.823629	-3.627696	28269.940027
HLA A*0101	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.374499	0.746693	-3.627806	23686.400982
HLA A*6901	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.392282	0.764363	-3.627920	24676.429978
HLA B*4501	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.572274	0.944277	-3.627997	37348.574074
HLA A*0212	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.001370	0.373369	-3.628001	10031.602510
HLA A*2902	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.374708	0.746693	-3.628015	23697.808259
HLA B*3801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.522975	0.894591	-3.628384	33340.705223
HLA B*4402	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.421858	0.793337	-3.628521	26415.427664
HLA B*3801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.546686	0.918162	-3.628524	35211.602008
HLA B*0802	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.458082	0.829510	-3.628573	28713.227109
HLA A*6901	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.013907	0.385288	-3.628619	10325.406715
HLA A*2403	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.403137	0.774481	-3.628656	25300.957073
HLA A*2603	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.603005	0.974301	-3.628704	40087.159995
HLA A*3001	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.295260	0.666540	-3.628720	19736.054961
HLA B*4403	1:332-340	9	WVAVVAVLA	1.133480	-0.118492	-4.643806	1.014988	-3.628819	44035.856313
HLA A*0250	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.575091	0.946270	-3.628821	37591.621402
HLA B*1502	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-3.896419	0.267585	-3.628834	7878.051588
HLA A*2402	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.522672	0.893801	-3.628871	33317.445672
HLA B*1509	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.460758	0.831818	-3.628940	28890.700323
HLA B*0801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.412744	0.783751	-3.628993	25866.876761
HLA B*1509	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.223932	0.594934	-3.628998	16746.819163
HLA A*2603	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.590280	0.961256	-3.629024	38929.648160
HLA B*7301	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.494187	0.865145	-3.629041	31202.295253
HLA B*5401	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.499076	0.869990	-3.629086	31555.554810
HLA A*0219	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.452923	0.823629	-3.629293	28374.128875
HLA B*3801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.502461	0.873123	-3.629339	31802.512225
HLA A*0206	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.412732	0.783381	-3.629351	25866.177085
HLA A*0206	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.393805	0.764421	-3.629384	24763.087678
HLA A*2902	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.412925	0.783381	-3.629544	25877.654149
HLA A*3301	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.591230	0.961636	-3.629594	39014.825661
HLA B*0702	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.380053	0.750403	-3.629650	23991.271175
HLA A*3301	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.545936	0.916286	-3.629651	35150.887826
HLA A*3301	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.644657	1.014994	-3.629663	44122.179747
HLA B*3801	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.536914	0.907250	-3.629664	34428.196759
HLA A*2602	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.538787	0.909118	-3.629668	34576.960663
HLA A*2602	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.584214	0.954333	-3.629881	38389.646086
HLA B*2705	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-3.937765	0.307875	-3.629890	8664.929977
HLA B*3801	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.495112	0.865145	-3.629967	31268.873761
HLA A*3002	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.528080	0.898050	-3.630030	33734.961022
HLA B*0801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.416917	0.786863	-3.630053	26116.602515
HLA A*3201	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.579186	0.949124	-3.630062	37947.765701
HLA B*3901	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.470029	0.839877	-3.630152	29514.072330
HLA B*5101	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.449504	0.819348	-3.630156	28151.661789
HLA B*1517	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.353131	0.722962	-3.630169	22549.167414
HLA A*2902	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.456722	0.826538	-3.630183	28623.428639
HLA A*3301	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.546517	0.916314	-3.630202	35197.889336
HLA A*2603	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.518586	0.888375	-3.630211	33005.471695
HLA A*0301	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.360907	0.730675	-3.630232	22956.586219
HLA A*2301	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.524272	0.894030	-3.630242	33440.418008
HLA B*3901	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.380697	0.750403	-3.630294	24026.860038
HLA B*5801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.356314	0.725976	-3.630338	22715.069146
HLA A*0202	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.385551	0.755176	-3.630375	24296.910534
HLA B*2705	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.449737	0.819348	-3.630389	28166.743267
HLA A*0202	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.292854	0.662443	-3.630412	19627.024891
HLA A*2501	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.124469	0.494046	-3.630423	13318.926817
HLA B*4002	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.548629	0.918162	-3.630467	35369.490884
HLA A*3301	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.586514	0.956046	-3.630468	38593.507835
HLA A*2301	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.524300	0.893801	-3.630499	33442.588986
HLA B*5701	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.380923	0.750403	-3.630520	24039.341613
HLA B*0801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.377220	0.746693	-3.630527	23835.253801
HLA B*5301	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.537793	0.907250	-3.630543	34497.925796

HLA A*6801	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.576895	0.946270	-3.630626	37748.131787
HLA A*0212	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.430640	0.799991	-3.630649	26955.042518
HLA B*5401	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.538773	0.908065	-3.630708	34575.838337
HLA B*3901	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.500866	0.869990	-3.630877	31685.905886
HLA A*2402	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.518924	0.887960	-3.630964	33031.193768
HLA A*2301	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.529852	0.898882	-3.630970	33872.848866
HLA A*2301	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.545849	0.914880	-3.630970	35143.852521
HLA A*0101	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.395344	0.764363	-3.630981	24850.990768
HLA A*2403	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.421987	0.790996	-3.630991	26423.288582
HLA A*0211	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.405486	0.774481	-3.631005	25438.203354
HLA A*2402	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.549404	0.918327	-3.631077	35432.691140
HLA B*1501	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.403760	0.772678	-3.631082	25337.255059
HLA B*4001	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.454772	0.823629	-3.631142	28495.191612
HLA B*4501	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.547494	0.916286	-3.631208	35277.191877
HLA B*5401	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.546110	0.914880	-3.631231	35164.962661
HLA A*3301	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.519197	0.887960	-3.631237	33051.928905
HLA A*0203	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.428723	0.797462	-3.631261	26836.312562
HLA B*0802	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.418150	0.786863	-3.631287	26190.884113
HLA B*1501	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.395760	0.764421	-3.631339	24874.798240
HLA A*0201	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.395811	0.764363	-3.631449	24877.758954
HLA B*1517	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.418364	0.786863	-3.631501	26203.781057
HLA A*2403	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.386679	0.755176	-3.631502	24360.085448
HLA B*4801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.413197	0.781690	-3.631507	25893.898694
HLA A*3002	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.504778	0.873256	-3.631522	31972.604865
HLA A*0101	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.343441	0.711889	-3.631552	22051.657313
HLA B*4002	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-3.922000	0.290447	-3.631553	8356.030434
HLA A*2501	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.446983	0.815296	-3.631687	27988.720092
HLA A*0216	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.462353	0.830662	-3.631692	28997.020111
HLA A*2403	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.404380	0.772678	-3.631702	25373.467852
HLA A*0301	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.364901	0.733042	-3.631860	23168.687448
HLA B*3901	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.345029	0.712902	-3.632127	22132.449742
HLA B*3501	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.429618	0.797462	-3.632156	26891.683749
HLA B*0803	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.502191	0.869990	-3.632202	31782.732851
HLA B*3901	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.416061	0.783751	-3.632311	26065.224314
HLA B*5701	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.415737	0.783381	-3.632356	26045.772200
HLA A*1101	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.463216	0.830662	-3.632554	29054.648835
HLA A*2902	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.286863	0.654207	-3.632656	19358.124850
HLA A*0203	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.402754	0.770046	-3.632708	25278.656221
HLA B*4501	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.452086	0.819348	-3.632738	28319.535146
HLA A*0206	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.405517	0.772678	-3.632839	25439.992450
HLA A*2603	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.226315	0.593391	-3.632924	16838.938412
HLA B*5401	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.366046	0.733042	-3.633004	23229.808523
HLA A*8001	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.424480	0.791452	-3.633028	26575.391525
HLA A*2501	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.463733	0.830662	-3.633071	29089.249556
HLA B*4001	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.365959	0.732827	-3.633132	23225.159173
HLA B*7301	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.607439	0.974301	-3.633138	40498.484118
HLA B*4002	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.634183	1.001026	-3.633157	43070.801681
HLA B*1503	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.328531	0.695361	-3.633170	21307.446321
HLA B*0802	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.473065	0.839877	-3.633188	29721.085830
HLA B*5801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.295693	0.662443	-3.633250	19755.710398
HLA B*0803	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.527286	0.894030	-3.633256	33673.331575
HLA B*1501	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.256656	0.623337	-3.633319	18057.430742
HLA B*1501	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.055380	0.421976	-3.633405	11360.050884
HLA A*6802	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.013964	0.380356	-3.633608	10326.747425
HLA A*0211	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.212772	0.578823	-3.633949	16321.958788
HLA A*0206	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.345859	0.711889	-3.633970	22174.756262
HLA A*0203	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.174372	0.540402	-3.633970	14940.746395
HLA B*0702	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.407869	0.773768	-3.634100	25578.131310
HLA A*2402	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.528698	0.894591	-3.634107	33782.993315
HLA A*0203	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.139168	0.505009	-3.634159	13777.410891
HLA B*4801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.432921	0.798696	-3.634225	27097.009971
HLA B*5701	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.399357	0.765110	-3.634246	25081.680331
HLA A*2902	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.416073	0.781690	-3.634383	26065.929374
HLA B*4801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.430231	0.795837	-3.634394	26929.681117
HLA B*5301	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.509585	0.875034	-3.634551	32328.463702

HLA B*4403	1:542-550	9	GTTVPVDSV	0.896728	0.099224	-4.630569	0.995952	-3.634618	42713.921726
HLA B*0803	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.385133	0.750403	-3.634730	24273.524836
HLA A*0216	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-3.808520	0.173777	-3.634743	6434.575299
HLA B*5101	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.482456	0.847664	-3.634792	30370.753257
HLA B*5101	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.442777	0.807959	-3.634819	27718.993762
HLA A*2403	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.434850	0.799991	-3.634859	27217.629524
HLA A*0216	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.365562	0.730675	-3.634887	23203.934781
HLA B*4501	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.529488	0.894591	-3.634897	33844.457276
HLA B*4601	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.330272	0.695361	-3.634911	21393.033508
HLA B*0801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.346867	0.711889	-3.634978	22226.280144
HLA A*2601	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.368026	0.733042	-3.634984	23335.990854
HLA B*5301	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.589428	0.954333	-3.635094	38853.273532
HLA B*4402	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.399620	0.764363	-3.635257	25096.882116
HLA B*7301	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.532676	0.897363	-3.635313	34093.831102
HLA A*6802	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-3.877534	0.242192	-3.635342	7542.818541
HLA A*2301	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.540572	0.905205	-3.635367	34719.417037
HLA A*2602	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.590062	0.954621	-3.635441	38910.066814
HLA A*0219	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.452150	0.816673	-3.635476	28323.671998
HLA B*5401	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.483339	0.847787	-3.635552	30432.593837
HLA B*0802	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.483219	0.847664	-3.635555	30424.198510
HLA A*0206	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.168437	0.532852	-3.635586	14737.964123
HLA B*1509	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.495751	0.860149	-3.635603	31314.919461
HLA B*0802	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.455004	0.819348	-3.635656	28510.457126
HLA B*3801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.480017	0.844164	-3.635853	30200.685309
HLA A*8001	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.452589	0.816673	-3.635916	28352.340119
HLA A*6802	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.435964	0.799991	-3.635973	27287.512912
HLA A*0203	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.290202	0.654207	-3.635995	19507.512986
HLA A*2301	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.534088	0.898050	-3.636038	34204.862257
HLA B*2705	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.467870	0.831818	-3.636052	29367.701723
HLA B*4501	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.541141	0.904921	-3.636220	34764.901228
HLA B*3901	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.410719	0.774481	-3.636237	25746.531944
HLA B*2705	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.433842	0.797462	-3.636380	27154.534939
HLA B*5101	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.480635	0.844164	-3.636471	30243.685453
HLA A*2301	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.451807	0.815296	-3.636510	28301.309554
HLA B*3801	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.496684	0.860149	-3.636535	31382.247603
HLA A*0216	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.453230	0.816673	-3.636557	28394.244619
HLA B*4402	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.418272	0.781690	-3.636582	26198.253018
HLA B*4801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.435431	0.798791	-3.636639	27254.023191
HLA B*3801	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.530503	0.893801	-3.636702	33923.646713
HLA A*0211	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.141729	0.505009	-3.636720	13858.893247
HLA A*3101	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.401156	0.764421	-3.636736	25185.833845
HLA B*5301	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.565937	0.929186	-3.636752	36807.596939
HLA A*0212	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.391303	0.754459	-3.636844	24620.824577
HLA A*2402	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.566156	0.929186	-3.636970	36826.120225
HLA B*1501	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.392155	0.755176	-3.636979	24669.222206
HLA B*1509	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.435691	0.798696	-3.636995	27270.394084
HLA B*7301	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.555327	0.918327	-3.637000	35919.244237
HLA A*2501	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.435882	0.798791	-3.637091	27282.346617
HLA A*2402	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.541703	0.904590	-3.637113	34809.880048
HLA A*2902	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.433337	0.796188	-3.637150	27122.969150
HLA A*0203	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.387574	0.750403	-3.637171	24410.347452
HLA B*2705	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.223274	0.586005	-3.637270	16721.470805
HLA A*3001	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.280510	0.643088	-3.637422	19077.008757
HLA A*0212	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.401856	0.764421	-3.637436	25226.469857
HLA B*4001	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.369492	0.732039	-3.637454	23414.900927
HLA A*0301	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.360524	0.722962	-3.637563	22936.351750
HLA B*1503	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.466956	0.829345	-3.637611	29305.963940
HLA A*0101	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.369683	0.732039	-3.637644	23425.163609
HLA A*3002	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.544935	0.907250	-3.637685	35069.971917
HLA A*8001	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.412182	0.774481	-3.637701	25833.453445
HLA B*3901	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.431051	0.793337	-3.637714	26980.573765
HLA B*1517	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.421489	0.783751	-3.637738	26393.001177
HLA B*5801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.328322	0.690572	-3.637751	21297.189678
HLA A*0101	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.370766	0.732827	-3.637939	23483.657915
HLA B*3801	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.535328	0.897363	-3.637966	34302.705433

HLA B*0803	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.513048	0.875034	-3.638014	32587.287161
HLA B*0702	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.333390	0.695361	-3.638029	21547.165033
HLA B*1801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.388462	0.750403	-3.638059	24460.316175
HLA B*0801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.392722	0.754459	-3.638263	24701.406502
HLA A*3201	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.537168	0.898882	-3.638286	34448.317931
HLA B*4002	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.599599	0.961256	-3.638342	39773.932848
HLA A*2402	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.559996	0.921444	-3.638551	36307.439050
HLA A*8001	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.462245	0.823629	-3.638616	28989.804958
HLA A*2402	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.554134	0.915512	-3.638622	35820.665640
HLA A*0201	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.389028	0.750403	-3.638625	24492.227925
HLA B*4001	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.393088	0.754459	-3.638629	24722.261873
HLA B*5801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.350588	0.711889	-3.638699	22417.561415
HLA B*0803	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.454151	0.815296	-3.638855	28454.523521
HLA B*0801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.408924	0.770046	-3.638878	25640.337140
HLA B*1501	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.334288	0.695361	-3.638926	21591.739966
HLA A*0250	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.544254	0.905205	-3.639049	35014.994902
HLA B*3501	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.432404	0.793337	-3.639068	27064.778955
HLA B*0802	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.468464	0.829345	-3.639119	29407.924874
HLA B*1502	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.555487	0.916314	-3.639173	35932.460369
HLA A*1101	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.437999	0.798791	-3.639207	27415.653861
HLA B*4601	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.394601	0.755176	-3.639425	24808.543671
HLA B*4402	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.337283	0.697848	-3.639435	21741.186156
HLA B*0802	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.487227	0.847787	-3.639440	30706.291433
HLA A*0211	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.438248	0.798696	-3.639552	27431.379829
HLA A*0216	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.351448	0.711889	-3.639559	22461.992594
HLA B*4801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.422950	0.783381	-3.639569	26481.961924
HLA A*2501	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.469085	0.829510	-3.639575	29449.955596
HLA B*5301	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.412283	0.772678	-3.639606	25839.463657
HLA A*0212	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.437259	0.797462	-3.639797	27368.974217
HLA B*4601	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.404911	0.765110	-3.639800	25404.509313
HLA B*3501	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.395012	0.755176	-3.639836	24832.041800
HLA A*2601	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.372314	0.732333	-3.639981	23567.529319
HLA A*8001	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.423756	0.783751	-3.640005	26531.147260
HLA B*1517	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.438804	0.798791	-3.640013	27466.573357
HLA B*2705	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.337880	0.697848	-3.640032	21771.081513
HLA A*6801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.191054	0.550986	-3.640068	15525.787496
HLA B*5301	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.601041	0.960920	-3.640121	39906.268471
HLA A*8001	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.438889	0.798696	-3.640193	27471.923158
HLA B*3801	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.513746	0.873492	-3.640254	32639.688450
HLA B*1801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.423859	0.783381	-3.640478	26537.463357
HLA B*4002	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.582858	0.942253	-3.640605	38269.999410
HLA B*1503	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.352529	0.711889	-3.640640	22517.959974
HLA B*4002	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.596525	0.955683	-3.640842	39493.480560
HLA B*1509	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.448938	0.807959	-3.640979	28114.982039
HLA A*1101	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.437317	0.796188	-3.641130	27372.676045
HLA A*6901	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.331703	0.690572	-3.641131	21463.631710
HLA A*2501	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.488813	0.847664	-3.641149	30818.625814
HLA A*2402	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.533277	0.892112	-3.641165	34141.081439
HLA B*3901	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.406316	0.765110	-3.641205	25486.828874
HLA A*2301	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.538575	0.897363	-3.641213	34560.129584
HLA A*6802	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.135282	0.494046	-3.641236	13654.681125
HLA B*1509	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.535279	0.894030	-3.641249	34298.808604
HLA B*4801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.413961	0.772678	-3.641283	25939.465755
HLA A*2403	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.422976	0.781690	-3.641286	26483.537880
HLA A*2301	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.549376	0.908065	-3.641311	35430.390971
HLA B*5701	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.411412	0.770046	-3.641366	25787.654084
HLA B*5701	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.303928	0.662443	-3.641485	20133.885574
HLA B*4501	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.516523	0.875034	-3.641489	32849.071312
HLA B*7301	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.602479	0.960920	-3.641559	40038.611189
HLA A*8001	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.414262	0.772678	-3.641584	25957.434168
HLA B*3501	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.474742	0.833148	-3.641595	29836.110312
HLA B*5801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.351063	0.709300	-3.641763	22442.072663
HLA A*0301	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.367742	0.725976	-3.641766	23320.720193
HLA A*0202	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.388591	0.746693	-3.641899	24467.595276
HLA B*7301	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.603158	0.961256	-3.641902	40101.258835

HLA A*2501	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.406367	0.764421	-3.641947	25489.862435
HLA A*8001	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.423406	0.781429	-3.641977	26509.769823
HLA B*2705	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.388744	0.746693	-3.642051	24476.200643
HLA B*7301	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.586347	0.944277	-3.642070	38578.686833
HLA A*0202	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.414842	0.772678	-3.642164	25992.142783
HLA B*1517	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.203346	0.561125	-3.642222	15971.516083
HLA B*5701	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.397463	0.755176	-3.642286	24972.552999
HLA A*2402	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.560562	0.918162	-3.642400	36354.806954
HLA A*2403	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-3.935777	0.293372	-3.642406	8625.363231
HLA A*0206	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.435757	0.793337	-3.642420	27274.525231
HLA B*1502	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.586820	0.944277	-3.642542	38620.659640
HLA B*1517	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.434004	0.791452	-3.642553	27164.673140
HLA A*0219	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.415234	0.772678	-3.642557	26015.636034
HLA B*0702	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.472085	0.829510	-3.642575	29654.112897
HLA B*0803	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.495998	0.853416	-3.642582	31332.712590
HLA A*0219	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.439486	0.796898	-3.642587	27509.698601
HLA A*0212	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.397815	0.755176	-3.642639	24992.826035
HLA B*3801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.462125	0.819348	-3.642778	28981.807648
HLA A*6801	1:137-145	9	RDVKPANIM	0.886768	0.128226	-4.657784	1.014994	-3.642790	45476.133449
HLA B*5701	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.417283	0.774481	-3.642802	26138.652735
HLA A*0219	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.357806	0.714935	-3.642871	22793.235945
HLA A*3301	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.628234	0.985326	-3.642908	42484.847078
HLA A*0250	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.398086	0.755176	-3.642909	25008.379840
HLA A*2403	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.393600	0.750403	-3.643197	24751.435416
HLA B*4601	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.407622	0.764421	-3.643202	25563.606076
HLA A*2501	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.462577	0.819348	-3.643229	29011.926654
HLA A*8001	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.443226	0.799991	-3.643235	27747.650291
HLA A*0301	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.365259	0.722004	-3.643254	23187.746968
HLA B*5401	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.531640	0.888375	-3.643264	34012.588317
HLA B*1509	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.443266	0.799991	-3.643275	27750.202307
HLA A*0101	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.375657	0.732333	-3.643324	23749.658717
HLA B*0802	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.442030	0.798696	-3.643334	27671.348531
HLA A*1101	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.376174	0.732827	-3.643347	23777.941809
HLA A*0212	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.744078	0.100651	-3.643427	5547.256055
HLA A*1101	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.476659	0.833148	-3.643512	29968.112057
HLA A*0212	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.413625	0.770046	-3.643579	25919.406377
HLA A*0201	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.376665	0.733042	-3.643623	23804.841944
HLA A*0211	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.440599	0.796898	-3.643701	27580.331899
HLA B*1502	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.418284	0.774481	-3.643803	26198.961676
HLA B*5301	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.599904	0.956046	-3.643858	39801.915121
HLA A*2403	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.427254	0.783381	-3.643873	26745.727368
HLA A*6802	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.441365	0.797462	-3.643903	27629.016148
HLA B*7301	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.542898	0.898882	-3.644016	34905.865797
HLA A*8001	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.440353	0.796188	-3.644165	27564.669662
HLA A*3001	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.262111	0.617889	-3.644223	18285.694596
HLA A*0216	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.394648	0.750403	-3.644245	24811.228046
HLA A*3001	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.046932	0.402654	-3.644277	11141.188664
HLA A*2403	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.376325	0.732039	-3.644286	23786.175940
HLA B*0801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.377368	0.733042	-3.644326	23843.378789
HLA B*4001	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.357273	0.712902	-3.644370	22765.262009
HLA B*0803	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.463718	0.819348	-3.644370	29088.305353
HLA B*4801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.409544	0.765110	-3.644434	25676.983107
HLA B*3501	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.359453	0.714935	-3.644518	22879.839581
HLA B*7301	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.538329	0.893801	-3.644528	34540.503679
HLA B*3901	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.475250	0.830662	-3.644588	29870.995261
HLA B*0803	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.492380	0.847787	-3.644593	31072.756956
HLA B*7301	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.492431	0.847787	-3.644645	31076.455379
HLA B*4403	1:514-522	9	VYGFTKFSQ	0.915578	0.085448	-4.645688	1.001026	-3.644662	44227.091866
HLA B*1517	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.492340	0.847664	-3.644676	31069.899384
HLA B*7301	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.532697	0.887960	-3.644737	34095.491137
HLA A*0202	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.426439	0.781690	-3.644749	26695.566542
HLA B*4402	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.409239	0.764421	-3.644818	25658.931203
HLA B*4801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.418594	0.773768	-3.644826	26217.677176
HLA B*5301	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.492509	0.847664	-3.644845	31082.003841
HLA A*0219	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.435849	0.790996	-3.644853	27280.280372

HLA B*5301	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.594028	0.949124	-3.644904	39267.016709
HLA A*3201	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.236988	0.592081	-3.644907	17257.918705
HLA A*2601	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.391662	0.746693	-3.644969	24641.211991
HLA B*0803	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.471601	0.826538	-3.645063	29621.083660
HLA B*5101	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.417751	0.772678	-3.645073	26166.807923
HLA B*0803	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.436121	0.790996	-3.645126	27297.405407
HLA A*2402	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.518259	0.873123	-3.645137	32980.661748
HLA B*0801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.288280	0.643088	-3.645192	19421.377325
HLA B*3501	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.445277	0.799991	-3.645286	27879.007761
HLA B*1801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.216564	0.571232	-3.645333	16465.098977
HLA B*3501	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.464696	0.819348	-3.645348	29153.842707
HLA A*0201	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.371365	0.725976	-3.645389	23516.076487
HLA B*1517	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.282230	0.636741	-3.645489	19152.704232
HLA B*4801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.377603	0.732039	-3.645564	23856.281282
HLA B*1503	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.493263	0.847664	-3.645599	31136.026947
HLA A*2902	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.444323	0.798696	-3.645627	27817.841089
HLA A*3101	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.048332	0.402654	-3.645678	11177.169105
HLA A*0202	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.493454	0.847664	-3.645790	31149.673776
HLA A*0219	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.378150	0.732333	-3.645817	23886.371184
HLA B*5701	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.343726	0.697848	-3.645877	22066.096978
HLA A*6802	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.427320	0.781429	-3.645891	26749.779035
HLA A*6802	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.186369	0.540402	-3.645967	15359.205973
HLA B*1503	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.410496	0.764421	-3.646075	25733.303184
HLA A*2902	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.418773	0.772678	-3.646095	26228.458832
HLA A*2301	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.534109	0.887960	-3.646149	34206.527698
HLA A*1101	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.437670	0.791452	-3.646218	27394.897532
HLA A*0101	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.359183	0.712902	-3.646281	22865.609607
HLA A*1101	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.462992	0.816673	-3.646319	29039.720341
HLA A*2402	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.521436	0.875034	-3.646402	33222.772258
HLA A*0219	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.410944	0.764421	-3.646524	25759.906861
HLA A*3001	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.170919	0.524138	-3.646780	14822.400754
HLA B*0801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.300993	0.654207	-3.646786	19998.300472
HLA A*2603	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.099518	0.452683	-3.646835	12575.281104
HLA B*7301	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.428347	0.781429	-3.646918	26813.093576
HLA B*3501	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.463674	0.816673	-3.647001	29085.315581
HLA B*4002	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.379351	0.732333	-3.647018	23952.495300
HLA A*3002	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.535443	0.888375	-3.647068	34311.799757
HLA B*4002	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.632395	0.985326	-3.647069	42893.846898
HLA B*0803	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.491254	0.844164	-3.647090	30992.341211
HLA A*2501	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.430478	0.783381	-3.647097	26944.982554
HLA A*0201	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.379445	0.732333	-3.647112	23957.679074
HLA A*3101	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.293115	0.645932	-3.647183	19638.814414
HLA B*0801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.444826	0.797462	-3.647364	27850.064906
HLA A*0203	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-3.889676	0.242192	-3.647484	7756.678631
HLA B*4801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.411863	0.764363	-3.647500	25814.453603
HLA A*0216	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.471140	0.823629	-3.647511	29589.691937
HLA A*3101	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.345391	0.697848	-3.647543	22150.896476
HLA A*2603	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.616397	0.968816	-3.647582	41342.558912
HLA A*3001	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.152687	0.505009	-3.647678	14213.025902
HLA A*0219	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.413021	0.765110	-3.647911	25883.394591
HLA B*4001	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.412504	0.764421	-3.648084	25852.607131
HLA B*4601	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.380180	0.732039	-3.648141	23998.280865
HLA B*4402	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.413291	0.765110	-3.648181	25899.502625
HLA A*3002	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.553140	0.904921	-3.648219	35738.787953
HLA A*2603	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.222457	0.574191	-3.648266	16690.019886
HLA A*2603	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.592632	0.944277	-3.648355	39141.035693
HLA A*3002	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.477733	0.829345	-3.648388	30042.294463
HLA A*8001	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.380490	0.732039	-3.648451	24015.424287
HLA B*1509	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.553133	0.904590	-3.648543	35738.207929
HLA B*4002	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.632611	0.984065	-3.648546	42915.200900
HLA A*3002	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.610223	0.961636	-3.648587	40758.942475
HLA B*5301	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.456548	0.807959	-3.648589	28611.972063
HLA A*2402	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.546653	0.898050	-3.648603	35208.935237
HLA A*1101	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.467976	0.819348	-3.648628	29374.852014
HLA A*2501	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.441969	0.793337	-3.648632	27667.456633

HLA B*1509	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.488510	0.839877	-3.648633	30797.125747
HLA A*2602	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.594942	0.946270	-3.648672	39349.739072
HLA B*1801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.456658	0.807959	-3.648700	28619.248005
HLA B*0702	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.242127	0.593391	-3.648736	17463.317203
HLA A*3301	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.578049	0.929186	-3.648863	37848.533760
HLA A*3101	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.418951	0.770046	-3.648905	26239.244921
HLA A*0216	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.444819	0.795837	-3.648982	27849.612912
HLA B*7301	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.522124	0.873123	-3.649002	33275.475351
HLA A*3201	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.610763	0.961636	-3.649128	40809.689353
HLA A*2501	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.382257	0.733042	-3.649215	24113.323720
HLA A*3001	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.303777	0.654485	-3.649292	20126.915767
HLA A*0216	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.344698	0.695361	-3.649337	22115.573671
HLA B*4402	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.448170	0.798696	-3.649473	28065.289654
HLA A*2602	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.473114	0.823629	-3.649485	29724.462565
HLA A*2301	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.537920	0.888375	-3.649545	34508.005286
HLA A*0212	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.433116	0.783381	-3.649735	27109.179824
HLA B*5701	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.182600	0.532852	-3.649749	15226.503637
HLA B*3501	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.431206	0.781429	-3.649777	26990.208972
HLA A*0301	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.361734	0.711889	-3.649845	23000.343659
HLA A*0212	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.446750	0.796898	-3.649852	27973.733934
HLA A*0250	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.375942	0.725976	-3.649966	23765.210252
HLA A*0301	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.359324	0.709300	-3.650024	22873.032837
HLA A*0203	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.145798	0.495678	-3.650120	13989.360358
HLA A*2602	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.542356	0.892112	-3.650243	34862.271726
HLA A*6901	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.276269	0.625924	-3.650345	18891.631195
HLA B*7301	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.544404	0.894030	-3.650374	35027.120345
HLA A*6802	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.433781	0.783381	-3.650400	27150.715729
HLA B*3901	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.479848	0.829345	-3.650502	30188.924070
HLA A*2402	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.538975	0.888375	-3.650600	34591.928504
HLA B*1502	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.483748	0.833148	-3.650600	30461.254155
HLA B*5701	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.414978	0.764363	-3.650616	26000.299710
HLA B*1502	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.524117	0.873492	-3.650625	33428.480148
HLA B*0802	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.483828	0.833148	-3.650680	30466.857598
HLA B*0702	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.383037	0.732333	-3.650704	24156.672172
HLA B*3901	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.423493	0.772678	-3.650815	26515.076706
HLA A*0211	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.498491	0.847664	-3.650827	31513.076126
HLA A*0212	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.244241	0.593391	-3.650850	17548.551682
HLA B*4501	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.600054	0.949124	-3.650930	39815.698239
HLA A*2602	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.625238	0.974301	-3.650937	42192.811561
HLA B*4402	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.446809	0.795837	-3.650972	27977.517560
HLA A*3201	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.348901	0.697848	-3.651053	22330.653769
HLA A*0219	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.447244	0.796188	-3.651056	28005.532301
HLA A*0212	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.442167	0.790996	-3.651171	27680.032431
HLA B*0802	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.432924	0.781690	-3.651234	27097.156563
HLA A*0202	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.442714	0.791452	-3.651262	27714.945227
HLA A*6802	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.083673	0.432298	-3.651375	12124.749509
HLA B*0801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.415782	0.764363	-3.651419	26048.449528
HLA B*1501	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.331543	0.680074	-3.651469	21455.737284
HLA B*1502	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.401873	0.750403	-3.651470	25227.425182
HLA B*7301	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.524746	0.873256	-3.651490	33476.981591
HLA A*0301	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.366443	0.714935	-3.651507	23251.056581
HLA B*5301	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.572969	0.921444	-3.651525	37408.429272
HLA B*4601	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.382241	0.730675	-3.651566	24112.410584
HLA A*0212	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.402040	0.750403	-3.651637	25237.116951
HLA A*3201	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.597977	0.946270	-3.651708	39625.740537
HLA B*1502	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.598121	0.946270	-3.651851	39638.819317
HLA B*5301	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.505300	0.853416	-3.651884	32011.026883
HLA A*2403	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.263946	0.612002	-3.651945	18363.117358
HLA A*0202	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.514803	0.862842	-3.651961	32719.244942
HLA A*6901	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.374929	0.722962	-3.651967	23709.862360
HLA A*3001	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.288099	0.635971	-3.652128	19413.288813
HLA B*1517	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.481523	0.829345	-3.652178	30305.595197
HLA B*0802	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.445538	0.793337	-3.652201	27895.754069
HLA A*0216	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.424903	0.772678	-3.652225	26601.282715
HLA B*4402	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.451022	0.798791	-3.652231	28250.218006

HLA A*0201	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.226803	0.574537	-3.652266	16857.897209
HLA A*3101	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.178188	0.525884	-3.652304	15072.589027
HLA A*2402	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.572547	0.920120	-3.652426	37372.019420
HLA A*3301	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.626810	0.974301	-3.652509	42345.793122
HLA A*1101	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.460476	0.807959	-3.652518	28871.950951
HLA B*5401	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.025918	0.373369	-3.652548	10614.944669
HLA A*6801	1:357-365	9	TRDVQVPDV	0.879739	0.143142	-4.675438	1.022881	-3.652556	47362.821092
HLA A*2902	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.444037	0.791452	-3.652585	27799.487191
HLA A*1101	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.176844	0.524138	-3.652705	15026.019645
HLA B*0801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.436126	0.783381	-3.652745	27297.700761
HLA A*2601	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.408007	0.755176	-3.652831	25586.296730
HLA A*0203	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-3.920492	0.267585	-3.652906	8327.059037
HLA A*8001	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.450505	0.797462	-3.653043	28216.615286
HLA B*1517	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.472536	0.819348	-3.653188	29684.930589
HLA B*5801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.350706	0.697387	-3.653318	22423.626061
HLA B*0702	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.449539	0.796188	-3.653352	28153.946342
HLA A*3301	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.608045	0.954621	-3.653424	40555.049400
HLA A*8001	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.449278	0.795837	-3.653442	28137.045037
HLA A*1101	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.482972	0.829510	-3.653463	30406.921306
HLA A*2403	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.385821	0.732333	-3.653488	24312.031250
HLA A*0219	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.449478	0.795837	-3.653641	28149.986568
HLA B*1509	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.547463	0.893801	-3.653663	35274.710970
HLA B*4002	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.497894	0.844164	-3.653730	31469.803373
HLA B*4002	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.598224	0.944464	-3.653760	39648.255872
HLA A*3002	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.526905	0.873123	-3.653783	33643.833126
HLA A*0219	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.423874	0.770046	-3.653828	26538.324759
HLA B*3801	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.558750	0.904921	-3.653829	36203.485964
HLA A*0212	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.386228	0.732333	-3.653895	24334.795795
HLA A*0203	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-3.929020	0.275124	-3.653897	8492.201185
HLA B*0803	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.501566	0.847664	-3.653902	31737.029421
HLA A*0206	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.409102	0.755176	-3.653926	25650.881372
HLA A*0201	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.384611	0.730675	-3.653936	24244.389944
HLA A*0216	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.453930	0.799991	-3.653939	28440.057233
HLA B*1501	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.000012	0.346054	-3.653958	10000.283524
HLA B*7301	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.527469	0.873492	-3.653977	33687.543754
HLA B*4601	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.386366	0.732333	-3.654033	24342.564299
HLA B*3801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.562237	0.908065	-3.654172	36495.307366
HLA A*0211	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.507604	0.853416	-3.654189	32181.364243
HLA B*5701	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.376217	0.722004	-3.654212	23780.257370
HLA B*3501	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.337163	0.682948	-3.654215	21735.188496
HLA A*3001	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.280144	0.625924	-3.654220	19060.915646
HLA B*1502	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.548843	0.894591	-3.654252	35386.907568
HLA A*0203	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.290352	0.635971	-3.654381	19514.268298
HLA A*2501	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.451903	0.797462	-3.654441	28307.587635
HLA B*3901	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.428234	0.773768	-3.654466	26806.131798
HLA A*3101	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.376506	0.722004	-3.654501	23796.086409
HLA A*0212	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.427285	0.772678	-3.654607	26747.608423
HLA A*0301	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.352592	0.697848	-3.654744	22521.249345
HLA B*1801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.300681	0.645932	-3.654749	19983.916565
HLA B*1503	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.405183	0.750403	-3.654780	25420.456844
HLA B*4002	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.609325	0.954333	-3.654992	40674.797931
HLA B*5401	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.559732	0.904590	-3.655143	36285.446760
HLA A*2402	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.554051	0.898882	-3.655169	35813.883778
HLA B*1509	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.478840	0.823629	-3.655210	30118.941575
HLA A*0203	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.451435	0.796188	-3.655248	28277.128992
HLA B*4402	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.427959	0.772678	-3.655281	26789.170037
HLA B*0702	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.446466	0.790996	-3.655471	27955.428415
HLA A*6802	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.386164	0.730675	-3.655489	24331.241543
HLA B*5101	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.487319	0.831818	-3.655501	30712.770704
HLA A*0212	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.448881	0.793337	-3.655544	28111.331902
HLA B*5701	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.388619	0.733042	-3.655578	24469.183731
HLA A*0216	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.447030	0.791452	-3.655578	27991.748573
HLA A*6802	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.281666	0.625924	-3.655742	19127.853007
HLA A*3002	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.378759	0.722962	-3.655797	23919.863301
HLA A*2402	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.563080	0.907250	-3.655830	36566.255609

HLA B*4001	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.346712	0.690866	-3.655846	22218.345608
HLA A*2501	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.430386	0.774481	-3.655905	26939.298148
HLA B*4001	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.411130	0.755176	-3.655953	25770.918515
HLA A*1101	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.388995	0.733042	-3.655954	24490.372992
HLA B*0803	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.449349	0.793337	-3.656012	28141.611957
HLA B*3801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.560621	0.904590	-3.656031	36359.724173
HLA B*4403	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.577516	0.921444	-3.656071	37802.082591
HLA A*6901	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.161192	0.505009	-3.656183	14494.114347
HLA B*5101	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.489344	0.833148	-3.656197	30856.328787
HLA B*5701	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.420758	0.764421	-3.656337	26348.632933
HLA B*0802	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.447462	0.790996	-3.656467	28019.625981
HLA B*0702	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.429174	0.772678	-3.656496	26864.201887
HLA B*5301	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.572789	0.916286	-3.656503	37392.849607
HLA B*0802	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.421644	0.765110	-3.656533	26402.426551
HLA B*5301	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.521708	0.865145	-3.656563	33243.627657
HLA B*1501	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.313927	0.657361	-3.656566	20602.835939
HLA B*2705	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.483123	0.826538	-3.656585	30417.451005
HLA B*1801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.310842	0.654207	-3.656635	20457.008727
HLA B*1502	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.550668	0.894030	-3.656638	35535.968932
HLA B*4002	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.521791	0.865145	-3.656645	33249.922805
HLA B*4002	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.630962	0.974301	-3.656661	42752.529119
HLA A*8001	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.438419	0.781690	-3.656729	27442.215221
HLA B*5401	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-3.775881	0.119114	-3.656766	5968.714994
HLA B*1517	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.421886	0.765110	-3.656775	26417.142574
HLA B*4801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.426963	0.770046	-3.656917	26727.791648
HLA B*5701	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.389294	0.732333	-3.656961	24507.205029
HLA A*0101	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.382997	0.725976	-3.657021	24154.450631
HLA A*3002	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.554474	0.897363	-3.657112	35848.775609
HLA A*2501	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.422245	0.765110	-3.657135	26439.017439
HLA A*3201	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.319596	0.662443	-3.657154	20873.549760
HLA B*3501	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.454071	0.796898	-3.657173	28449.290185
HLA A*2301	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.527223	0.869990	-3.657233	33668.413371
HLA B*7301	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.545713	0.888375	-3.657338	35132.827039
HLA B*5401	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.562625	0.905205	-3.657420	36527.898779
HLA B*1801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.486861	0.829345	-3.657516	30680.388014
HLA A*3002	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.162536	0.505009	-3.657527	14539.035221
HLA A*8001	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.440926	0.783381	-3.657545	27601.079408
HLA B*0803	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.474359	0.816673	-3.657686	29809.812071
HLA B*3501	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.481335	0.823629	-3.657706	30292.482042
HLA A*2902	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.457701	0.799991	-3.657710	28688.073801
HLA A*3301	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.562643	0.904921	-3.657722	36529.479708
HLA A*2602	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.574027	0.916286	-3.657741	37499.609168
HLA B*4002	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.562676	0.904921	-3.657755	36532.246499
HLA A*2301	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.531012	0.873256	-3.657756	33963.494626
HLA B*5101	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.439491	0.781690	-3.657800	27509.996251
HLA A*2603	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.556859	0.898882	-3.657977	36046.164017
HLA A*6802	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.428051	0.770046	-3.658005	26794.822765
HLA A*2902	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.444946	0.786863	-3.658083	27857.749920
HLA A*2603	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.116660	0.458556	-3.658104	13081.560211
HLA B*7301	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.562719	0.904590	-3.658129	36535.804109
HLA A*3201	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.061334	0.403047	-3.658287	11516.854275
HLA B*1509	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.442044	0.783751	-3.658294	27672.246740
HLA B*5301	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.353704	0.695361	-3.658342	22578.952260
HLA A*0101	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.356237	0.697848	-3.658388	22711.014269
HLA B*4403	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.502612	0.844164	-3.658448	31813.525208
HLA A*2902	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.349061	0.690572	-3.658489	22338.870112
HLA A*3101	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.080473	0.421976	-3.658497	12035.739420
HLA B*4002	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.607747	0.949124	-3.658623	40527.195383
HLA B*1503	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.457415	0.798791	-3.658624	28669.145734
HLA B*7301	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-3.928052	0.269402	-3.658651	8473.294214
HLA A*2501	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.449650	0.790996	-3.658654	28161.105810
HLA A*2501	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.445519	0.786863	-3.658656	27894.546791
HLA B*1517	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.488207	0.829510	-3.658698	30775.640680
HLA B*5301	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.577067	0.918327	-3.658740	37763.042295
HLA B*1801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.478508	0.819348	-3.659160	30095.975776

HLA A*6801	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.551357	0.892112	-3.659244	35592.341574
HLA A*6801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.534332	0.875034	-3.659298	34224.112301
HLA A*3301	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.443290	0.783751	-3.659539	27751.703603
HLA B*3501	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.088658	0.429083	-3.659575	12264.741022
HLA B*1509	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.489260	0.829510	-3.659750	30850.319917
HLA A*6901	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.349080	0.689311	-3.659769	22339.836940
HLA A*1101	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.483431	0.823629	-3.659801	30439.015356
HLA B*0803	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.459863	0.799991	-3.659872	28831.213070
HLA B*4801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.415079	0.755176	-3.659903	26006.348739
HLA A*2402	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.574858	0.914880	-3.659979	37571.493509
HLA B*5301	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.578176	0.918162	-3.660014	37859.592219
HLA B*4001	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.355424	0.695361	-3.660062	22668.543063
HLA A*3002	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.329751	0.669685	-3.660066	21367.355996
HLA B*2705	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.441774	0.781690	-3.660084	27655.036158
HLA A*0219	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.350657	0.690572	-3.660085	22421.078710
HLA A*0216	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.453432	0.793337	-3.660095	28407.458128
HLA B*0803	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.489443	0.829345	-3.660098	30863.340615
HLA A*0212	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.424480	0.764363	-3.660117	26575.391525
HLA B*4801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.414668	0.754459	-3.660209	25981.739384
HLA B*1509	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.314442	0.654207	-3.660234	20627.259938
HLA B*4001	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.393389	0.733042	-3.660347	24739.387123
HLA A*0201	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.372333	0.711889	-3.660444	23568.549323
HLA B*1509	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.433201	0.772678	-3.660523	27114.460014
HLA B*4801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.424945	0.764421	-3.660524	26603.873221
HLA A*1101	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.424950	0.764363	-3.660587	26604.161070
HLA A*6801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.260314	0.599665	-3.660649	18210.174438
HLA A*0219	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.458145	0.797462	-3.660683	28717.421470
HLA A*8001	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.415895	0.755176	-3.660718	26055.214529
HLA B*0802	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.458301	0.797462	-3.660839	28727.676933
HLA A*3001	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.298254	0.637402	-3.660851	19872.549608
HLA A*3002	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.508763	0.847787	-3.660976	32267.308926
HLA B*4402	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-3.978449	0.317460	-3.660988	9515.875246
HLA B*5301	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.605463	0.944464	-3.660999	40314.646008
HLA A*3002	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.425384	0.764363	-3.661021	26630.800628
HLA B*2705	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.469129	0.807959	-3.661171	29452.982850
HLA B*5401	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.415648	0.754459	-3.661189	26040.418370
HLA A*2902	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.431385	0.770046	-3.661339	27001.308320
HLA A*1101	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.487885	0.826538	-3.661347	30752.839616
HLA B*0801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.370698	0.709300	-3.661397	23479.973929
HLA B*1502	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.566097	0.904590	-3.661508	36821.139931
HLA A*6801	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.610841	0.949124	-3.661717	40816.975608
HLA B*1502	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.577379	0.915512	-3.661868	37790.223157
HLA A*2603	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.583359	0.921444	-3.661915	38314.123592
HLA B*1801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.493747	0.831818	-3.661930	31170.745435
HLA B*5301	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.172427	0.510481	-3.661946	14873.970661
HLA B*3801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.535291	0.873256	-3.662035	34299.736381
HLA A*2403	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.416527	0.754459	-3.662068	26093.159248
HLA B*0702	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.459565	0.797462	-3.662103	28811.411218
HLA B*1501	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.183930	0.521798	-3.662132	15273.198603
HLA A*3201	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-3.997226	0.334871	-3.662354	9936.325819
HLA A*3201	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.515863	0.853416	-3.662447	32799.172786
HLA B*1502	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.436523	0.773768	-3.662755	27322.669676
HLA A*3101	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.385793	0.722962	-3.662832	24310.452997
HLA A*0250	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.577753	0.914880	-3.662873	37822.743248
HLA B*4001	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.409626	0.746693	-3.662933	25681.845405
HLA A*0211	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.158706	0.495678	-3.663028	14411.391888
HLA B*0803	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.492577	0.829510	-3.663068	31086.880579
HLA B*4601	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.375970	0.712902	-3.663068	23766.753108
HLA A*2602	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.624752	0.961636	-3.663116	42145.588511
HLA A*2603	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.618855	0.955683	-3.663171	41577.169045
HLA A*0206	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.459402	0.796188	-3.663215	28800.658433
HLA B*5101	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.437766	0.774481	-3.663285	27400.974544
HLA B*5801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.352637	0.689311	-3.663326	22523.564376
HLA B*3901	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.496562	0.833148	-3.663414	31373.420571
HLA B*4403	1:52-60	9	FYLRFRREA	1.095023	-0.126207	-4.632332	0.968816	-3.663516	42887.581980

HLA A*0250	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.561652	0.898050	-3.663602	36446.179007
HLA B*4501	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.617969	0.954333	-3.663636	41492.457651
HLA A*3201	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.552167	0.888375	-3.663792	35658.833571
HLA A*0101	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.287171	0.623337	-3.663834	19371.848728
HLA A*0203	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.373155	0.709300	-3.663855	23613.217732
HLA B*4001	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.389848	0.725976	-3.663872	24538.514190
HLA A*3301	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.557832	0.893801	-3.664031	36126.986873
HLA A*0219	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.397118	0.733042	-3.664076	24952.701378
HLA A*0201	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.387055	0.722962	-3.664093	24381.180234
HLA A*0250	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.487772	0.823629	-3.664143	30744.854919
HLA B*2705	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.243036	0.578823	-3.664213	17499.917177
HLA A*0202	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.494995	0.830662	-3.664333	31260.416848
HLA B*0802	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.438828	0.774481	-3.664347	27468.059308
HLA A*3101	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.170947	0.506563	-3.664384	14823.363036
HLA B*3801	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.558436	0.894030	-3.664405	36177.250657
HLA B*3801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.512224	0.847787	-3.664437	32525.466817
HLA A*6802	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.438934	0.774481	-3.664452	27474.747084
HLA A*3002	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.287794	0.623337	-3.664457	19399.640526
HLA B*5301	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.580782	0.916314	-3.664467	38087.416120
HLA B*3901	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.418951	0.754459	-3.664492	26239.244921
HLA A*0202	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.579381	0.914880	-3.664502	37964.808863
HLA B*0801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.359876	0.695361	-3.664514	22902.130363
HLA B*4601	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.390506	0.725976	-3.664530	24575.712536
HLA B*0803	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.472491	0.807959	-3.664533	29681.879494
HLA B*0803	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.438422	0.773768	-3.664653	27442.363681
HLA A*2902	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.379626	0.714935	-3.664690	23967.660999
HLA B*4402	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.144449	0.479739	-3.664710	13945.986906
HLA B*2705	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.397764	0.733042	-3.664722	24989.851626
HLA A*3101	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.397804	0.733042	-3.664762	24992.150002
HLA A*2602	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.572100	0.907250	-3.664850	37333.625244
HLA B*4403	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.619334	0.954333	-3.665001	41623.079660
HLA A*2601	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.379955	0.714935	-3.665019	23985.820609
HLA B*0802	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.488663	0.823629	-3.665034	30807.957239
HLA B*5701	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.379983	0.714935	-3.665048	23987.377788
HLA A*2601	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.374356	0.709300	-3.665056	23678.585682
HLA B*1501	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.395797	0.730675	-3.665122	24876.951452
HLA A*8001	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.435175	0.770046	-3.665129	27237.956833
HLA B*5401	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.463920	0.798696	-3.665224	29101.841850
HLA B*4501	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.650702	0.985326	-3.665376	44740.639197
HLA A*0219	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.448816	0.783381	-3.665434	28107.074007
HLA A*0301	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.360858	0.695361	-3.665497	22953.978322
HLA A*2603	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.580387	0.914880	-3.665507	38052.815665
HLA A*0212	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.388469	0.722962	-3.665508	24460.713161
HLA A*2902	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.447199	0.781429	-3.665770	28002.653819
HLA B*0802	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.439580	0.773768	-3.665811	27515.652222
HLA B*1501	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.328341	0.662443	-3.665898	21298.111422
HLA B*4501	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.608162	0.942253	-3.665909	40566.020800
HLA A*6801	1:14-22	9	GEILGFGGM	0.948298	0.046073	-4.660295	0.994371	-3.665924	45739.891672
HLA A*3201	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.496597	0.830662	-3.665935	31375.966575
HLA A*2902	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.461916	0.795837	-3.666080	28967.856843
HLA A*0101	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.396756	0.730675	-3.666081	24931.921368
HLA A*3101	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.378054	0.711889	-3.666165	23881.073644
HLA B*0802	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.474157	0.807959	-3.666199	29795.946268
HLA B*5301	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.558327	0.892112	-3.666215	36168.248891
HLA A*2402	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.539515	0.873256	-3.666259	34634.997148
HLA B*0803	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.496971	0.830662	-3.666309	31402.966926
HLA A*0206	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.483062	0.816673	-3.666389	30413.172875
HLA A*0101	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.389397	0.722962	-3.666436	24513.039299
HLA B*3901	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.399338	0.732827	-3.666511	25080.594841
HLA A*0216	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.375885	0.709300	-3.666585	23762.124841
HLA B*4402	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.129121	0.462438	-3.666683	13462.360403
HLA A*2402	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.431089	0.764363	-3.666726	26982.909257
HLA B*3501	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.462957	0.796188	-3.666770	29037.363911
HLA B*1801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.440703	0.773768	-3.666935	27586.897768
HLA B*5101	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.496282	0.829345	-3.666937	31353.229591

HLA A*1101	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.422187	0.755176	-3.667010	26435.441877
HLA B*5701	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.390017	0.722962	-3.667056	24548.074098
HLA B*3501	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.290395	0.623337	-3.667058	19516.168651
HLA B*7301	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.572051	0.904921	-3.667130	37329.384099
HLA A*3001	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.280672	0.613540	-3.667133	19084.131197
HLA B*0802	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.458615	0.791452	-3.667164	28748.509899
HLA A*2602	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.520675	0.853416	-3.667259	33164.590253
HLA B*5401	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.514942	0.847664	-3.667278	32729.690051
HLA B*5301	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.582353	0.914880	-3.667474	38225.512449
HLA B*0802	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.440188	0.772678	-3.667510	27554.233111
HLA A*2601	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.052852	0.385288	-3.667564	11294.115657
HLA B*1502	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.589374	0.921765	-3.667609	38848.439419
HLA B*3901	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.321828	0.654207	-3.667621	20981.103314
HLA A*6801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.507501	0.839877	-3.667624	32173.704860
HLA B*1801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.464651	0.796898	-3.667753	29150.846199
HLA A*0212	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.246673	0.578823	-3.667850	17647.085752
HLA A*2403	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.365252	0.697387	-3.667864	23187.370642
HLA A*3101	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.423044	0.755176	-3.667868	26487.693123
HLA A*0206	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.330329	0.662443	-3.667886	21395.811303
HLA A*2403	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.433076	0.765110	-3.667966	27106.686759
HLA B*0702	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.380871	0.712902	-3.667969	24036.480679
HLA B*1502	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.537967	0.869990	-3.667977	34511.739178
HLA B*5401	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.541517	0.873492	-3.668025	34795.006137
HLA A*6802	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.423244	0.755176	-3.668067	26499.876040
HLA A*2501	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.464343	0.796188	-3.668156	29130.194445
HLA B*1509	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.432658	0.764421	-3.668238	27080.596660
HLA A*2602	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.588359	0.920120	-3.668238	38757.753825
HLA B*1509	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.465739	0.797462	-3.668277	29223.954138
HLA B*4501	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.423580	0.755176	-3.668403	26520.384651
HLA A*6801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.358990	0.690572	-3.668418	22855.468423
HLA B*4501	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.586596	0.918162	-3.668435	38600.816058
HLA B*0802	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.485148	0.816673	-3.668475	30559.628701
HLA A*2501	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.501686	0.833148	-3.668539	31745.787014
HLA A*2601	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.391570	0.722962	-3.668609	24636.013597
HLA B*3801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.498143	0.829510	-3.668634	31487.854852
HLA B*4501	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.652699	0.984065	-3.668634	44946.848565
HLA A*6802	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.306042	0.637402	-3.668640	20232.154490
HLA A*0301	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.359223	0.690572	-3.668651	22867.712611
HLA A*3101	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.338345	0.669685	-3.668661	21794.414276
HLA A*2601	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.190607	0.521798	-3.668809	15509.837065
HLA A*0301	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.366241	0.697387	-3.668853	23240.241532
HLA A*2501	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.450284	0.781429	-3.668855	28202.269950
HLA B*5801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.351925	0.682948	-3.668977	22486.674073
HLA B*1509	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.439096	0.770046	-3.669050	27485.004837
HLA A*2603	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.456003	0.786863	-3.669139	28576.083867
HLA B*3501	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.395132	0.725976	-3.669156	24838.894014
HLA B*1502	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.452986	0.783751	-3.669235	28378.273702
HLA B*7301	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.120315	0.451064	-3.669252	13192.142782
HLA A*1101	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.381169	0.711889	-3.669280	24053.000760
HLA B*5101	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.469435	0.799991	-3.669443	29473.703994
HLA B*1501	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-3.707722	0.038251	-3.669471	5101.786520
HLA A*3001	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-3.887994	0.218420	-3.669574	7726.691401
HLA A*2501	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.465506	0.795837	-3.669670	29208.306592
HLA A*2403	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.439735	0.770046	-3.669689	27525.478514
HLA A*2501	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.493350	0.823629	-3.669721	31142.259942
HLA B*5101	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.493477	0.823629	-3.669848	31151.358984
HLA A*6901	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.241128	0.571232	-3.669896	17423.211616
HLA B*0702	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.212406	0.542449	-3.669956	16308.189801
HLA A*0212	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.365367	0.695361	-3.670005	23193.518071
HLA A*0219	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.463380	0.793337	-3.670043	29065.653688
HLA A*3101	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.332497	0.662443	-3.670055	21502.914778
HLA A*0301	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.332692	0.662443	-3.670250	21512.572202
HLA B*1517	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.453634	0.783381	-3.670253	28420.677786
HLA B*5401	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.514524	0.844164	-3.670360	32698.187830
HLA A*0101	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.361168	0.690572	-3.670596	22970.375735

HLA B*0802	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.466787	0.796188	-3.670599	29294.551138
HLA A*2603	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.590882	0.920120	-3.670762	38983.600412
HLA B*0803	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.452478	0.781690	-3.670788	28345.132033
HLA A*6802	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.882266	0.211378	-3.670887	7625.450790
HLA A*0101	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.353840	0.682948	-3.670892	22586.038051
HLA A*1101	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.445479	0.774481	-3.670998	27891.981500
HLA A*2902	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.346277	0.675193	-3.671084	22196.119956
HLA B*5801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.351206	0.680074	-3.671132	22449.479841
HLA B*4403	1:179-187	9	TAQYLSPEQ	1.016496	-0.060813	-4.626942	0.955683	-3.671258	42358.623884
HLA B*5101	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.488036	0.816673	-3.671363	30763.489105
HLA A*2402	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.468328	0.796898	-3.671430	29398.698892
HLA A*0211	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.462903	0.791452	-3.671451	29033.751091
HLA A*2501	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.488181	0.816673	-3.671508	30773.809313
HLA A*3201	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.565571	0.894030	-3.671541	36776.546540
HLA B*5801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.362613	0.690866	-3.671747	23046.927331
HLA B*3501	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.362876	0.690866	-3.672010	23060.895871
HLA B*3901	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.468915	0.796898	-3.672017	29438.486718
HLA A*2603	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.579292	0.907250	-3.672042	37957.005020
HLA B*1801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.463039	0.790996	-3.672044	29042.862544
HLA A*0206	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.468960	0.796898	-3.672062	29441.512793
HLA A*2402	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.511996	0.839877	-3.672119	32508.403255
HLA A*0203	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.329488	0.657361	-3.672126	21354.413274
HLA B*1517	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.223157	0.550986	-3.672171	16716.948351
HLA B*4001	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.347391	0.675193	-3.672198	22253.110226
HLA B*3901	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.501752	0.829510	-3.672242	31750.596131
HLA A*0101	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.381686	0.709300	-3.672386	24081.645097
HLA A*1101	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.469938	0.797462	-3.672476	29507.845940
HLA A*2301	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.465908	0.793337	-3.672571	29235.339437
HLA B*0702	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.403381	0.730675	-3.672706	25315.196117
HLA B*1517	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.496393	0.823629	-3.672763	31361.202627
HLA B*1502	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.504585	0.831818	-3.672768	31958.424614
HLA B*2705	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.471559	0.798696	-3.672863	29618.199358
HLA A*0101	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.348067	0.675193	-3.672874	22287.808666
HLA B*1509	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.446720	0.773768	-3.672952	27971.766651
HLA B*4402	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.446776	0.773768	-3.673008	27975.398666
HLA A*0219	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.385029	0.711889	-3.673140	24267.747572
HLA B*4601	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.396126	0.722962	-3.673165	24895.800006
HLA A*0301	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.356319	0.682948	-3.673371	22715.314919
HLA B*4601	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.385403	0.711889	-3.673514	24288.630999
HLA B*4001	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.396495	0.722962	-3.673533	24916.954301
HLA B*3801	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.562002	0.888375	-3.673627	36475.569149
HLA B*3901	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.443922	0.770046	-3.673876	27792.118953
HLA A*0301	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.363210	0.689311	-3.673899	23078.618155
HLA B*4402	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.407007	0.733042	-3.673965	25527.398119
HLA A*0201	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.386902	0.712902	-3.674000	24372.608275
HLA B*1517	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.471462	0.797462	-3.674000	29611.630609
HLA B*0801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.387184	0.712902	-3.674282	24388.435785
HLA A*2301	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.518464	0.844164	-3.674300	32996.188091
HLA B*0801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.406675	0.732333	-3.674342	25507.933388
HLA A*2603	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.168447	0.494046	-3.674401	14738.283049
HLA B*4403	1:581-589	9	LGWTGMLDK	0.753795	0.230270	-4.658479	0.984065	-3.674414	45549.013955
HLA A*3001	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.274141	0.599665	-3.674476	18799.263067
HLA B*7301	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.590821	0.916286	-3.674535	38978.117477
HLA A*8001	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.439011	0.764421	-3.674591	27479.652488
HLA B*3901	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.498251	0.823629	-3.674622	31495.691734
HLA A*6801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.407516	0.732827	-3.674689	25557.383501
HLA A*2501	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.448461	0.773768	-3.674693	28084.122903
HLA B*4501	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.568773	0.894030	-3.674743	37048.727238
HLA A*3002	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.458195	0.783381	-3.674814	28720.684175
HLA B*4001	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.389799	0.714935	-3.674864	24535.726585
HLA A*2301	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.471815	0.796898	-3.674916	29635.669707
HLA A*3001	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.291480	0.616515	-3.674965	19565.007762
HLA B*0801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.425434	0.750403	-3.675031	26633.826263
HLA A*3301	1:360-368	9	VQVPDVRGQ	0.963310	-0.014186	-4.624165	0.949124	-3.675041	42088.626299
HLA B*5801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.344743	0.669685	-3.675058	22117.847001

HLA A*2301	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.537964	0.862842	-3.675123	34511.552474
HLA B*1502	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.568931	0.893801	-3.675130	37062.158449
HLA B*3901	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.471326	0.796188	-3.675138	29602.340719
HLA A*8001	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.390154	0.714935	-3.675218	24555.777843
HLA B*1503	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.133350	0.458095	-3.675256	13594.094542
HLA A*0216	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.458723	0.783381	-3.675342	28755.664997
HLA B*4501	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.649711	0.974301	-3.675410	44638.614021
HLA B*5801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.329631	0.654207	-3.675424	21361.461462
HLA B*0803	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.499069	0.823629	-3.675440	31555.042678
HLA B*5301	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.563825	0.888375	-3.675450	36629.018157
HLA B*1502	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.580746	0.905205	-3.675541	38084.325515
HLA A*2902	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.450023	0.774481	-3.675542	28185.339636
HLA B*4403	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.660904	0.985326	-3.675577	45804.025558
HLA A*2603	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.637218	0.961636	-3.675583	43372.902906
HLA B*3901	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.475579	0.799991	-3.675587	29893.627659
HLA A*2403	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.387485	0.711889	-3.675596	24405.329791
HLA B*3901	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.495035	0.819348	-3.675687	31263.291942
HLA A*2501	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.457424	0.781690	-3.675734	28669.766128
HLA B*0801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.373592	0.697848	-3.675744	23636.990240
HLA A*2601	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.406436	0.730675	-3.675761	25493.861771
HLA B*3801	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.529177	0.853416	-3.675762	33820.297395
HLA B*1503	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.228190	0.552387	-3.675803	16911.790792
HLA B*0702	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.440200	0.764363	-3.675837	27554.978448
HLA A*0301	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.366729	0.690866	-3.675863	23266.407494
HLA A*2403	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.388812	0.712902	-3.675910	24480.040936
HLA A*0203	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.254753	0.578823	-3.675930	17978.476013
HLA B*5401	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.549115	0.873123	-3.675993	35409.121490
HLA A*0211	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.366877	0.690866	-3.676011	23274.338573
HLA A*0202	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.476023	0.799991	-3.676031	29924.208599
HLA B*5801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.351249	0.675193	-3.676056	22451.666033
HLA A*6801	1:472-480	9	PPANQTSAI	1.026064	-0.040738	-4.661397	0.985326	-3.676071	45856.092016
HLA B*0802	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.476100	0.799991	-3.676109	29929.551335
HLA A*0201	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.367070	0.690866	-3.676204	23284.665614
HLA B*4002	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.630833	0.954621	-3.676211	42739.810257
HLA B*5801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.268739	0.592477	-3.676263	18566.898326
HLA B*0802	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.472273	0.795837	-3.676436	29666.949712
HLA B*4501	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.605632	0.929186	-3.676446	40330.352106
HLA B*0702	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.391406	0.714935	-3.676471	24626.685896
HLA B*4402	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.389378	0.712902	-3.676476	24511.978420
HLA A*6801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.095007	0.418508	-3.676499	12445.337848
HLA A*0216	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.440926	0.764421	-3.676505	27601.079408
HLA B*1517	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.346324	0.669685	-3.676640	22198.521657
HLA B*3501	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.441758	0.765110	-3.676647	27653.988903
HLA B*4403	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.638008	0.961256	-3.676752	43451.814516
HLA A*0101	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.374147	0.697387	-3.676759	23667.187658
HLA B*4403	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.651191	0.974301	-3.676890	44791.012248
HLA A*2402	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.585006	0.908065	-3.676941	38459.699341
HLA A*3101	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.386261	0.709300	-3.676960	24336.638944
HLA B*4601	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.374389	0.697387	-3.677001	23680.379130
HLA A*6801	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.592557	0.915512	-3.677045	39134.260322
HLA B*2705	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.392193	0.714935	-3.677258	24671.357623
HLA A*2601	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.375124	0.697848	-3.677276	23720.510972
HLA A*3301	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.638595	0.961256	-3.677339	43510.621650
HLA B*0803	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.509223	0.831818	-3.677406	32301.541334
HLA B*3801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.501063	0.823629	-3.677434	31700.308206
HLA A*0250	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.277106	0.599665	-3.677441	18928.050034
HLA A*3002	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.496849	0.819348	-3.677501	31394.134067
HLA B*4403	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.619802	0.942253	-3.677549	41667.913863
HLA A*1101	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.424308	0.746693	-3.677615	26564.898393
HLA A*0216	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.375479	0.697848	-3.677630	23739.896015
HLA A*2402	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.551218	0.873492	-3.677726	35580.982901
HLA B*5301	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.551234	0.873492	-3.677743	35582.330350
HLA B*1801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.510894	0.833148	-3.677746	32426.026248
HLA A*2301	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.517656	0.839877	-3.677779	32934.839227
HLA A*2602	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.622114	0.944277	-3.677836	41890.317395

HLA B*3801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.508521	0.830662	-3.677859	32249.333990
HLA B*0802	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.461348	0.783381	-3.677967	28929.957137
HLA B*2705	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.452483	0.774481	-3.678002	28345.438723
HLA B*4002	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.607239	0.929186	-3.678053	40479.865553
HLA A*2402	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.572100	0.894030	-3.678070	37333.625244
HLA A*3201	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.575439	0.897363	-3.678076	37621.731697
HLA A*3201	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.511272	0.833148	-3.678124	32454.281365
HLA A*2301	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.531546	0.853416	-3.678130	34005.228940
HLA B*4001	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.368726	0.690572	-3.678155	23373.642242
HLA A*6801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.252450	0.574191	-3.678259	17883.411905
HLA A*0203	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.442622	0.764363	-3.678260	27709.098387
HLA A*0219	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.376256	0.697848	-3.678408	23782.444497
HLA B*0702	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.051912	0.373369	-3.678543	11269.702116
HLA A*2602	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.465699	0.786863	-3.678836	29221.266590
HLA A*0301	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.348629	0.669685	-3.678944	22316.644627
HLA B*4402	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.425807	0.746693	-3.679114	26656.745801
HLA B*4601	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.388424	0.709300	-3.679124	24458.199025
HLA A*2902	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.405146	0.725976	-3.679170	25418.256589
HLA A*2301	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.539355	0.860149	-3.679207	34622.258229
HLA A*1101	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.475156	0.795837	-3.679319	29864.532009
HLA B*4002	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.600764	0.921444	-3.679320	39880.801759
HLA B*5301	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.584552	0.905205	-3.679347	38419.564195
HLA A*3001	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.258235	0.578823	-3.679412	18123.197020
HLA A*3201	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.476314	0.796898	-3.679416	29944.289278
HLA B*4002	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.595705	0.916286	-3.679420	39418.985190
HLA A*3301	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.444587	0.765110	-3.679476	27834.701237
HLA B*1503	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.349216	0.669685	-3.679532	22346.847690
HLA B*4501	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.625889	0.946270	-3.679619	42256.086545
HLA B*0803	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.471072	0.791452	-3.679621	29585.050070
HLA A*0202	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.496496	0.816673	-3.679823	31368.668583
HLA B*5401	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.540098	0.860149	-3.679949	34681.496465
HLA B*1502	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.527805	0.847787	-3.680018	33713.614998
HLA A*0212	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.393091	0.712902	-3.680188	24722.395618
HLA A*2501	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.378040	0.697848	-3.680191	23880.298493
HLA B*5101	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.510861	0.830662	-3.680199	32423.570444
HLA A*2402	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.550327	0.869990	-3.680338	35508.104243
HLA B*3501	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.427031	0.746693	-3.680338	26731.985215
HLA A*2501	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.413204	0.732827	-3.680377	25894.318947
HLA B*5101	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.479317	0.798791	-3.680525	30152.036591
HLA A*0250	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.533982	0.853416	-3.680566	34196.536267
HLA B*5701	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.393476	0.712902	-3.680574	24744.339600
HLA B*1503	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.476439	0.795837	-3.680602	29952.876259
HLA A*2902	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.403607	0.722962	-3.680645	25328.346962
HLA A*3002	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.504350	0.823629	-3.680721	31941.140136
HLA A*2601	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.393704	0.712902	-3.680802	24757.327828
HLA B*4601	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.395755	0.714935	-3.680820	24874.529102
HLA B*5301	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.588913	0.908065	-3.680848	38807.268763
HLA A*0206	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.089951	0.409024	-3.680926	12301.288356
HLA A*3101	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.371811	0.690866	-3.680945	23540.260594
HLA B*0801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.221414	0.540402	-3.681012	16649.978721
HLA B*5101	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.451076	0.770046	-3.681030	28253.733327
HLA A*2902	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.232024	0.550986	-3.681038	17061.765045
HLA A*2601	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.392957	0.711889	-3.681068	24714.773304
HLA A*0211	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.462960	0.781690	-3.681269	29037.521000
HLA B*5101	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.428004	0.746693	-3.681311	26791.923781
HLA B*4403	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.573437	0.892112	-3.681325	37448.723673
HLA B*4001	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.412030	0.730675	-3.681355	25824.370894
HLA A*2501	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.472931	0.791452	-3.681479	29711.922340
HLA A*6802	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.445844	0.764363	-3.681481	27915.379651
HLA B*0801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.436772	0.755176	-3.681596	27338.342307
HLA B*4402	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.436119	0.754459	-3.681660	27297.257732
HLA A*0203	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.103756	0.421976	-3.681780	12698.609635
HLA B*4002	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.643419	0.961636	-3.681783	43996.566050
HLA A*2602	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.407963	0.725976	-3.681987	25583.666903
HLA A*6802	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.325202	0.643088	-3.682114	21144.731890

HLA A*2601	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.372739	0.690572	-3.682168	23590.617708
HLA B*4402	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.339532	0.657361	-3.682170	21854.037894
HLA B*1502	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.478078	0.795837	-3.682242	30066.195211
HLA B*0702	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.452359	0.770046	-3.682313	28337.312567
HLA A*0212	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.357625	0.675193	-3.682432	22783.743139
HLA A*0219	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.446812	0.764363	-3.682449	27977.668916
HLA B*1509	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.511819	0.829345	-3.682474	32495.215916
HLA A*2402	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.579919	0.897363	-3.682557	38011.871267
HLA A*6901	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.114879	0.432298	-3.682581	13028.026547
HLA B*4002	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.643508	0.960920	-3.682588	44005.611608
HLA A*3201	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.552609	0.869990	-3.682619	35695.119163
HLA B*1517	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.482719	0.799991	-3.682727	30389.160703
HLA A*2301	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.512083	0.829345	-3.682737	32514.910980
HLA A*3101	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.378129	0.695361	-3.682768	23885.208209
HLA B*1502	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.587738	0.904921	-3.682817	38702.439095
HLA B*4001	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.380328	0.697387	-3.682941	24006.461426
HLA B*1509	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.473950	0.790996	-3.682955	29781.764680
HLA B*5101	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.415852	0.732827	-3.683025	26052.677448
HLA A*0202	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.337267	0.654207	-3.683060	21740.362850
HLA A*6802	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.358266	0.675193	-3.683074	22817.417303
HLA A*6901	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.282752	0.599665	-3.683087	19175.720360
HLA A*0101	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.363360	0.680074	-3.683286	23086.610116
HLA A*8001	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.416137	0.732827	-3.683310	26069.737024
HLA A*6801	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.645012	0.961636	-3.683376	44158.237584
HLA A*0211	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.510013	0.826538	-3.683474	32360.309977
HLA A*2603	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.448642	0.765110	-3.683531	28095.824104
HLA A*3101	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.363715	0.680074	-3.683641	23105.477117
HLA A*3301	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.629919	0.946270	-3.683649	42649.961172
HLA B*0702	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.430410	0.746693	-3.683717	26940.755574
HLA B*5301	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.416839	0.733042	-3.683797	26111.940430
HLA A*2501	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.484025	0.799991	-3.684034	30480.705820
HLA A*2601	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.406088	0.722004	-3.684083	25473.457934
HLA B*0803	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.456773	0.772678	-3.684095	28626.835532
HLA A*6802	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.341489	0.657361	-3.684127	21952.743993
HLA A*0250	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.456830	0.772678	-3.684152	28630.552605
HLA B*4601	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.338362	0.654207	-3.684155	21795.239629
HLA B*1502	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.547083	0.862842	-3.684241	35243.809685
HLA A*2402	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.589547	0.905205	-3.684342	38863.994798
HLA B*1509	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.481370	0.796898	-3.684472	30294.940326
HLA B*4801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.417586	0.733042	-3.684544	26156.900632
HLA A*0211	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.508192	0.823629	-3.684563	32224.918092
HLA B*1801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.416628	0.732039	-3.684589	26099.229881
HLA A*2501	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.439831	0.755176	-3.684655	27531.584492
HLA B*0802	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.466094	0.781429	-3.684665	29247.836743
HLA A*0202	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-3.857239	0.172544	-3.684695	7198.446951
HLA B*0802	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.483510	0.798791	-3.684719	30444.614708
HLA B*4402	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.406767	0.722004	-3.684762	25513.315764
HLA A*0202	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.557973	0.873123	-3.684850	36138.715356
HLA B*1517	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.483562	0.798696	-3.684866	30448.238368
HLA A*2602	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.483788	0.798791	-3.684997	30464.055748
HLA A*3002	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.180768	0.495678	-3.685090	15162.387524
HLA A*8001	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.435511	0.750403	-3.685107	27259.036654
HLA A*0201	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.278509	0.593391	-3.685117	18989.280855
HLA A*0212	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.397007	0.711889	-3.685118	24946.357591
HLA B*7301	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.603353	0.918162	-3.685191	40119.269177
HLA A*2301	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.532859	0.847664	-3.685195	34108.220758
HLA A*2403	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.408191	0.722962	-3.685229	25597.095692
HLA B*1517	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.501914	0.816673	-3.685241	31762.450281
HLA A*0201	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.308584	0.623337	-3.685247	20350.930697
HLA A*3001	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.211142	0.525884	-3.685258	16260.793490
HLA B*5401	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.440447	0.755176	-3.685270	27570.635179
HLA B*0802	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.469028	0.783751	-3.685277	29446.132140
HLA B*4001	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.397181	0.711889	-3.685292	24956.346410
HLA A*3301	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.594411	0.909118	-3.685293	39301.658104
HLA B*4403	1:602-610	9	RVVYQNPPA	0.935310	0.029991	-4.650700	0.965301	-3.685399	44740.397156

HLA B*4403	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.594531	0.909118	-3.685412	39312.503099
HLA B*3501	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.374739	0.689311	-3.685428	23699.474951
HLA B*1503	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.439897	0.754459	-3.685438	27535.755207
HLA A*3301	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.525409	0.839877	-3.685532	33528.092675
HLA A*0212	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.376116	0.690572	-3.685544	23774.726126
HLA B*3501	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.460086	0.774481	-3.685605	28846.034377
HLA A*0203	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.277705	0.592081	-3.685624	18954.179709
HLA A*2403	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.400614	0.714935	-3.685678	25154.379159
HLA B*4001	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.383554	0.697848	-3.685706	24185.439970
HLA B*2705	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.450141	0.764363	-3.685778	28192.964645
HLA A*2403	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.381176	0.695361	-3.685815	24053.391135
HLA B*5701	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.416548	0.730675	-3.685873	26094.429729
HLA A*3201	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.578011	0.892112	-3.685899	37845.257799
HLA A*2301	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.467341	0.781429	-3.685912	29331.976368
HLA A*0212	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.383462	0.697387	-3.686075	24180.337727
HLA A*3201	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.591293	0.905205	-3.686088	39020.524856
HLA A*2301	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.505443	0.819348	-3.686095	32021.592369
HLA B*5101	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.441300	0.755176	-3.686123	27624.831308
HLA A*2603	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.604469	0.918327	-3.686142	40222.496131
HLA B*3901	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.483743	0.797462	-3.686281	30460.924573
HLA B*3901	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.469707	0.783381	-3.686326	29492.205938
HLA A*0212	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.377412	0.690866	-3.686546	23845.829725
HLA B*4402	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.401495	0.714935	-3.686559	25205.461859
HLA A*1101	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.486586	0.799991	-3.686595	30660.974792
HLA A*0301	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.366725	0.680074	-3.686650	23266.155758
HLA A*0216	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.409638	0.722962	-3.686676	25682.540094
HLA B*1517	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.399601	0.712902	-3.686699	25095.795969
HLA A*2602	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.592052	0.905205	-3.686847	39088.768701
HLA B*5101	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.477858	0.790996	-3.686862	30050.909549
HLA B*1517	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.482712	0.795837	-3.686875	30388.667501
HLA B*4002	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.642994	0.956046	-3.686948	43953.506141
HLA B*0802	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.433932	0.746693	-3.687239	27160.117828
HLA A*0216	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.419783	0.732333	-3.687450	26289.543867
HLA B*0801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.378080	0.690572	-3.687508	23882.494820
HLA A*3201	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.609004	0.921444	-3.687559	40644.662778
HLA A*2501	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.471342	0.783751	-3.687592	29603.461758
HLA B*1501	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.413726	0.725976	-3.687750	25925.436587
HLA B*4002	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.517120	0.829345	-3.687775	32894.240637
HLA A*0206	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.511413	0.823629	-3.687784	32464.817519
HLA A*0216	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.061353	0.373369	-3.687983	11517.352725
HLA A*0216	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.788653	0.100651	-3.688001	6146.850383
HLA A*2301	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.518790	0.830662	-3.688129	33021.009718
HLA B*0702	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.342349	0.654207	-3.688142	21996.253913
HLA A*0201	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.397456	0.709300	-3.688156	24972.147706
HLA A*3301	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.587066	0.898882	-3.688184	38642.603888
HLA B*0702	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.411196	0.722962	-3.688234	25774.822510
HLA B*0702	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.410286	0.722004	-3.688282	25720.916092
HLA A*2603	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.642914	0.954621	-3.688292	43945.422242
HLA B*2705	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.418994	0.730675	-3.688319	26241.800171
HLA B*0801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.368397	0.680074	-3.688323	23355.946111
HLA B*1801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.442834	0.754459	-3.688375	27722.592956
HLA A*2301	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.517912	0.829510	-3.688402	32954.265901
HLA B*5401	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.551446	0.862842	-3.688604	35599.659250
HLA B*2705	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.484469	0.795837	-3.688632	30511.887336
HLA A*0212	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.397935	0.709300	-3.688635	24999.722615
HLA B*5301	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.576618	0.887960	-3.688658	37724.042318
HLA B*7301	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.421125	0.732039	-3.689086	26370.879056
HLA B*1501	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.281199	0.592081	-3.689117	19107.271655
HLA A*0216	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.459191	0.770046	-3.689145	28786.639093
HLA A*1101	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.351594	0.662443	-3.689151	22469.527905
HLA B*5101	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.364422	0.675193	-3.689229	23143.132186
HLA B*4002	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.586596	0.897363	-3.689234	38600.816058
HLA B*1502	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.586627	0.897363	-3.689264	38603.530893
HLA A*1101	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.470957	0.781690	-3.689267	29577.208569
HLA B*4002	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.536950	0.847664	-3.689286	34430.990663

HLA A*0250	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.351730	0.662443	-3.689288	22476.579355
HLA B*1509	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.453660	0.764363	-3.689298	28422.369117
HLA A*6901	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.386789	0.697387	-3.689402	24366.280147
HLA B*5101	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.384783	0.695361	-3.689421	24253.966475
HLA A*2403	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.378796	0.689311	-3.689485	23921.933852
HLA A*2602	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.488214	0.798696	-3.689518	30776.140162
HLA B*3801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.518889	0.829345	-3.689544	33028.513450
HLA A*0101	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.378897	0.689311	-3.689586	23927.499345
HLA B*5801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.356377	0.666540	-3.689837	22718.387310
HLA B*1509	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.485691	0.795837	-3.689854	30597.842464
HLA B*5301	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.588868	0.898882	-3.689986	38803.280051
HLA A*0206	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.523153	0.833148	-3.690006	33354.416125
HLA A*8001	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.380601	0.690572	-3.690029	24021.531340
HLA B*4402	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.422170	0.732039	-3.690131	26434.440806
HLA B*5301	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.560296	0.869990	-3.690307	36332.589417
HLA A*2603	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.422391	0.732039	-3.690352	26447.886920
HLA A*3301	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.610547	0.920120	-3.690427	40789.383025
HLA B*4801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.437150	0.746693	-3.690458	27362.164161
HLA B*7301	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.269301	0.578823	-3.690478	18590.920175
HLA B*3801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.517176	0.826538	-3.690638	32898.511815
HLA B*3901	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.489506	0.798791	-3.690715	30867.849060
HLA B*0803	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.477752	0.786863	-3.690889	30043.594695
HLA A*0250	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.478010	0.786863	-3.691147	30061.478593
HLA B*5301	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.589228	0.898050	-3.691178	38835.411327
HLA B*0803	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.445672	0.754459	-3.691213	27904.357432
HLA A*6801	1:352-360	9	TFGGITRDV	0.726621	0.189665	-4.607650	0.916286	-3.691365	40518.207227
HLA B*1509	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.269801	0.578365	-3.691437	18612.354958
HLA A*6901	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.371630	0.680074	-3.691556	23530.456671
HLA A*2601	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.265784	0.574191	-3.691593	18440.967696
HLA B*1503	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.400896	0.709300	-3.691595	25170.714350
HLA A*0219	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.382525	0.690866	-3.691659	24128.199653
HLA B*3801	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.561732	0.869990	-3.691742	36452.883396
HLA B*4001	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.345965	0.654207	-3.691757	22180.155253
HLA B*4002	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.414720	0.722962	-3.691758	25984.831851
HLA A*0219	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.792412	0.100651	-3.691760	6200.287366
HLA B*5101	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.489342	0.797462	-3.691880	30856.161858
HLA B*7301	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.599979	0.908065	-3.691914	39808.806084
HLA B*4501	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.652845	0.960920	-3.691925	44961.926856
HLA A*3002	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.525073	0.833148	-3.691925	33502.164898
HLA B*2705	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.284549	0.592477	-3.692072	19255.244774
HLA A*2402	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-3.985469	0.293372	-3.692097	9670.946949
HLA A*0206	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.462172	0.770046	-3.692127	28984.943585
HLA A*0301	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.367397	0.675193	-3.692204	23302.181676
HLA B*4501	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.234857	0.542619	-3.692238	17173.445491
HLA A*2301	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.540041	0.847787	-3.692254	34676.993804
HLA A*3101	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.382875	0.690572	-3.692303	24147.656596
HLA A*3002	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.509183	0.816673	-3.692510	32298.570759
HLA A*3002	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.442925	0.750403	-3.692522	27728.442643
HLA B*4403	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.610928	0.918327	-3.692601	40825.146592
HLA A*0250	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.467142	0.774481	-3.692660	29318.491436
HLA A*2403	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.418794	0.725976	-3.692818	26229.735900
HLA B*4402	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.443252	0.750403	-3.692849	27749.301569
HLA B*3801	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.567892	0.875034	-3.692858	36973.642362
HLA A*8001	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.415838	0.722962	-3.692877	26051.831809
HLA B*1801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.267125	0.574191	-3.692934	18498.020781
HLA A*3002	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.355395	0.662443	-3.692953	22667.071499
HLA A*0211	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.426019	0.733042	-3.692977	26669.727864
HLA B*0801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.245381	0.552387	-3.692994	17594.655964
HLA B*1501	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-3.793742	0.100651	-3.693090	6219.301725
HLA A*3301	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.587823	0.894591	-3.693232	38709.977362
HLA B*1509	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.524046	0.830662	-3.693385	33423.055257
HLA B*1501	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.376412	0.682948	-3.693464	23790.937598
HLA A*2902	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.457950	0.764421	-3.693530	28704.529645
HLA A*3001	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.299097	0.605498	-3.693599	19911.182588
HLA B*1801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.523229	0.829510	-3.693719	33360.190823

HLA B*4403	1:26-34	9	HLARDLRLH	1.195772	-0.234852	-4.654666	0.960920	-3.693746	45150.832845
HLA A*6901	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.384644	0.690866	-3.693778	24246.226246
HLA B*4403	1:258-266	9	NPENRYQTA	1.327644	-0.366008	-4.655443	0.961636	-3.693808	45231.755668
HLA B*4403	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.650206	0.956046	-3.694160	44689.597494
HLA B*1801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.524868	0.830662	-3.694207	33486.400467
HLA A*0206	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.420190	0.725976	-3.694213	26314.160053
HLA A*3101	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.369455	0.675193	-3.694262	23412.874263
HLA B*0803	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.426683	0.732333	-3.694350	26710.590453
HLA B*4001	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.416414	0.722004	-3.694409	26086.384395
HLA A*0201	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.348735	0.654207	-3.694527	22322.078164
HLA A*3001	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.274458	0.579907	-3.694551	18812.997842
HLA B*0801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.420669	0.725976	-3.694693	26343.216849
HLA A*0216	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.459144	0.764363	-3.694781	28783.524611
HLA A*2602	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.557717	0.862842	-3.694875	36117.411436
HLA A*0202	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.469592	0.774481	-3.695111	29484.389045
HLA B*4801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.425788	0.730675	-3.695113	26655.592145
HLA A*3001	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.075003	0.379878	-3.695125	11885.109174
HLA A*2601	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.341082	0.645932	-3.695151	21932.207794
HLA A*2601	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.390687	0.695361	-3.695326	24585.951963
HLA A*1101	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.468112	0.772678	-3.695434	29384.070512
HLA B*1517	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.407333	0.711889	-3.695444	25546.601293
HLA B*4501	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.616888	0.921444	-3.695444	41389.330009
HLA A*3201	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.477167	0.781690	-3.695477	30003.151344
HLA B*4801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.418514	0.722962	-3.695553	26212.855239
HLA A*2402	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.386434	0.690866	-3.695568	24346.383625
HLA B*2705	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.478967	0.783381	-3.695585	30127.741627
HLA A*2602	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.613947	0.918327	-3.695620	41109.939825
HLA B*2705	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.450801	0.755176	-3.695624	28235.855587
HLA B*5101	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.482679	0.786863	-3.695815	30386.365997
HLA A*3301	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.640162	0.944277	-3.695885	43667.908812
HLA A*8001	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.426655	0.730675	-3.695980	26708.856494
HLA A*6802	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.385333	0.689311	-3.696021	24284.689355
HLA B*5101	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.469820	0.773768	-3.696052	29499.865311
HLA B*7301	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.610949	0.914880	-3.696069	40827.134377
HLA B*5801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.353445	0.657361	-3.696084	22565.519798
HLA B*1503	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.461233	0.765110	-3.696122	28922.289268
HLA B*3501	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.466216	0.770046	-3.696170	29256.065733
HLA A*0101	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.288320	0.592081	-3.696239	19423.163555
HLA B*5101	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.492431	0.796188	-3.696244	31076.455379
HLA B*4001	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.405545	0.709300	-3.696245	25441.644034
HLA A*0211	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.492601	0.796188	-3.696413	31088.562390
HLA A*6801	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.604540	0.908065	-3.696475	40229.024638
HLA A*0203	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.218298	0.521798	-3.696500	16530.967257
HLA B*4001	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.385875	0.689311	-3.696564	24315.056523
HLA A*0216	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.248971	0.552387	-3.696584	17740.701653
HLA A*2902	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.429451	0.732827	-3.696624	26881.356580
HLA B*5801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.351213	0.654485	-3.696728	22449.844192
HLA A*2601	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.386115	0.689311	-3.696804	24328.477485
HLA B*4002	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.602190	0.905205	-3.696985	40011.977704
HLA B*4501	1:526-534	9	DSPRPAGEV	0.926748	0.029298	-4.653087	0.956046	-3.697041	44986.987459
HLA B*1517	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.493315	0.796188	-3.697127	31139.732902
HLA A*0201	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.394709	0.697387	-3.697322	24814.718167
HLA B*3801	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.494323	0.796898	-3.697424	31212.087245
HLA B*4002	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.643715	0.946270	-3.697445	44026.566358
HLA B*4801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.410362	0.712902	-3.697459	25725.369192
HLA B*1501	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.311021	0.613540	-3.697481	20465.421388
HLA A*3101	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.380493	0.682948	-3.697545	24015.554208
HLA B*5801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.046015	0.348457	-3.697558	11117.707132
HLA B*4801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.351808	0.654207	-3.697601	22480.592375
HLA A*2403	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.406955	0.709300	-3.697655	25524.360091
HLA A*6901	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.219586	0.521798	-3.697788	16580.047998
HLA A*3201	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.488832	0.790996	-3.697836	30819.959646
HLA B*4601	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.380911	0.682948	-3.697963	24038.691371
HLA A*6802	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.420974	0.722962	-3.698013	26361.750170
HLA A*0211	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.388676	0.690572	-3.698104	24472.360951

HLA A*2603	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.606233	0.908065	-3.698169	40386.245582
HLA B*1502	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.573284	0.875034	-3.698250	37435.557414
HLA B*1509	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.430372	0.732039	-3.698333	26938.423731
HLA A*3002	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.420572	0.722004	-3.698568	26337.374428
HLA A*0202	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.239016	0.540402	-3.698614	17338.679722
HLA B*3901	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.480339	0.781690	-3.698649	30223.076989
HLA A*0216	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.352865	0.654207	-3.698658	22535.386926
HLA A*2501	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.413599	0.714935	-3.698664	25917.863991
HLA B*0801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.344778	0.645932	-3.698846	22119.641900
HLA B*4002	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.593513	0.894591	-3.698923	39220.522042
HLA B*0702	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.390003	0.690866	-3.699137	24547.277297
HLA B*0803	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.480583	0.781429	-3.699154	30240.086138
HLA B*5401	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.209671	0.510481	-3.699190	16205.817982
HLA B*5701	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.408498	0.709300	-3.699198	25615.242668
HLA A*0250	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.518569	0.819348	-3.699222	33004.221827
HLA A*6801	1:585-593	9	GMLDKGADV	0.832496	0.121837	-4.653559	0.954333	-3.699226	45035.932363
HLA A*6901	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.408562	0.709300	-3.699262	25618.984483
HLA A*0219	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.412168	0.712902	-3.699266	25832.614922
HLA A*3002	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.205832	0.506563	-3.699269	16063.193769
HLA B*1517	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.162489	0.463212	-3.699276	14537.462215
HLA A*0206	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.499268	0.799991	-3.699277	31569.556304
HLA B*0702	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.454461	0.755176	-3.699285	28474.850306
HLA B*4801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.397141	0.697848	-3.699293	24954.051328
HLA B*3901	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.498007	0.798696	-3.699311	31477.976345
HLA A*6901	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.369100	0.669685	-3.699415	23393.756253
HLA A*1101	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.390046	0.690572	-3.699474	24549.667778
HLA B*4002	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.621308	0.921765	-3.699543	41812.658133
HLA A*2403	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.390137	0.690572	-3.699565	24554.847953
HLA B*3801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.397068	0.697387	-3.699681	24949.866721
HLA A*6802	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.395050	0.695361	-3.699689	24834.191311
HLA A*3101	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.425755	0.725976	-3.699779	26653.573369
HLA B*4601	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.369516	0.669685	-3.699831	23416.167682
HLA A*6801	1:497-505	9	IPDVAGQTV	1.097862	-0.123561	-4.674303	0.974301	-3.700002	47239.224703
HLA B*1801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.472698	0.772678	-3.700020	29696.013518
HLA B*4403	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.486884	0.786863	-3.700021	30682.047834
HLA A*0206	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.498900	0.798696	-3.700203	31542.754003
HLA B*0801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.280125	0.579907	-3.700218	19060.090725
HLA B*1502	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.431108	0.730675	-3.700433	26984.077079
HLA A*2402	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.553889	0.853416	-3.700473	35800.517582
HLA B*1801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.517165	0.816673	-3.700491	32897.621941
HLA A*3001	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.165938	0.465424	-3.700514	14653.374291
HLA A*2603	1:87-95	9	LPYIVMEYV	0.918913	0.023340	-4.642864	0.942253	-3.700611	43940.429988
HLA A*0216	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.398212	0.697387	-3.700825	25015.686706
HLA B*4002	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.599002	0.898050	-3.700952	39719.316549
HLA B*5701	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.426970	0.725976	-3.700994	26728.225435
HLA A*2902	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.390537	0.689311	-3.701226	24577.440971
HLA A*0211	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-3.653365	-0.047884	-3.701248	4501.576106
HLA B*4403	1:404-412	9	PAANTSVSA	1.424782	-0.470161	-4.655972	0.954621	-3.701351	45286.846416
HLA A*0212	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-3.875165	0.173777	-3.701389	7501.798229
HLA B*4403	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.623305	0.921765	-3.701540	42005.372451
HLA A*3301	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.617116	0.915512	-3.701604	41411.055142
HLA B*7301	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.499092	0.797462	-3.701630	31556.749817
HLA B*4002	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.609715	0.908065	-3.701650	40711.341998
HLA B*4002	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.620067	0.918327	-3.701740	41693.393974
HLA B*4801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.416686	0.714935	-3.701751	26102.759969
HLA A*0202	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.434176	0.732333	-3.701843	27175.403183
HLA A*0301	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.368437	0.666540	-3.701897	23358.094212
HLA A*0212	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.364373	0.662443	-3.701930	23140.503098
HLA A*2402	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.531318	0.829345	-3.701973	33987.389063
HLA B*2705	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.466434	0.764421	-3.702014	29270.788739
HLA A*0211	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.532744	0.830662	-3.702082	34099.180393
HLA A*1101	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.500854	0.798696	-3.702158	31685.048811
HLA B*1502	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.590675	0.888375	-3.702300	38965.045897
HLA B*3801	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.495770	0.793337	-3.702433	31316.274772
HLA B*5101	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.501153	0.798696	-3.702457	31706.825692

HLA A*0201	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.364979	0.662443	-3.702536	23172.824038
HLA B*3801	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.493559	0.790996	-3.702564	31157.257932
HLA A*0206	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.393488	0.690866	-3.702622	24745.008930
HLA A*3001	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.224473	0.521798	-3.702675	16767.669773
HLA A*0250	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.550483	0.847787	-3.702696	35520.784770
HLA A*2601	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.400139	0.697387	-3.702752	25126.905528
HLA A*2402	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.532328	0.829510	-3.702819	34066.544338
HLA A*6901	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.345911	0.643088	-3.702823	22177.395605
HLA B*4402	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.433647	0.730675	-3.702972	27142.344725
HLA B*7301	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.578037	0.875034	-3.703003	37847.509992
HLA B*5101	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.486386	0.783381	-3.703005	30646.878872
HLA B*1502	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.501705	0.798696	-3.703009	31747.160973
HLA B*5101	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.499973	0.796898	-3.703075	31620.834244
HLA B*1503	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.494100	0.790996	-3.703104	31196.050242
HLA A*2902	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.436173	0.733042	-3.703131	27300.654471
HLA A*1101	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.486520	0.783381	-3.703139	30656.330714
HLA A*0219	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.426183	0.722962	-3.703222	26679.829396
HLA B*5801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.349247	0.645932	-3.703315	22348.419367
HLA A*3301	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.621616	0.918162	-3.703454	41842.301077
HLA B*4002	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.520191	0.816673	-3.703518	33127.650988
HLA B*1801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.494971	0.791452	-3.703520	31258.725740
HLA A*0216	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.326929	0.623337	-3.703592	21228.976400
HLA A*3001	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.289640	0.586005	-3.703635	19482.306782
HLA A*3301	1:418-426	9	VNVSTGPEQ	0.969813	-0.048369	-4.625105	0.921444	-3.703660	42179.802836
HLA A*0203	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.416604	0.712902	-3.703702	26097.817980
HLA A*6901	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.277961	0.574191	-3.703770	18965.359867
HLA A*2402	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.519122	0.815296	-3.703825	33046.207567
HLA B*0803	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.468944	0.765110	-3.703833	29440.397887
HLA A*3101	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.418839	0.714935	-3.703903	26232.432138
HLA B*1801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.436309	0.732333	-3.703976	27309.222039
HLA A*0203	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.401375	0.697387	-3.703987	25198.508522
HLA A*3201	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.602058	0.898050	-3.704008	39999.857759
HLA B*0802	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.436469	0.732333	-3.704136	27319.270198
HLA B*0801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.434857	0.730675	-3.704182	27218.071261
HLA A*2603	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.487669	0.783381	-3.704288	30737.537435
HLA B*1801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.469414	0.765110	-3.704303	29472.268984
HLA B*3801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.552097	0.847664	-3.704433	35653.046730
HLA A*2902	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.374123	0.669685	-3.704439	23665.907324
HLA B*7301	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.544571	0.839877	-3.704694	35040.576921
HLA B*1517	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.459955	0.755176	-3.704778	28837.296685
HLA B*1501	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.374485	0.669685	-3.704800	23685.632150
HLA B*3501	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.384926	0.680074	-3.704852	24261.971684
HLA B*4801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.430960	0.725976	-3.704983	26974.881851
HLA A*2402	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.459595	0.754459	-3.705136	28813.437554
HLA A*3001	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.244805	0.539629	-3.705177	17571.351053
HLA A*6802	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.437594	0.732333	-3.705261	27390.155435
HLA B*0801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.321781	0.616515	-3.705266	20978.833328
HLA B*5801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.342793	0.637402	-3.705391	22018.755904
HLA B*1502	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.437432	0.732039	-3.705394	27379.933081
HLA A*0219	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.455918	0.750403	-3.705515	28570.519045
HLA A*3301	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.498855	0.793337	-3.705518	31539.511957
HLA B*1801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.505563	0.799991	-3.705572	32030.428485
HLA A*3301	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.199620	0.494046	-3.705574	15835.065347
HLA A*6801	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.600172	0.894591	-3.705581	39826.469622
HLA B*4601	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.396248	0.690572	-3.705677	24902.804534
HLA B*0802	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.470217	0.764421	-3.705796	29526.848523
HLA B*0803	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.503399	0.797462	-3.705937	31871.233546
HLA B*0702	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.214455	0.508438	-3.706017	16385.304184
HLA A*2301	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.529683	0.823629	-3.706053	33859.657554
HLA B*0803	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.470523	0.764421	-3.706102	29547.621634
HLA B*3801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.461362	0.755176	-3.706185	28930.896199
HLA B*4601	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.386345	0.680074	-3.706271	24341.379112
HLA A*6801	1:595-603	9	AGGSQHNRV	1.010046	-0.048790	-4.667543	0.961256	-3.706287	46509.673735
HLA B*0803	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.505114	0.798791	-3.706323	31997.348894
HLA B*0802	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.470725	0.764363	-3.706362	29561.371877

HLA B*1801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.488057	0.781690	-3.706367	30764.986985
HLA B*4601	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.397237	0.690866	-3.706371	24959.586886
HLA A*2301	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.539520	0.833148	-3.706372	34635.371893
HLA A*0202	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.470856	0.764421	-3.706436	29570.328964
HLA B*3801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.523174	0.816673	-3.706501	33356.040158
HLA A*2501	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.344066	0.637402	-3.706664	22083.413164
HLA A*2902	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.230880	0.524138	-3.706741	17016.873009
HLA A*0201	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.396058	0.689311	-3.706747	24891.894490
HLA B*5301	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.579889	0.873123	-3.706766	38009.198041
HLA A*2902	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.173080	0.466242	-3.706838	14896.357187
HLA B*1509	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.402232	0.695361	-3.706871	25248.314895
HLA B*5401	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.031500	0.324517	-3.706984	10752.268755
HLA A*0203	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.332974	0.625924	-3.707050	21526.542412
HLA A*2902	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.323661	0.616515	-3.707145	21069.824617
HLA B*1503	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.479829	0.772678	-3.707151	30187.617549
HLA A*2603	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.611759	0.904590	-3.707170	40903.405775
HLA B*5401	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.523879	0.816673	-3.707206	33410.219856
HLA A*2402	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.526654	0.819348	-3.707306	33624.363755
HLA A*2301	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.506148	0.798791	-3.707357	32073.604544
HLA B*4501	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.429446	0.722004	-3.707442	26881.065731
HLA A*0301	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.365007	0.657361	-3.707646	23174.328436
HLA A*2501	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.430626	0.722962	-3.707664	26954.167590
HLA A*3201	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.481459	0.773768	-3.707691	30301.168872
HLA B*0803	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.477825	0.770046	-3.707779	30048.633626
HLA A*2902	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.390734	0.682948	-3.707786	24588.612253
HLA A*2902	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.405226	0.697387	-3.707838	25422.932358
HLA A*0206	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.438595	0.730675	-3.707920	27453.351931
HLA B*1801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.472393	0.764363	-3.708030	29675.136082
HLA B*0802	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.462541	0.754459	-3.708082	29009.572480
HLA A*2403	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.321676	0.613540	-3.708136	20973.726757
HLA A*6801	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.628260	0.920120	-3.708140	42487.375375
HLA B*5401	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.531795	0.823629	-3.708166	34024.734772
HLA A*0211	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.260615	0.552387	-3.708228	18222.788728
HLA B*7301	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.294494	0.586005	-3.708489	19701.278658
HLA A*1101	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.478663	0.770046	-3.708618	30106.723543
HLA A*0101	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.399530	0.690866	-3.708665	25091.723335
HLA B*3801	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.540485	0.831818	-3.708668	34712.468089
HLA A*0216	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.441770	0.733042	-3.708728	27654.736938
HLA B*4501	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.573879	0.865145	-3.708733	37486.830616
HLA A*0202	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.354749	0.645932	-3.708818	22633.374327
HLA B*0803	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.441896	0.733042	-3.708855	27662.817008
HLA B*0702	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.399432	0.690572	-3.708860	25086.022758
HLA A*0212	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.434843	0.725976	-3.708867	27217.187795
HLA B*5701	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.406405	0.697387	-3.709018	25492.068888
HLA B*4501	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.653486	0.944464	-3.709022	45028.380174
HLA A*0212	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.363311	0.654207	-3.709104	23083.987449
HLA B*1501	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.406504	0.697387	-3.709116	25497.861735
HLA A*8001	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.431159	0.722004	-3.709155	26987.288849
HLA A*6802	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.422078	0.712902	-3.709176	26428.864106
HLA B*4402	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.421122	0.711889	-3.709233	26370.736392
HLA B*3501	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.432200	0.722962	-3.709239	27052.043634
HLA B*3801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.542593	0.833148	-3.709445	34881.325635
HLA A*3301	1:166-174	9	SGNSVTQTA	1.343767	-0.425440	-4.627795	0.918327	-3.709468	42441.889047
HLA A*0202	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.432637	0.722962	-3.709676	27079.278165
HLA B*5701	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.421566	0.711889	-3.709677	26397.713443
HLA A*0206	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.367105	0.657361	-3.709744	23286.555203
HLA A*2603	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.627919	0.918162	-3.709758	42454.059905
HLA B*1502	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.529121	0.819348	-3.709773	33815.906543
HLA B*0802	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.432755	0.722962	-3.709793	27086.603951
HLA A*3301	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.392804	0.682948	-3.709856	24706.084060
HLA A*0201	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.345866	0.635971	-3.709894	22175.116154
HLA A*2602	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.385140	0.675193	-3.709947	24273.918791
HLA A*2501	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.442329	0.732333	-3.709996	27690.366828
HLA B*4001	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.390095	0.680074	-3.710021	24552.456967
HLA A*3301	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.618098	0.908065	-3.710033	41504.805315

HLA A*0203	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.400950	0.690866	-3.710084	25173.846472
HLA B*0702	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.422227	0.711889	-3.710337	26437.873206
HLA B*1517	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.400947	0.690572	-3.710375	25173.710285
HLA A*3201	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.501844	0.791452	-3.710392	31757.295759
HLA B*4403	1:237-245	9	SARHEGLSA	1.147924	-0.227804	-4.630527	0.920120	-3.710407	42709.762532
HLA A*0211	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-3.973834	0.263371	-3.710463	9415.304091
HLA B*5301	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.583963	0.873256	-3.710707	38367.430357
HLA A*2402	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.573630	0.862842	-3.710788	37465.340021
HLA A*2603	1:446-454	9	AAGFGRFKQ	0.949923	-0.028158	-4.632557	0.921765	-3.710793	42909.861403
HLA B*1503	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.282052	0.571232	-3.710820	19144.831186
HLA A*0301	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.365028	0.654207	-3.710821	23175.456799
HLA B*4002	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.618084	0.907250	-3.710834	41503.458119
HLA A*1101	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.475292	0.764421	-3.710871	29873.904180
HLA A*2301	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.542739	0.831818	-3.710921	34893.027252
HLA B*1503	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.441626	0.730675	-3.710951	27645.612291
HLA B*1501	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.347757	0.636741	-3.711016	22271.898503
HLA A*8001	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.409046	0.697848	-3.711197	25647.551146
HLA A*6801	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.616414	0.905205	-3.711209	41344.124553
HLA B*5401	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.502245	0.790996	-3.711250	31786.687742
HLA B*5701	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.406652	0.695361	-3.711290	25506.553474
HLA A*3101	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.408900	0.697387	-3.711513	25638.950063
HLA B*5801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.348347	0.636741	-3.711606	22302.161660
HLA A*2403	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.374069	0.662443	-3.711626	23662.962819
HLA A*2601	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.402850	0.690866	-3.711984	25284.263787
HLA B*4002	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.551862	0.839877	-3.711985	35633.764043
HLA A*3001	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.255991	0.543984	-3.712007	18029.805992
HLA A*0203	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.401344	0.689311	-3.712033	25196.736409
HLA A*0101	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.358006	0.645932	-3.712074	22803.719610
HLA A*2301	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.476622	0.764363	-3.712259	29965.518182
HLA B*1517	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.476758	0.764421	-3.712337	29974.922045
HLA A*2601	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.387612	0.675193	-3.712419	24412.460460
HLA A*6802	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.138641	0.426183	-3.712458	13760.725328
HLA A*6801	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.585725	0.873256	-3.712469	38523.419258
HLA B*1501	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.401786	0.689311	-3.712475	25222.376017
HLA B*1801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.536144	0.823629	-3.712514	34367.160033
HLA B*3801	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.552414	0.839877	-3.712537	35679.094910
HLA B*4501	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.610625	0.898050	-3.712574	40796.665654
HLA A*3301	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.459360	0.746693	-3.712667	28797.854019
HLA A*0211	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.421970	0.709300	-3.712670	26422.287972
HLA A*0206	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.265161	0.552387	-3.712775	18414.549286
HLA B*0803	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.496160	0.783381	-3.712779	31344.410721
HLA A*0211	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.529488	0.816673	-3.712814	33844.457276
HLA B*1801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.329356	0.616515	-3.712841	21347.944853
HLA B*1801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.511819	0.798791	-3.713028	32495.215916
HLA B*0801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.388232	0.675193	-3.713039	24447.351508
HLA A*0301	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.325120	0.612002	-3.713118	21140.728596
HLA B*3501	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.443861	0.730675	-3.713186	27788.210068
HLA A*2402	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.325310	0.612002	-3.713309	21149.994515
HLA B*4002	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.628194	0.914880	-3.713314	42480.940007
HLA B*7301	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.583422	0.869990	-3.713433	38319.720430
HLA B*1517	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.483536	0.770046	-3.713490	30446.426484
HLA B*0802	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.446382	0.732827	-3.713554	27949.984458
HLA B*7301	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.573705	0.860149	-3.713556	37471.826449
HLA A*0301	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.368245	0.654485	-3.713760	23347.734604
HLA A*0206	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.509660	0.795837	-3.713823	32334.060776
HLA B*4001	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.396775	0.682948	-3.713827	24933.000422
HLA B*1509	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.510055	0.796188	-3.713867	32363.461313
HLA B*5101	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.507219	0.793337	-3.713882	32152.824897
HLA A*0203	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.117801	0.403854	-3.713947	13115.999583
HLA A*2403	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.394066	0.680074	-3.713991	24777.962320
HLA B*5101	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.495432	0.781429	-3.714003	31291.888142
HLA A*0219	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.411447	0.697387	-3.714060	25789.746794
HLA B*1517	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.488877	0.774481	-3.714395	30823.127728
HLA A*3301	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.608578	0.894030	-3.714548	40604.883412
HLA A*2603	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.437519	0.722962	-3.714558	27385.414159

HLA B*5101	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.447629	0.733042	-3.714587	28030.390446
HLA B*1502	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.522575	0.807959	-3.714617	33310.056501
HLA B*5801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.350619	0.635971	-3.714647	22419.138065
HLA A*2301	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.541277	0.826538	-3.714739	34775.811247
HLA A*3201	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.609389	0.894591	-3.714798	40680.739611
HLA B*3501	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.240736	0.525884	-3.714852	17407.477698
HLA A*2602	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.588312	0.873123	-3.715189	38753.560549
HLA B*0702	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.441175	0.725976	-3.715199	27616.911738
HLA B*5301	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.575387	0.860149	-3.715238	37617.254317
HLA A*0206	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.465659	0.750403	-3.715256	29218.579289
HLA B*1517	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.446031	0.730675	-3.715357	27927.463794
HLA A*0203	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.352762	0.637402	-3.715359	22530.023351
HLA A*2603	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.568863	0.853416	-3.715447	37056.344343
HLA A*3301	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.588737	0.873256	-3.715481	38791.526230
HLA B*1509	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.502457	0.786863	-3.715593	31802.168131
HLA A*0212	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.125494	0.409720	-3.715774	13350.379405
HLA B*5101	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.499546	0.783751	-3.715795	31589.715698
HLA A*2603	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.589106	0.873256	-3.715850	38824.487910
HLA B*1509	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.497546	0.781690	-3.715856	31444.616731
HLA B*0802	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.448964	0.733042	-3.715922	28116.655177
HLA A*3101	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.287305	0.571232	-3.716073	19377.823223
HLA A*8001	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.413540	0.697387	-3.716153	25914.358909
HLA B*0803	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.512343	0.796188	-3.716156	32534.441973
HLA B*3501	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.378658	0.662443	-3.716215	23914.299585
HLA A*2402	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.515099	0.798791	-3.716308	32741.555489
HLA A*3201	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.591396	0.875034	-3.716362	39029.814216
HLA A*3001	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.277494	0.561125	-3.716369	18944.953355
HLA B*5301	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.507456	0.790996	-3.716461	32170.397962
HLA A*0202	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.308864	0.592081	-3.716782	20364.036372
HLA B*3901	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.481253	0.764363	-3.716890	30286.746821
HLA A*0201	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.396974	0.680074	-3.716900	24944.468264
HLA B*5801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.223481	0.506563	-3.716918	16729.433295
HLA A*8001	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.450185	0.733042	-3.717144	28195.862690
HLA B*3801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.514897	0.797462	-3.717435	32726.326008
HLA A*2501	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.464170	0.746693	-3.717477	29118.535036
HLA B*5701	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.408066	0.690572	-3.717494	25589.757439
HLA B*1509	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.550722	0.833148	-3.717575	35540.390857
HLA B*4601	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.392797	0.675193	-3.717604	24705.683092
HLA B*5101	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.509150	0.791452	-3.717699	32296.124608
HLA A*0211	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.517867	0.799991	-3.717876	32950.878776
HLA B*1502	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.482404	0.764421	-3.717983	30367.138819
HLA A*0301	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.363962	0.645932	-3.718030	23118.605643
HLA B*5401	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.491832	0.773768	-3.718064	31033.614291
HLA B*1801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.450942	0.732827	-3.718115	28245.022245
HLA B*0702	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.451186	0.733042	-3.718144	28260.918170
HLA B*4002	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.509602	0.791452	-3.718150	32329.687979
HLA A*3301	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.623368	0.905205	-3.718163	42011.508498
HLA A*6801	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.622833	0.904590	-3.718243	41959.721150
HLA B*0802	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.431164	0.712902	-3.718262	26987.580847
HLA B*0801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.441248	0.722962	-3.718286	27621.543663
HLA B*7301	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.505166	0.786863	-3.718302	32001.157367
HLA A*0203	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.147386	0.429083	-3.718303	14040.614301
HLA B*0801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.401361	0.682948	-3.718413	25197.690608
HLA A*2501	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.293010	0.574537	-3.718472	19634.034025
HLA A*0202	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.242625	0.524138	-3.718486	17483.357310
HLA B*4501	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.558365	0.839877	-3.718488	36171.379686
HLA A*0212	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.137011	0.418508	-3.718503	13709.158057
HLA A*2501	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.472968	0.754459	-3.718509	29714.494262
HLA A*2603	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.664816	0.946270	-3.718546	46218.467468
HLA A*2402	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.566236	0.847664	-3.718572	36832.894505
HLA A*0203	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.242747	0.524138	-3.718609	17488.276319
HLA A*3001	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.296987	0.578365	-3.718622	19814.687042
HLA A*2501	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.491565	0.772678	-3.718887	31014.480912
HLA B*0702	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.239925	0.521039	-3.718887	17375.018478
HLA A*6901	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.355776	0.636741	-3.719035	22686.945675

HLA A*3002	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.251915	0.532852	-3.719063	17861.367124
HLA B*5401	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.489121	0.770046	-3.719075	30840.474576
HLA B*5401	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.552238	0.833148	-3.719090	35664.621350
HLA A*3301	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.611221	0.892112	-3.719109	40852.763369
HLA B*4403	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.261938	0.542619	-3.719318	18278.375717
HLA B*4002	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.345243	0.625924	-3.719319	22143.348227
HLA B*7301	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.567014	0.847664	-3.719350	36898.909274
HLA A*2902	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.417267	0.697848	-3.719418	26137.662903
HLA A*0202	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.432390	0.712902	-3.719488	27063.900464
HLA B*3801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.374017	0.654485	-3.719533	23660.146678
HLA B*4501	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.519615	0.799991	-3.719624	33083.771928
HLA A*0301	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.336238	0.616515	-3.719722	21688.909361
HLA B*4403	1:522-530	9	QASVDSPRP	0.852450	0.093820	-4.666009	0.946270	-3.719739	46345.660853
HLA B*3801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.519993	0.799991	-3.720002	33112.600187
HLA A*3001	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.294210	0.574191	-3.720019	19688.386489
HLA B*1501	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.100533	0.380356	-3.720177	12604.704812
HLA B*0803	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.503977	0.783751	-3.720226	31913.677063
HLA A*0211	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.513979	0.793337	-3.720642	32657.174265
HLA B*1509	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.453754	0.733042	-3.720712	28428.520257
HLA A*0202	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.299539	0.578823	-3.720716	19931.443740
HLA B*7301	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.519418	0.798696	-3.720722	33068.741063
HLA A*2601	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.400816	0.680074	-3.720741	25166.084969
HLA B*4402	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.418148	0.697387	-3.720760	26190.742423
HLA A*2603	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.625692	0.904921	-3.720771	42236.888445
HLA A*2602	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.932206	0.211378	-3.720828	8554.727416
HLA A*2603	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.636401	0.915512	-3.720889	43291.324098
HLA A*8001	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.446873	0.725976	-3.720896	27981.604451
HLA A*0101	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.378371	0.657361	-3.721010	23898.521200
HLA A*2603	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.615199	0.894030	-3.721169	41228.650207
HLA B*0802	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.491320	0.770046	-3.721274	30997.036190
HLA B*3501	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-3.642096	-0.079239	-3.721335	4386.281164
HLA B*4403	1:140-148	9	KPANIMISA	1.205138	-0.289626	-4.636913	0.915512	-3.721401	43342.410092
HLA B*4403	1:486-494	9	IIVGSGPAT	1.132825	-0.203639	-4.650885	0.929186	-3.721700	44759.522449
HLA B*1502	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.245865	0.524138	-3.721726	17614.275032
HLA B*4402	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.411083	0.689311	-3.721772	25768.130310
HLA A*0202	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.315191	0.593391	-3.721800	20662.888261
HLA B*4403	1:293-301	9	RTSLLSSAA	1.125440	-0.209126	-4.638121	0.916314	-3.721806	43463.099317
HLA B*2705	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-3.987969	0.266144	-3.721825	9726.774621
HLA B*4801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.443844	0.722004	-3.721840	27787.157770
HLA A*3001	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.293096	0.571232	-3.721865	19637.964482
HLA A*0219	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.384339	0.662443	-3.721896	24229.180219
HLA A*6901	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.388504	0.666540	-3.721964	24462.698188
HLA A*3201	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.538702	0.816673	-3.722029	34570.227248
HLA A*3001	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.306573	0.584529	-3.722044	20256.906158
HLA B*3801	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.472604	0.750403	-3.722201	29689.588127
HLA B*3501	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.419677	0.697387	-3.722290	26283.144588
HLA B*4002	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.597428	0.875034	-3.722394	39575.609492
HLA A*2603	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.537734	0.815296	-3.722438	34493.260363
HLA B*1517	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.216508	0.494046	-3.722462	16462.961332
HLA B*1501	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.301315	0.578823	-3.722492	20013.127802
HLA B*4403	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.596018	0.873492	-3.722526	39447.357957
HLA B*3901	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.307121	0.584529	-3.722592	20282.456172
HLA A*3101	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.263044	0.540402	-3.722642	18325.009462
HLA A*2902	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.418080	0.695361	-3.722718	26186.633764
HLA A*0202	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-3.964986	0.242192	-3.722794	9225.420925
HLA A*2403	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.405815	0.682948	-3.722867	25457.477153
HLA B*5801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.348972	0.625924	-3.723048	22334.278254
HLA A*2301	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.506824	0.783751	-3.723074	32123.615712
HLA B*3501	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.307696	0.584529	-3.723167	20309.356826
HLA A*6801	1:226-234	9	YQHVREDPI	0.574108	0.335010	-4.632289	0.909118	-3.723171	42883.405876
HLA A*3201	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.570838	0.847664	-3.723175	37225.324328
HLA B*5401	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.552529	0.829345	-3.723184	35688.554141
HLA A*3002	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.520670	0.797462	-3.723208	33164.231421
HLA B*5101	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.420772	0.697387	-3.723385	26349.488206
HLA A*0250	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.552783	0.829345	-3.723438	35709.411915

HLA B*5301	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.571283	0.847787	-3.723496	37263.405535
HLA A*2402	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.567890	0.844164	-3.723726	36973.442339
HLA B*4403	1:439-447	9	EAVKKLTAA	1.094052	-0.196689	-4.621296	0.897363	-3.723933	41811.527139
HLA A*2301	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.455972	0.732039	-3.723933	28574.074223
HLA A*3101	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.390516	0.666540	-3.723975	24576.244349
HLA B*5401	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.543326	0.819348	-3.723978	34940.251031
HLA A*2902	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.435933	0.711889	-3.724044	27285.593888
HLA B*2705	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.433349	0.709300	-3.724049	27123.702821
HLA A*8001	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.378298	0.654207	-3.724091	23894.513597
HLA A*0202	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.435999	0.711889	-3.724110	27289.727338
HLA B*1502	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.505819	0.781690	-3.724129	32049.321691
HLA A*0211	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.507724	0.783381	-3.724343	32190.244446
HLA A*0301	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.360440	0.635971	-3.724468	22931.885192
HLA A*3001	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.299099	0.574537	-3.724562	19911.290305
HLA B*1502	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.523454	0.798791	-3.724663	33377.520917
HLA B*4403	1:143-151	9	NIMISATNA	0.971550	-0.064300	-4.631939	0.907250	-3.724689	42848.852628
HLA B*4601	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.387163	0.662443	-3.724720	24387.248365
HLA A*0211	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.348098	0.623337	-3.724761	22289.376190
HLA A*2602	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.447841	0.722962	-3.724879	28044.041487
HLA B*1517	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-3.973317	0.248296	-3.725022	9404.104891
HLA A*0301	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.368141	0.643088	-3.725053	23342.177685
HLA B*4501	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.598391	0.873256	-3.725135	39663.487776
HLA A*3002	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.143669	0.418508	-3.725162	13920.961234
HLA B*7301	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.578646	0.853416	-3.725230	37900.577627
HLA A*0101	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.387713	0.662443	-3.725270	24418.140075
HLA B*5801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.339142	0.613866	-3.725275	21834.420869
HLA A*0202	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.420716	0.695361	-3.725354	26346.067281
HLA A*0212	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.408318	0.682948	-3.725370	25604.574567
HLA A*2902	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.447444	0.722004	-3.725439	28018.413343
HLA B*1801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.521636	0.796188	-3.725448	33238.052950
HLA B*5701	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.414788	0.689311	-3.725477	25988.908848
HLA B*1502	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.325324	0.599665	-3.725659	21150.681041
HLA B*1501	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.363149	0.637402	-3.725747	23075.372212
HLA B*4001	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.305666	0.579907	-3.725759	20214.649474
HLA B*5401	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.556507	0.830662	-3.725845	36016.925019
HLA B*0802	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.421207	0.695361	-3.725845	26375.872752
HLA A*2601	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.388291	0.662443	-3.725848	24450.658168
HLA A*3201	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.598988	0.873123	-3.725865	39718.027308
HLA B*4403	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.600921	0.875034	-3.725887	39895.259677
HLA A*2602	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.620544	0.894591	-3.725953	41739.207123
HLA B*4501	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.318050	0.592081	-3.725969	20799.378131
HLA B*1801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.451955	0.725976	-3.725978	28310.956935
HLA A*0301	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.349324	0.623337	-3.725987	22352.409505
HLA B*4501	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.619799	0.893801	-3.725999	41667.688445
HLA B*7301	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.545525	0.819348	-3.726177	35117.625153
HLA A*2301	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.542941	0.816673	-3.726268	34909.265026
HLA A*0250	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.435623	0.709300	-3.726323	27266.116055
HLA A*0206	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.287477	0.561125	-3.726352	19385.477462
HLA B*0803	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.522232	0.795837	-3.726395	33283.757146
HLA B*4801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.438295	0.711889	-3.726406	27434.348004
HLA B*5701	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.417368	0.690866	-3.726502	26143.743890
HLA B*4402	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.452523	0.725976	-3.726547	28348.045720
HLA A*2301	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.500392	0.773768	-3.726623	31651.298517
HLA A*0301	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.363410	0.636741	-3.726668	23089.233081
HLA B*1503	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.277740	0.550986	-3.726755	18955.717872
HLA B*4403	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.206499	0.479739	-3.726760	16087.892366
HLA A*0219	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.305619	0.578823	-3.726796	20212.462412
HLA B*4002	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.542149	0.815296	-3.726853	34845.678786
HLA B*5801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.277898	0.550986	-3.726912	18962.589855
HLA A*3201	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.525717	0.798791	-3.726925	33551.862304
HLA A*0101	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.370033	0.643088	-3.726945	23444.053625
HLA B*4801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.424407	0.697387	-3.727019	26570.935031
HLA B*5801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.319164	0.592081	-3.727083	20852.782157
HLA A*0301	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.364622	0.637402	-3.727220	23153.776785
HLA A*0250	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.575136	0.847664	-3.727472	37595.485564

HLA A*2603	1:263-271	9	YQTAAEMRA	1.057768	-0.165656	-4.619618	0.892112	-3.727506	41650.334906
HLA A*6802	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.436812	0.709300	-3.727512	27340.856678
HLA A*0211	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.525005	0.797462	-3.727543	33496.909263
HLA B*3501	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.364453	0.636741	-3.727712	23144.759866
HLA B*1509	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.418291	0.690572	-3.727719	26199.386879
HLA B*0801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.351119	0.623337	-3.727782	22444.986671
HLA A*0101	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.382029	0.654207	-3.727822	24100.673350
HLA B*4501	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.642740	0.914880	-3.727860	43927.833013
HLA B*1501	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.191115	0.463212	-3.727902	15527.971462
HLA A*0203	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.364765	0.636741	-3.728024	23161.418867
HLA A*3301	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.632623	0.904590	-3.728033	42916.361748
HLA B*1501	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.327730	0.599665	-3.728065	21268.175171
HLA A*2603	1:256-264	9	AKNPENRYQ	0.888017	0.017188	-4.633441	0.905205	-3.728235	42997.233971
HLA A*3001	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.063115	0.334871	-3.728243	11564.178357
HLA B*0802	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.458989	0.730675	-3.728314	28773.249211
HLA A*8001	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.408477	0.680074	-3.728403	25613.995517
HLA B*4501	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.633004	0.904590	-3.728414	42953.990221
HLA A*8001	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.419405	0.690866	-3.728539	26266.655850
HLA B*3801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.498615	0.770046	-3.728569	31522.112981
HLA A*1101	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.425960	0.697387	-3.728572	26666.121102
HLA B*4402	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.437935	0.709300	-3.728635	27411.649631
HLA A*3301	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.502454	0.773768	-3.728686	31801.996085
HLA B*5301	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.591542	0.862842	-3.728700	39042.907524
HLA A*0101	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.398555	0.669685	-3.728871	25035.452997
HLA A*6801	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.647068	0.918162	-3.728906	44367.762876
HLA A*0211	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.493334	0.764421	-3.728913	31141.080631
HLA A*0212	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.418232	0.689311	-3.728921	26195.843725
HLA A*6802	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.290080	0.561125	-3.728955	19502.026016
HLA A*3301	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.627193	0.898050	-3.729143	42383.150616
HLA B*0801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.426636	0.697387	-3.729249	26707.700583
HLA A*0101	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.365999	0.636741	-3.729258	23227.295245
HLA B*3801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.511042	0.781690	-3.729352	32437.079667
HLA A*0202	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.251172	0.521798	-3.729374	17830.858756
HLA A*0201	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.399101	0.669685	-3.729416	25066.894577
HLA A*0203	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.399112	0.669685	-3.729428	25067.572632
HLA B*5801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.372558	0.643088	-3.729470	23580.792813
HLA B*1509	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.460185	0.730675	-3.729510	28852.589383
HLA A*0211	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.452652	0.722962	-3.729691	28356.481763
HLA B*4601	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.419015	0.689311	-3.729704	26243.077889
HLA B*4403	1:339-347	9	LAVLTVVVT	1.133135	-0.228214	-4.634632	0.904921	-3.729711	43115.329260
HLA B*0801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.308617	0.578823	-3.729794	20352.472103
HLA A*2301	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.537859	0.807959	-3.729900	34503.151831
HLA A*0250	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.460711	0.730675	-3.730036	28887.574582
HLA B*1502	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.603254	0.873123	-3.730132	40110.154499
HLA A*2402	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.563304	0.833148	-3.730156	36585.053281
HLA B*4601	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.387536	0.657361	-3.730175	24408.234627
HLA A*2602	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.560851	0.830662	-3.730189	36379.006088
HLA A*2603	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.549559	0.819348	-3.730211	35445.344736
HLA A*2402	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.562113	0.831818	-3.730295	36484.844781
HLA B*1501	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-3.972537	0.242192	-3.730345	9387.229496
HLA A*0250	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.425847	0.695361	-3.730486	26659.197484
HLA A*2602	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.605583	0.875034	-3.730549	40325.770529
HLA B*4403	1:349-357	9	AINTFGGIT	1.133244	-0.225179	-4.638699	0.908065	-3.730634	43520.979938
HLA A*2301	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.530690	0.799991	-3.730699	33938.331744
HLA B*5301	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.485174	0.754459	-3.730715	30561.447321
HLA B*5401	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.522169	0.791452	-3.730717	33278.895842
HLA B*0801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.344644	0.613866	-3.730778	22112.822058
HLA B*1509	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.529572	0.798791	-3.730781	33851.049330
HLA A*2403	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.428697	0.697848	-3.730849	26834.715613
HLA B*5301	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.575023	0.844164	-3.730859	37585.724236
HLA B*3801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.512369	0.781429	-3.730940	32536.378115
HLA A*0101	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.397496	0.666540	-3.730955	24974.444453
HLA A*2403	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.385448	0.654485	-3.730963	24291.127704
HLA B*5401	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.524363	0.793337	-3.731026	33447.474201
HLA B*0803	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.443950	0.712902	-3.731048	27793.923239

HLA A*0101	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.367042	0.635971	-3.731070	23283.154054
HLA A*6901	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.309982	0.578823	-3.731159	20416.543526
HLA B*4403	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.625048	0.893801	-3.731247	42174.326678
HLA B*1801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.512724	0.781429	-3.731295	32562.967722
HLA B*5701	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.411480	0.680074	-3.731406	25791.700144
HLA B*1801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.446377	0.714935	-3.731442	27949.682047
HLA A*2902	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.367500	0.635971	-3.731529	23307.729074
HLA A*6901	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.388932	0.657361	-3.731571	24486.796018
HLA B*3801	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.546961	0.815296	-3.731665	35233.896494
HLA B*0801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.389045	0.657361	-3.731683	24493.155444
HLA B*4403	1:53-61	9	YLRFRREAQ	1.015867	-0.071403	-4.676178	0.944464	-3.731714	47443.601600
HLA A*3201	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.594561	0.862842	-3.731719	39315.267987
HLA A*3301	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.591873	0.860149	-3.731725	39072.700596
HLA A*6802	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.398316	0.666540	-3.731775	25021.642027
HLA B*1509	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.411901	0.680074	-3.731826	25816.688153
HLA A*0250	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.227781	0.495678	-3.732103	16895.878863
HLA B*4001	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.375192	0.643088	-3.732104	23724.232699
HLA A*0101	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.369734	0.637402	-3.732332	23427.951781
HLA A*3001	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.127467	0.395099	-3.732368	13411.185682
HLA A*0219	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.441671	0.709300	-3.732371	27648.454072
HLA A*0211	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.139426	0.407006	-3.732421	13785.612101
HLA B*1501	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.346402	0.613866	-3.732535	22202.485032
HLA A*0201	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.399192	0.666540	-3.732652	25072.183891
HLA B*1517	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.306888	0.574191	-3.732697	20271.596222
HLA A*0101	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.387203	0.654485	-3.732718	24389.491317
HLA B*5301	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.548020	0.815296	-3.732724	35319.967226
HLA B*1503	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.346611	0.613866	-3.732744	22213.177661
HLA B*1503	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.497163	0.764363	-3.732801	31416.900715
HLA B*0801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.423714	0.690866	-3.732848	26528.563836
HLA B*5301	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.572821	0.839877	-3.732944	37395.681790
HLA B*4801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.442246	0.709300	-3.732946	27685.124261
HLA B*1501	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.424036	0.690866	-3.733170	26548.232896
HLA A*6901	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.185932	0.452683	-3.733249	15343.758709
HLA B*4001	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.395753	0.662443	-3.733310	24874.394534
HLA A*6801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.370799	0.637402	-3.733396	23485.436598
HLA A*3201	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.944837	0.211378	-3.733459	8807.182734
HLA B*3801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.507351	0.773768	-3.733582	32162.567193
HLA A*3301	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.541609	0.807959	-3.733650	34802.348159
HLA B*4001	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.391234	0.657361	-3.733873	24616.962198
HLA A*0219	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.388091	0.654207	-3.733884	24439.417348
HLA B*1801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.503986	0.770046	-3.733940	31914.367668
HLA B*5101	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.466033	0.732039	-3.733994	29243.723116
HLA B*1503	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.240574	0.506563	-3.734011	17400.981007
HLA B*1501	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.186735	0.452683	-3.734053	15372.173734
HLA B*5701	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.403912	0.669685	-3.734228	25346.166289
HLA B*5801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.193060	0.458556	-3.734504	15597.683291
HLA B*0802	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.466557	0.732039	-3.734518	29279.024187
HLA B*4002	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.639129	0.904590	-3.734539	43564.087466
HLA A*2602	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.632705	0.898050	-3.734655	42924.488564
HLA A*2301	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.481351	0.746693	-3.734659	30293.629216
HLA A*3001	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.207655	0.472905	-3.734750	16130.769991
HLA A*2501	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.499123	0.764363	-3.734760	31558.969236
HLA A*3002	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.561340	0.826538	-3.734801	36419.964857
HLA B*0801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.401342	0.666540	-3.734802	25196.600098
HLA B*5301	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.566830	0.831818	-3.735013	36883.342276
HLA A*0101	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.360945	0.625924	-3.735021	22958.573386
HLA B*7301	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.530871	0.795837	-3.735035	33952.472090
HLA B*1503	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.449976	0.714935	-3.735041	28182.290210
HLA A*3001	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.144778	0.409720	-3.735059	13956.553381
HLA A*0101	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.309289	0.574191	-3.735098	20383.986398
HLA A*3002	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.533855	0.798696	-3.735159	34186.547755
HLA A*3001	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.287547	0.552387	-3.735160	19388.623915
HLA B*4002	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.204253	0.469073	-3.735180	16004.902925
HLA A*2601	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.401723	0.666540	-3.735182	25218.692129
HLA A*2601	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.404885	0.669685	-3.735200	25402.997567

HLA B*1509	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.433074	0.697848	-3.735226	27106.540115
HLA B*3901	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.401807	0.666540	-3.735267	25223.604099
HLA B*4002	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.629463	0.894030	-3.735433	42605.222730
HLA B*3501	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.392827	0.657361	-3.735466	24707.420668
HLA A*3002	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.447385	0.711889	-3.735496	28014.624186
HLA A*2402	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.566217	0.830662	-3.735555	36831.300445
HLA A*3001	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.149764	0.414162	-3.735601	14117.694774
HLA A*0201	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.276030	0.540402	-3.735628	18881.209504
HLA A*0301	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.361732	0.625924	-3.735808	23000.219230
HLA B*4402	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.431220	0.695361	-3.735859	26991.085070
HLA A*2602	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.307135	0.571232	-3.735903	20283.114538
HLA A*0219	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.393372	0.657361	-3.736011	24738.450279
HLA A*2501	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.506122	0.770046	-3.736076	32071.695940
HLA B*1509	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.060403	0.324299	-3.736104	11492.207942
HLA B*3501	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.402665	0.666540	-3.736124	25273.460075
HLA A*8001	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.352658	0.616515	-3.736143	22524.661052
HLA A*6901	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.314585	0.578365	-3.736220	20634.068124
HLA A*0203	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.288849	0.552387	-3.736462	19446.820311
HLA B*0702	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.403003	0.666540	-3.736463	25293.156379
HLA A*3002	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.336191	0.599665	-3.736526	21686.562796
HLA B*1502	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.432108	0.695361	-3.736747	27046.336642
HLA A*1101	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.458813	0.722004	-3.736808	28761.577073
HLA A*6802	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.416924	0.680074	-3.736850	26117.026383
HLA B*1501	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.362780	0.625924	-3.736856	23055.781405
HLA B*3501	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.082968	0.346054	-3.736914	12105.087403
HLA A*3001	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.291189	0.554273	-3.736916	19551.887442
HLA A*6802	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.241927	0.505009	-3.736918	17455.288707
HLA A*0211	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.487382	0.750403	-3.736979	30717.257154
HLA B*1501	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.340291	0.603309	-3.736982	21892.258897
HLA B*0803	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.469822	0.732827	-3.736995	29500.024903
HLA A*0250	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.563541	0.826538	-3.737003	36605.048772
HLA B*4001	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.360343	0.623337	-3.737007	22926.799339
HLA B*1801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.449950	0.712902	-3.737048	28180.613166
HLA B*3801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.532911	0.795837	-3.737074	34112.280477
HLA B*3501	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.315901	0.578823	-3.737078	20696.674602
HLA B*1801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.492307	0.755176	-3.737130	31067.546287
HLA B*4501	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.567805	0.830662	-3.737144	36966.242240
HLA A*2902	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.417248	0.680074	-3.737174	26136.531713
HLA A*2601	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.391667	0.654485	-3.737182	24641.478605
HLA B*4002	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.610441	0.873256	-3.737185	40779.454261
HLA A*6802	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.406870	0.669685	-3.737186	25519.389552
HLA B*3801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.469522	0.732333	-3.737189	29479.604215
HLA B*5701	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.394573	0.657361	-3.737212	24806.933186
HLA B*0801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.363163	0.625924	-3.737239	23076.121235
HLA B*5701	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.329741	0.592477	-3.737265	21366.893620
HLA B*0702	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.420401	0.682948	-3.737453	26326.975275
HLA B*0702	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.360839	0.623337	-3.737502	22952.984916
HLA B*5401	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.534981	0.797462	-3.737519	34275.251498
HLA A*3002	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.533733	0.796188	-3.737545	34176.931945
HLA B*0702	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.363536	0.625924	-3.737612	23095.979216
HLA A*3001	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-3.850012	0.112336	-3.737676	7079.650079
HLA A*2902	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.447054	0.709300	-3.737753	27993.262937
HLA B*1501	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.383718	0.645932	-3.737787	24194.600543
HLA A*6901	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.278292	0.540402	-3.737890	18979.832055
HLA A*0216	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.427261	0.689311	-3.737950	26746.161446
HLA A*6801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.471091	0.733042	-3.738049	29586.330512
HLA B*4002	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.626035	0.887960	-3.738075	42270.262168
HLA A*0211	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.141982	0.403854	-3.738128	13866.992921
HLA B*4403	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.636344	0.898050	-3.738294	43285.703633
HLA A*6901	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.374274	0.635971	-3.738302	23674.102659
HLA A*0250	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.290855	0.552387	-3.738468	19536.873367
HLA B*4002	1:344-352	9	VVVTIAINT	1.075829	-0.182028	-4.632322	0.893801	-3.738521	42886.653921
HLA A*3201	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.502915	0.764363	-3.738552	31835.734843
HLA A*2402	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.531950	0.793337	-3.738613	34036.885564
HLA B*1517	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.502985	0.764363	-3.738623	31840.902096

HLA A*6901	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.393149	0.654485	-3.738664	24725.739480
HLA B*4001	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.374659	0.635971	-3.738687	23695.116159
HLA B*4001	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.405259	0.666540	-3.738718	25424.857924
HLA B*5101	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.503932	0.765110	-3.738822	31910.396892
HLA B*0802	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.494010	0.755176	-3.738834	31189.637749
HLA B*5401	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.535032	0.796188	-3.738845	34279.331098
HLA B*3901	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.461822	0.722962	-3.738861	28961.589005
HLA A*0201	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.384837	0.645932	-3.738905	24256.984522
HLA B*5701	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.393234	0.654207	-3.739027	24730.555435
HLA A*3101	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.375782	0.636741	-3.739041	23756.469293
HLA A*0201	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.396441	0.657361	-3.739080	24913.854140
HLA A*6802	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.436502	0.697387	-3.739115	27321.339395
HLA B*4801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.429766	0.690572	-3.739194	26900.850616
HLA B*4601	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.405768	0.666540	-3.739228	25454.722859
HLA A*3201	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.025044	0.285730	-3.739313	10593.603800
HLA A*6802	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.430219	0.690866	-3.739353	26928.952694
HLA B*3901	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.437289	0.697848	-3.739441	27370.899105
HLA B*1509	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.325472	0.586005	-3.739467	21157.890908
HLA A*0206	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-3.954357	0.214737	-3.739620	9002.375430
HLA A*2601	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.377039	0.637402	-3.739637	23825.327020
HLA A*3001	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.142772	0.403047	-3.739725	13892.222192
HLA A*2301	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.536050	0.796188	-3.739862	34359.723937
HLA B*1502	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.587555	0.847664	-3.739891	38686.111220
HLA A*0201	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.394397	0.654485	-3.739912	24796.870021
HLA B*0803	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.486689	0.746693	-3.739997	30668.274049
HLA B*0803	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.504369	0.764363	-3.740006	31942.522550
HLA A*3201	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.166140	0.426123	-3.740016	14660.193366
HLA B*4402	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.402514	0.662443	-3.740072	25264.711087
HLA B*4601	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.363478	0.623337	-3.740141	23092.855761
HLA B*4402	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.406708	0.666540	-3.740168	25509.865392
HLA A*2403	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.332840	0.592477	-3.740364	21519.905432
HLA B*4801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.435769	0.695361	-3.740407	27275.263002
HLA A*0250	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.537332	0.796898	-3.740434	34461.365712
HLA B*4801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.403005	0.662443	-3.740563	25293.293213
HLA A*3101	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.335526	0.594934	-3.740591	21653.386101
HLA B*5401	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.524450	0.783751	-3.740699	33454.169915
HLA A*2603	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.473036	0.732333	-3.740703	29719.156439
HLA B*4403	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.571409	0.830662	-3.740748	37274.293033
HLA B*0801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.340650	0.599665	-3.740985	21910.386906
HLA A*2601	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.398360	0.657361	-3.740999	25024.214081
HLA A*0301	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.333515	0.592477	-3.741038	21553.344011
HLA B*1503	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.416278	0.675193	-3.741085	26078.200461
HLA A*3101	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.206518	0.465424	-3.741094	16088.588651
HLA B*4403	1:172-180	9	QTAAVIGTA	1.111745	-0.223785	-4.629085	0.887960	-3.741125	42568.130071
HLA B*5801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.353168	0.612002	-3.741167	22551.119314
HLA B*7301	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.438567	0.697387	-3.741180	27451.569754
HLA B*1501	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.336177	0.594934	-3.741242	21685.858876
HLA A*0301	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.355116	0.613866	-3.741250	22652.483660
HLA B*5701	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.424221	0.682948	-3.741273	26559.581538
HLA A*1101	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.472120	0.730675	-3.741445	29656.519377
HLA A*0250	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.541465	0.799991	-3.741474	34790.865167
HLA A*3002	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.114869	0.373369	-3.741500	13027.744630
HLA A*6901	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.326046	0.584529	-3.741517	21185.838039
HLA A*2403	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.416755	0.675193	-3.741562	26106.855468
HLA B*5801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.357968	0.616392	-3.741576	22801.745846
HLA B*4002	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.640571	0.898882	-3.741689	43709.033671
HLA A*8001	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.417020	0.675193	-3.741827	26122.819924
HLA B*2705	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.463913	0.722004	-3.741909	29101.369540
HLA B*1503	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.345276	0.603309	-3.741968	22145.025394
HLA A*3201	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.571522	0.829510	-3.742013	37283.973480
HLA A*2301	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.497330	0.755176	-3.742154	31428.970331
HLA B*1501	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.156324	0.414162	-3.742161	14332.552798
HLA B*0801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-3.874324	0.132130	-3.742194	7487.283255
HLA B*4801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.425234	0.682948	-3.742286	26621.581765
HLA A*3001	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.300918	0.558588	-3.742329	19994.838736

HLA A*6801	1:95-103	9	VDGVTLRDI	0.912845	0.031432	-4.686633	0.944277	-3.742355	48599.618328
HLA B*4501	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.538566	0.796188	-3.742378	34559.381726
HLA A*3201	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.164439	0.421976	-3.742463	14602.885215
HLA A*2602	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.586629	0.844164	-3.742465	38603.739735
HLA B*0801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.335944	0.593391	-3.742553	21674.247495
HLA A*0203	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.168724	0.426123	-3.742601	14747.694485
HLA B*3801	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.550616	0.807959	-3.742658	35531.739779
HLA B*4801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.422736	0.680074	-3.742662	26468.928065
HLA A*0219	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.295216	0.552387	-3.742829	19734.026437
HLA A*8001	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.438297	0.695361	-3.742936	27434.496421
HLA B*4403	1:242-250	9	GLSADLDAV	0.926669	-0.008507	-4.661160	0.918162	-3.742998	45831.043146
HLA A*0212	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.366403	0.623337	-3.743066	23248.918324
HLA A*2902	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.389009	0.645932	-3.743078	24491.167946
HLA A*3001	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.283964	0.540737	-3.743227	19229.324220
HLA A*3201	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.575086	0.831818	-3.743269	37591.214671
HLA A*6901	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.264318	0.521039	-3.743279	18378.820172
HLA A*2603	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.637888	0.894591	-3.743297	43439.827625
HLA B*0801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.348822	0.605498	-3.743323	22326.546730
HLA B*4402	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.369311	0.625924	-3.743387	23405.149213
HLA A*2602	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.583291	0.839877	-3.743414	38308.113084
HLA A*3002	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.165425	0.421976	-3.743450	14636.102935
HLA B*4402	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.434023	0.690572	-3.743452	27165.848828
HLA A*0203	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.254194	0.510481	-3.743713	17955.342657
HLA B*4002	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.603891	0.860149	-3.743742	40169.002320
HLA B*1509	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.527145	0.783381	-3.743764	33662.403209
HLA B*5401	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.518438	0.774481	-3.743956	32994.224587
HLA B*4501	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.632346	0.888375	-3.743970	42888.974105
HLA A*2403	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.367321	0.623337	-3.743985	23298.148034
HLA B*1801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.455942	0.711889	-3.744053	28572.064720
HLA A*3201	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.295054	0.550986	-3.744068	19726.661448
HLA A*0206	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.398292	0.654207	-3.744085	25020.288420
HLA A*3101	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.401485	0.657361	-3.744124	25204.916430
HLA A*2301	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.541686	0.797462	-3.744224	34808.561850
HLA B*2705	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.470203	0.725976	-3.744227	29525.890117
HLA A*1101	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.439643	0.695361	-3.744282	27519.671644
HLA A*3101	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.380323	0.635971	-3.744352	24006.201683
HLA B*5801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.362258	0.617889	-3.744370	23028.108139
HLA B*1509	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.435240	0.690866	-3.744374	27242.083066
HLA B*3901	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.435304	0.690866	-3.744438	27246.062526
HLA B*4001	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.414184	0.669685	-3.744500	25952.800496
HLA A*0203	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.324417	0.579907	-3.744511	21106.559908
HLA B*3801	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.477533	0.732827	-3.744706	30028.482973
HLA B*2705	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.398915	0.654207	-3.744708	25056.183746
HLA B*4801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.435715	0.690866	-3.744849	27271.869422
HLA A*3301	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.560172	0.815296	-3.744876	36322.173480
HLA B*5701	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.368221	0.623337	-3.744884	23346.471552
HLA B*7301	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.526722	0.781690	-3.745032	33629.639387
HLA A*2402	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.592827	0.847787	-3.745040	39158.614778
HLA A*0301	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.319328	0.574191	-3.745137	20860.680440
HLA B*5801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.358722	0.613540	-3.745182	22841.377176
HLA A*0250	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.536656	0.791452	-3.745204	34407.715053
HLA A*2301	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.543932	0.798696	-3.745236	34989.052985
HLA B*5701	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.203830	0.458556	-3.745274	15989.325255
HLA A*0301	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.337436	0.592081	-3.745355	21748.832632
HLA B*3901	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.492182	0.746693	-3.745490	31058.639749
HLA A*0202	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.495904	0.750403	-3.745501	31325.933063
HLA B*5801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.351002	0.605498	-3.745503	22438.916247
HLA B*0801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.359047	0.613540	-3.745507	22858.436109
HLA A*0301	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.363414	0.617889	-3.745526	23089.482903
HLA B*4501	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.598969	0.853416	-3.745553	39716.308384
HLA A*2601	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.211076	0.465424	-3.745652	16258.330542
HLA A*2501	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.164270	0.418508	-3.745762	14597.198324
HLA B*4801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.412314	0.666540	-3.745774	25841.280974
HLA A*3101	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.345452	0.599665	-3.745788	22154.012377
HLA A*0301	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.359465	0.613540	-3.745925	22880.458476

HLA A*3301	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-3.957313	0.211378	-3.745935	9063.851315
HLA A*0250	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.460991	0.714935	-3.746055	28906.177720
HLA B*5801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.362648	0.616515	-3.746133	23048.797627
HLA B*3801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.478269	0.732039	-3.746230	30079.373136
HLA B*5101	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.496675	0.750403	-3.746272	31381.568512
HLA A*6901	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.234738	0.488312	-3.746426	17168.707917
HLA B*7301	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.575937	0.829510	-3.746427	37664.904682
HLA B*4403	1:97-105	9	GVTLRDIVH	1.240170	-0.325290	-4.661345	0.914880	-3.746466	45850.634660
HLA B*5301	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.479418	0.732827	-3.746591	30159.051532
HLA A*3301	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.609516	0.862842	-3.746674	40692.625575
HLA B*0803	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.502067	0.755176	-3.746890	31773.621281
HLA A*3201	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.594747	0.847787	-3.746960	39332.074187
HLA B*7301	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.173085	0.426123	-3.746961	14896.518363
HLA B*5801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.268779	0.521798	-3.746981	18568.605968
HLA B*1509	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.469009	0.722004	-3.747005	29444.857765
HLA A*0101	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.360931	0.613866	-3.747064	22957.828178
HLA B*5701	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.392999	0.645932	-3.747067	24717.180097
HLA B*1502	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.480209	0.733042	-3.747168	30214.085635
HLA A*0301	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.346907	0.599665	-3.747242	22228.324347
HLA B*5801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.350555	0.603309	-3.747247	22415.863608
HLA A*3301	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.622316	0.875034	-3.747282	41909.811420
HLA B*1501	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.422485	0.675193	-3.747292	26453.610744
HLA B*0702	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.456609	0.709300	-3.747309	28615.996824
HLA B*1517	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.271519	0.524138	-3.747380	18686.105648
HLA B*1509	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.459294	0.711889	-3.747405	28793.492140
HLA A*2501	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.437989	0.690572	-3.747417	27415.060605
HLA A*0101	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.363901	0.616392	-3.747508	23115.354075
HLA B*0803	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.478226	0.730675	-3.747552	30076.444209
HLA B*5701	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.422750	0.675193	-3.747558	26469.787243
HLA B*4002	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.529004	0.781429	-3.747575	33806.760764
HLA A*3002	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.529276	0.781690	-3.747586	33827.982759
HLA B*4002	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.479723	0.732039	-3.747684	30180.269418
HLA B*4801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.437021	0.689311	-3.747710	27354.023927
HLA A*3201	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.166267	0.418508	-3.747759	14664.476733
HLA A*8001	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.459710	0.711889	-3.747821	28821.076564
HLA B*5401	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.252314	0.504447	-3.747867	17877.801443
HLA A*2301	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.543742	0.795837	-3.747905	34973.724105
HLA B*4002	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.621416	0.873492	-3.747924	41823.064713
HLA A*2602	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.574473	0.826538	-3.747935	37538.174043
HLA A*6802	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.353438	0.605498	-3.747940	22565.153571
HLA B*5401	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.333975	0.586005	-3.747970	21576.209967
HLA A*8001	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.457318	0.709300	-3.748018	28662.787466
HLA B*1801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.423277	0.675193	-3.748084	26501.883176
HLA A*8001	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.437423	0.689311	-3.748112	27379.340598
HLA B*1501	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.414680	0.666540	-3.748140	25982.442185
HLA B*5301	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.470205	0.722004	-3.748201	29526.049849
HLA A*2601	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.348056	0.599665	-3.748391	22287.205801
HLA B*1502	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.539877	0.791452	-3.748425	34663.864381
HLA B*5701	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.415028	0.666540	-3.748487	26003.253711
HLA A*0212	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.428587	0.680074	-3.748512	26827.893357
HLA A*0202	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.474535	0.725976	-3.748559	29821.909608
HLA B*1509	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.503072	0.754459	-3.748613	31847.276197
HLA A*2301	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.540126	0.791452	-3.748674	34683.748014
HLA A*0201	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.386077	0.637402	-3.748675	24326.371746
HLA A*0211	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.544578	0.795837	-3.748741	35041.145622
HLA A*1101	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.458174	0.709300	-3.748873	28719.285827
HLA A*2501	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.479589	0.730675	-3.748914	30170.964354
HLA A*0212	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.335028	0.586005	-3.749023	21628.566144
HLA B*4402	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-3.889624	0.140490	-3.749134	7755.755505
HLA A*3201	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.593513	0.844164	-3.749349	39220.522042
HLA B*4403	1:72-80	9	VAVYDTGEA	1.038007	-0.143977	-4.643388	0.894030	-3.749358	43993.471944
HLA B*3501	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.202082	0.452683	-3.749399	15925.098243
HLA B*1503	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.411844	0.662443	-3.749402	25813.336401
HLA B*0802	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.464355	0.714935	-3.749420	29130.982411
HLA A*1101	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.472397	0.722962	-3.749436	29675.457162

HLA A*0202	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.546900	0.797462	-3.749438	35228.940944
HLA A*2403	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.365867	0.616392	-3.749475	23220.259514
HLA A*6901	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-3.922070	0.172544	-3.749527	8357.386700
HLA B*3901	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.440104	0.690572	-3.749532	27548.867281
HLA B*5701	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.385513	0.635971	-3.749542	24294.807528
HLA B*3901	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.471636	0.722004	-3.749632	29623.487459
HLA A*2601	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.366257	0.616515	-3.749742	23241.121639
HLA A*2301	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.524319	0.774481	-3.749837	33444.036383
HLA B*0801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.324450	0.574537	-3.749913	21108.158546
HLA B*0702	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.412387	0.662443	-3.749944	25845.615089
HLA B*5101	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.461879	0.711889	-3.749990	28965.349545
HLA A*2902	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.373404	0.623337	-3.750067	23626.762573
HLA B*4601	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.387593	0.637402	-3.750191	24411.403933
HLA B*4002	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.425511	0.675193	-3.750318	26638.581527
HLA A*2501	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.463241	0.712902	-3.750339	29056.377893
HLA A*3002	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.558349	0.807959	-3.750390	36170.009930
HLA B*5401	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.549209	0.798791	-3.750418	35416.784696
HLA A*0301	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.283454	0.532852	-3.750603	19206.763278
HLA A*3201	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.537469	0.786863	-3.750605	34472.180474
HLA B*2705	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.462508	0.711889	-3.750619	29007.375424
HLA A*6802	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.164791	0.414162	-3.750629	14614.740023
HLA A*6901	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.311794	0.561125	-3.750669	20501.879275
HLA B*1502	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.523579	0.772678	-3.750901	33387.092429
HLA A*2501	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.325099	0.574191	-3.750908	21139.699300
HLA B*4501	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.649833	0.898882	-3.750951	44651.173265
HLA B*1501	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.405498	0.654485	-3.751013	25438.891453
HLA B*5101	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.515567	0.764363	-3.751204	32776.822978
HLA A*0301	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.367601	0.616392	-3.751209	23313.151670
HLA A*3101	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.170012	0.418508	-3.751504	14791.480657
HLA A*0202	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.534922	0.783381	-3.751541	34270.616179
HLA B*0801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.260258	0.508438	-3.751820	18207.810230
HLA B*5301	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.533564	0.781690	-3.751874	34163.622211
HLA A*2501	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.473880	0.722004	-3.751876	29776.931591
HLA B*0702	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.449311	0.697387	-3.751924	28139.176174
HLA B*5701	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.292328	0.540402	-3.751926	19603.254970
HLA B*5101	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.449835	0.697848	-3.751987	28173.143910
HLA B*1517	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.247683	0.495678	-3.752005	17688.185112
HLA B*1801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.475144	0.722962	-3.752182	29863.724201
HLA B*5401	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.447599	0.695361	-3.752237	28028.419179
HLA A*2301	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.539139	0.786863	-3.752276	34605.030680
HLA B*3801	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.536045	0.783751	-3.752294	34359.352174
HLA A*3002	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.582969	0.830662	-3.752307	38279.731361
HLA B*3901	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.427522	0.675193	-3.752329	26762.227277
HLA B*7301	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.585544	0.833148	-3.752396	38507.375228
HLA B*4002	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.571797	0.819348	-3.752449	37307.580104
HLA A*2601	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.256983	0.504447	-3.752535	18071.014578
HLA B*4801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.422243	0.669685	-3.752558	26438.874407
HLA A*3101	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.303646	0.550986	-3.752660	20120.819165
HLA B*1503	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.018883	0.266144	-3.752739	10444.397127
HLA A*3002	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.525479	0.772678	-3.752801	33533.534614
HLA B*0702	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.427995	0.675193	-3.752802	26791.344022
HLA A*3002	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.539666	0.786863	-3.752802	34646.991000
HLA B*1501	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.327627	0.574537	-3.753090	21263.113200
HLA B*5101	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.483802	0.730675	-3.753127	30465.044607
HLA A*0212	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.410721	0.657361	-3.753360	25746.671230
HLA B*3901	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.061287	0.307875	-3.753412	11515.608244
HLA B*4002	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.641842	0.888375	-3.753467	43837.146473
HLA B*4001	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.407982	0.654485	-3.753497	25584.774166
HLA B*2705	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.436462	0.682948	-3.753514	27318.826819
HLA A*6801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.407737	0.654207	-3.753530	25570.383492
HLA A*2601	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.389524	0.635971	-3.753553	24520.201438
HLA B*0803	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.286440	0.532852	-3.753589	19339.283469
HLA A*0203	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.433690	0.680074	-3.753615	27144.987921
HLA A*6901	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.296073	0.542449	-3.753624	19773.031932
HLA A*0201	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.390372	0.636741	-3.753631	24568.135447

HLA B*3501	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.462945	0.709300	-3.753645	29036.578477
HLA B*5401	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.504184	0.750403	-3.753781	31928.873832
HLA A*3002	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.222283	0.468482	-3.753801	16683.339678
HLA B*5401	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.540681	0.786863	-3.753817	34728.058209
HLA A*2301	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.486727	0.732827	-3.753900	30670.928755
HLA B*1801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.500648	0.746693	-3.753955	31669.968092
HLA B*3801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.528442	0.774481	-3.753961	33763.078103
HLA B*4403	1:286-294	9	KVLTDAERT	1.160173	-0.255583	-4.658672	0.904590	-3.754082	45569.224477
HLA A*2301	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.545112	0.790996	-3.754116	35084.204153
HLA B*2705	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.477115	0.722962	-3.754154	29999.580655
HLA B*3801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.550689	0.796188	-3.754502	35537.699185
HLA B*4801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.400447	0.645932	-3.754515	25144.719164
HLA B*3801	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.519636	0.765110	-3.754526	33085.382783
HLA B*7301	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.518948	0.764421	-3.754527	33032.980767
HLA A*3301	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.553323	0.798791	-3.754532	35753.871880
HLA A*3001	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.297337	0.542619	-3.754718	19830.665575
HLA A*2402	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.528602	0.773768	-3.754833	33775.500894
HLA B*0801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.392245	0.637402	-3.754843	24674.294122
HLA B*5101	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.480957	0.725976	-3.754980	30266.109015
HLA A*0219	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.378348	0.623337	-3.755011	23897.228351
HLA A*2603	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.536717	0.781690	-3.755027	34412.555084
HLA A*0211	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.381174	0.625924	-3.755250	24053.261010
HLA A*0101	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.360773	0.605498	-3.755275	22949.508332
HLA B*3901	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.486001	0.730675	-3.755326	30619.700351
HLA A*0250	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.446283	0.690866	-3.755417	27943.634514
HLA A*8001	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.425149	0.669685	-3.755465	26616.397556
HLA A*3101	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.392886	0.637402	-3.755484	24710.762504
HLA B*3501	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.430901	0.675193	-3.755708	26971.233820
HLA B*5801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.349273	0.593391	-3.755882	22349.749334
HLA B*0802	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.467816	0.711889	-3.755927	29364.047802
HLA B*4402	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.425657	0.669685	-3.755972	26647.517956
HLA A*0211	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.224477	0.468482	-3.755995	16767.851196
HLA A*3101	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.399086	0.643088	-3.755998	25066.080936
HLA B*4001	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.401939	0.645932	-3.756007	25231.246843
HLA B*0702	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.413515	0.657361	-3.756153	25912.816823
HLA B*0801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.170326	0.414162	-3.756164	14802.207261
HLA A*0201	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.399267	0.643088	-3.756179	25076.524674
HLA A*1101	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.379656	0.623337	-3.756319	23969.346669
HLA B*0801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.426047	0.669685	-3.756362	26671.459284
HLA B*7301	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.587078	0.830662	-3.756416	38643.649163
HLA B*4402	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.393189	0.636741	-3.756448	24728.013564
HLA B*1801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.478515	0.722004	-3.756511	30096.464227
HLA A*0211	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.488884	0.732333	-3.756551	30823.627981
HLA A*2501	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.431789	0.675193	-3.756596	27026.444756
HLA B*4002	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.610143	0.853416	-3.756727	40751.446119
HLA B*4402	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.402754	0.645932	-3.756822	25278.656221
HLA B*1509	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.521943	0.765110	-3.756833	33261.616956
HLA B*5401	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.414217	0.657361	-3.756856	25954.766196
HLA A*3002	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.411151	0.654207	-3.756944	25772.173306
HLA A*2602	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.447573	0.690572	-3.757001	28026.751291
HLA B*3501	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.281170	0.524138	-3.757032	19106.031276
HLA B*1501	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.400123	0.643088	-3.757035	25125.954010
HLA B*1517	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.402972	0.645932	-3.757041	25291.377610
HLA B*1502	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.573731	0.816673	-3.757058	37474.056418
HLA A*2301	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.529739	0.772678	-3.757061	33864.054087
HLA B*0802	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.479072	0.722004	-3.757068	30135.076968
HLA B*3501	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.394484	0.637402	-3.757082	24801.834005
HLA A*0203	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.400325	0.643088	-3.757237	25137.646592
HLA A*0211	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.521633	0.764363	-3.757270	33237.873136
HLA B*0802	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.448219	0.690866	-3.757353	28068.478267
HLA B*1501	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.393344	0.635971	-3.757373	24736.844344
HLA B*1801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.490451	0.733042	-3.757409	30935.052750
HLA B*5701	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.308415	0.550986	-3.757430	20343.005308
HLA A*3002	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.331630	0.574191	-3.757439	21460.032420
HLA B*1502	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.469385	0.711889	-3.757496	29470.355745

HLA B*0802	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.411745	0.654207	-3.757538	25807.471881
HLA B*1501	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.350170	0.592477	-3.757693	22395.984584
HLA B*1501	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.176214	0.418508	-3.757707	15004.249951
HLA A*3002	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.605437	0.847664	-3.757773	40312.247004
HLA B*0802	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.483788	0.725976	-3.757812	30464.055748
HLA B*7301	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.589634	0.831818	-3.757817	38871.774823
HLA A*6901	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.371778	0.613866	-3.757912	23538.477759
HLA A*3101	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.412138	0.654207	-3.757931	25830.798215
HLA A*2301	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.541322	0.783381	-3.757941	34779.385963
HLA B*3801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.544823	0.786863	-3.757959	35060.866315
HLA B*4601	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.403898	0.645932	-3.757966	25345.343583
HLA B*5801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.352959	0.594934	-3.758025	22540.264012
HLA B*4501	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.541428	0.783381	-3.758046	34787.853861
HLA B*7301	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.566020	0.807959	-3.758061	36814.566974
HLA A*2402	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.581745	0.823629	-3.758116	38171.989847
HLA B*4801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.433403	0.675193	-3.758210	27127.077964
HLA B*4402	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.441182	0.682948	-3.758234	27617.359955
HLA A*2301	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.539938	0.781690	-3.758248	34668.740444
HLA B*5801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.357949	0.599665	-3.758284	22800.759028
HLA B*5101	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.441283	0.682948	-3.758335	27623.785197
HLA A*3002	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.558393	0.799991	-3.758402	36173.727960
HLA A*0202	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.554672	0.796188	-3.758484	35865.070095
HLA B*0802	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.456339	0.697848	-3.758490	28598.199283
HLA A*3101	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.361939	0.603309	-3.758630	23011.171557
HLA B*4402	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.438823	0.680074	-3.758749	27467.762112
HLA B*4402	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.413306	0.654485	-3.758821	25900.343319
HLA A*2601	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.401922	0.643088	-3.758834	25230.291374
HLA B*1502	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.588204	0.829345	-3.758858	38743.917736
HLA B*1517	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.449758	0.690866	-3.758892	28168.114711
HLA A*0206	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.254682	0.495678	-3.759005	17975.558403
HLA A*8001	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.441969	0.682948	-3.759021	27667.456633
HLA A*0216	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.254753	0.495678	-3.759075	17978.476013
HLA B*1501	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.338989	0.579907	-3.759082	21826.744302
HLA A*2601	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.395912	0.636741	-3.759171	24883.546822
HLA A*2601	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.372798	0.613540	-3.759258	23593.808490
HLA A*0219	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.448585	0.689311	-3.759274	28092.176453
HLA A*2301	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.524422	0.765110	-3.759312	33451.998185
HLA A*0301	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.362752	0.603309	-3.759443	23054.284703
HLA A*0202	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.583084	0.823629	-3.759455	38289.880072
HLA A*2402	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.585995	0.826538	-3.759457	38547.393569
HLA A*0219	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.405446	0.645932	-3.759515	25435.863958
HLA A*0212	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.429219	0.669685	-3.759534	26866.963343
HLA A*6802	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.395534	0.635971	-3.759563	24861.882884
HLA A*0212	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.426162	0.666540	-3.759622	26678.530413
HLA A*2602	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.543159	0.783381	-3.759778	34926.832983
HLA B*0802	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.450399	0.690572	-3.759827	28209.746928
HLA A*0206	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.122688	0.362756	-3.759932	13264.421778
HLA B*4801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.395910	0.635971	-3.759939	24883.412205
HLA A*0301	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.353335	0.593391	-3.759944	22559.782911
HLA A*0211	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.530169	0.770046	-3.760123	33897.596430
HLA B*5701	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.414633	0.654485	-3.760148	25979.631095
HLA B*5401	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.541604	0.781429	-3.760175	34801.971608
HLA B*0803	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.492232	0.732039	-3.760193	31062.168449
HLA B*0801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.355130	0.594934	-3.760195	22653.218957
HLA A*6801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.422739	0.662443	-3.760296	26469.071259
HLA B*1517	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.352851	0.592477	-3.760374	22534.655454
HLA A*6901	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.378430	0.617889	-3.760541	23901.753627
HLA A*2602	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.608320	0.847664	-3.760656	40580.727129
HLA B*1801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.458051	0.697387	-3.760664	28711.207820
HLA B*5301	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.591368	0.830662	-3.760707	39027.280535
HLA B*3901	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.303202	0.542449	-3.760752	20100.256764
HLA A*0202	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.587377	0.826538	-3.760838	38670.208634
HLA B*1502	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.544256	0.783381	-3.760875	35015.184330
HLA B*2705	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.456261	0.695361	-3.760900	28593.094207
HLA B*0702	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.441161	0.680074	-3.761087	27616.015326

HLA A*0212	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.397092	0.635971	-3.761120	24951.216517
HLA A*2602	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.576428	0.815296	-3.761132	37707.515225
HLA B*4501	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.569227	0.807959	-3.761268	37087.430335
HLA A*2402	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.569260	0.807959	-3.761301	37090.239386
HLA B*0801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.398123	0.636741	-3.761382	25010.544615
HLA A*0201	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.387372	0.625924	-3.761448	24398.993168
HLA A*0216	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.474355	0.712902	-3.761452	29809.489537
HLA B*4601	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.364765	0.603309	-3.761457	23161.418867
HLA A*0202	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.470788	0.709300	-3.761488	29565.690134
HLA B*0803	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.484493	0.722962	-3.761531	30513.538040
HLA B*1509	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.354984	0.593391	-3.761593	22645.622044
HLA A*3101	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.387534	0.625924	-3.761610	24408.102581
HLA B*4801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.419151	0.657361	-3.761790	26251.313565
HLA A*2402	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.557977	0.796188	-3.761790	36139.106371
HLA A*0203	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.428340	0.666540	-3.761799	26812.658412
HLA B*2705	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.459240	0.697387	-3.761853	28789.909662
HLA A*0216	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.399444	0.637402	-3.762041	25086.701330
HLA A*3201	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.577490	0.815296	-3.762194	37799.833102
HLA B*5101	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.494553	0.732333	-3.762220	31228.639317
HLA A*0101	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.355628	0.593391	-3.762237	22679.214759
HLA A*6801	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.660297	0.898050	-3.762247	45740.139121
HLA B*4001	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.336569	0.574191	-3.762378	21705.459850
HLA B*4001	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.378911	0.616515	-3.762396	23928.276028
HLA B*5401	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.477345	0.714935	-3.762410	30015.489724
HLA A*6901	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.367956	0.605498	-3.762457	23332.203808
HLA B*5301	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.561267	0.798791	-3.762476	36413.857502
HLA B*1517	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.471855	0.709300	-3.762554	29638.395369
HLA A*0101	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-3.844678	0.082090	-3.762589	6993.240462
HLA B*1502	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.559542	0.796898	-3.762644	36269.549924
HLA B*5301	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.592085	0.829345	-3.762740	39091.729336
HLA A*3001	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.305201	0.542449	-3.762752	20193.007982
HLA B*1801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.242538	0.479739	-3.762799	17479.858088
HLA B*4002	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.625704	0.862842	-3.762862	42238.030945
HLA B*3501	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.432574	0.669685	-3.762889	27075.323065
HLA A*2402	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.518111	0.755176	-3.762935	32969.423095
HLA B*4801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.341775	0.578823	-3.762952	21967.237729
HLA A*3001	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.257093	0.494046	-3.763047	18075.609985
HLA A*2603	1:387-395	9	LQKPDSTIP	0.816382	0.081668	-4.661103	0.898050	-3.763053	45825.092951
HLA B*0702	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.341909	0.578823	-3.763086	21974.012671
HLA B*4601	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.417600	0.654485	-3.763116	26157.749681
HLA A*3001	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.231768	0.468482	-3.763286	17051.707065
HLA A*0201	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.355471	0.592081	-3.763389	22670.995882
HLA A*3002	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.496440	0.733042	-3.763398	31364.596023
HLA A*0301	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.368964	0.605498	-3.763465	23386.417062
HLA B*5401	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.560393	0.796898	-3.763494	36340.649077
HLA B*1503	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.071371	0.307875	-3.763496	11786.120354
HLA A*2501	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.458890	0.695361	-3.763529	28766.712230
HLA B*1801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.454149	0.690572	-3.763577	28454.369586
HLA A*3301	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.518055	0.754459	-3.763596	32965.142710
HLA A*0250	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.475525	0.711889	-3.763635	29889.908302
HLA A*6802	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.314655	0.550986	-3.763670	20637.417236
HLA A*2603	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.593025	0.829345	-3.763679	39176.413698
HLA B*4402	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.454588	0.690866	-3.763722	28483.169994
HLA B*4601	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.406819	0.643088	-3.763731	25516.352477
HLA B*2705	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.172765	0.409024	-3.763741	14885.562356
HLA A*0216	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.342577	0.578823	-3.763754	22007.799680
HLA A*2402	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.554761	0.790996	-3.763765	35872.443843
HLA A*0250	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.557122	0.793337	-3.763785	36068.011279
HLA A*3201	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.560040	0.796188	-3.763853	36311.171207
HLA B*7301	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.590508	0.826538	-3.763970	38950.082214
HLA B*4403	1:484-492	9	VIIIVGSGP	0.721868	0.177014	-4.662854	0.898882	-3.763972	46010.157601
HLA A*3002	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.444049	0.680074	-3.763974	27800.239162
HLA A*0206	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.222631	0.458556	-3.764075	16696.702769
HLA A*0301	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.338625	0.574537	-3.764088	21808.449532
HLA B*5401	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.461980	0.697848	-3.764131	28972.088400

HLA B*4403	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.612025	0.847664	-3.764361	40928.418386
HLA A*0211	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.418620	0.654207	-3.764413	26219.237405
HLA A*6901	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.376444	0.612002	-3.764443	23792.739555
HLA A*6901	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.378040	0.613540	-3.764500	23880.298493
HLA A*3101	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.381024	0.616515	-3.764508	24044.934421
HLA A*0211	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.144872	0.380356	-3.764516	13959.573844
HLA A*0201	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.343359	0.578823	-3.764536	22047.482312
HLA B*5801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.350645	0.586005	-3.764640	22420.472240
HLA A*3001	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.173442	0.408742	-3.764700	14908.772855
HLA A*1101	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.434653	0.669685	-3.764968	27205.263808
HLA A*0211	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.462382	0.697387	-3.764994	28998.902620
HLA A*1101	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.440193	0.675193	-3.765000	27554.531244
HLA B*0801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.351126	0.586005	-3.765121	22445.350948
HLA B*5401	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.548605	0.783381	-3.765224	35367.577486
HLA B*5301	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.598379	0.833148	-3.765232	39662.414915
HLA A*2603	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.448249	0.682948	-3.765301	28070.452352
HLA B*4801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.298265	0.532852	-3.765414	19873.087157
HLA B*4403	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.488489	0.722962	-3.765528	30795.626303
HLA A*0101	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.379132	0.613540	-3.765592	23940.447359
HLA B*4402	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.388941	0.623337	-3.765604	24487.325907
HLA B*3801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.564530	0.798791	-3.765739	36688.514102
HLA B*1509	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.318161	0.552387	-3.765774	20804.667352
HLA A*0101	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.358271	0.592477	-3.765794	22817.664184
HLA B*1501	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.382189	0.616392	-3.765797	24109.540955
HLA A*1101	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.357942	0.592081	-3.765861	22800.388982
HLA A*3002	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.455251	0.689311	-3.765940	28526.656760
HLA B*1509	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.488964	0.722962	-3.766002	30829.298084
HLA A*6901	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.290174	0.524138	-3.766035	19506.246625
HLA A*2403	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.308507	0.542449	-3.766057	20347.297844
HLA A*2603	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.597909	0.831818	-3.766092	39619.524269
HLA B*3801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.549670	0.783381	-3.766288	35454.358385
HLA A*6901	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.270866	0.504447	-3.766418	18658.023817
HLA A*0216	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.436114	0.669685	-3.766430	27296.962383
HLA A*2301	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.520994	0.754459	-3.766535	33188.999910
HLA B*1503	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.457107	0.690572	-3.766535	28648.835238
HLA A*0216	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.402528	0.635971	-3.766557	25265.531176
HLA B*4501	1:191-199	9	DSVDARSDV	0.837527	0.035965	-4.640078	0.873492	-3.766586	43659.405052
HLA B*4601	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.403466	0.636741	-3.766725	25320.126883
HLA B*3801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.531318	0.764421	-3.766897	33987.389063
HLA B*1503	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.447054	0.680074	-3.766979	27993.262937
HLA B*5401	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.307468	0.540402	-3.767066	20298.702099
HLA A*0216	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.447213	0.680074	-3.767139	28003.562782
HLA B*1501	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.379182	0.612002	-3.767180	23943.167332
HLA A*3301	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.640332	0.873123	-3.767209	43684.921300
HLA A*3001	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-3.805564	0.038251	-3.767313	6390.932570
HLA A*0250	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.030870	0.263371	-3.767499	10736.690870
HLA B*4601	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.393443	0.625924	-3.767519	24742.465573
HLA A*0203	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.147908	0.380356	-3.767552	14057.487144
HLA B*0702	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.456865	0.689311	-3.767554	28632.876021
HLA A*0250	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.598222	0.830662	-3.767560	39648.041380
HLA B*4403	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.627750	0.860149	-3.767601	42437.526759
HLA A*0250	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.518029	0.750403	-3.767626	32963.181053
HLA A*0250	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.465520	0.697848	-3.767672	29209.254690
HLA A*2501	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.465123	0.697387	-3.767736	29182.561711
HLA B*0802	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.442940	0.675193	-3.767747	27729.342704
HLA A*2402	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.542276	0.774481	-3.767794	34855.859881
HLA B*1501	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.346202	0.578365	-3.767837	22192.277775
HLA A*3002	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.404713	0.636741	-3.767972	25392.967347
HLA B*1501	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.373696	0.605498	-3.768197	23642.617343
HLA A*2601	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.380255	0.612002	-3.768254	24002.435722
HLA B*5301	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.542062	0.773768	-3.768294	34838.704567
HLA A*0216	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.425666	0.657361	-3.768305	26648.094602
HLA B*1801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.451257	0.682948	-3.768309	28265.505195
HLA B*3901	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.494386	0.725976	-3.768410	31216.646634
HLA A*0211	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.036100	0.267585	-3.768515	10866.768189

HLA A*3301	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.422809	0.654207	-3.768602	26473.367450
HLA A*2402	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.500678	0.732039	-3.768639	31672.195474
HLA A*6901	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.363698	0.594934	-3.768764	23104.602147
HLA B*5301	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.524074	0.755176	-3.768898	33425.225108
HLA A*2402	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.515607	0.746693	-3.768914	32779.837539
HLA A*3001	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.289995	0.521039	-3.768957	19498.228250
HLA A*0301	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.363924	0.594934	-3.768990	23116.604624
HLA B*5801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.353589	0.584529	-3.769060	22572.967722
HLA A*2402	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.585751	0.816673	-3.769078	38525.711808
HLA A*2301	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.308735	0.539629	-3.769106	20357.978079
HLA A*3002	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.257514	0.488312	-3.769202	18093.122344
HLA B*5801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.340486	0.571232	-3.769254	21902.091184
HLA B*5701	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.406142	0.636741	-3.769401	25476.627728
HLA A*3101	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.293646	0.524138	-3.769508	19662.840199
HLA B*5101	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.484681	0.714935	-3.769745	30526.746887
HLA A*2403	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.436328	0.666540	-3.769788	27310.403984
HLA B*1509	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.502187	0.732333	-3.769853	31782.388971
HLA A*2501	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.459186	0.689311	-3.769875	28786.327630
HLA A*1101	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.395837	0.625924	-3.769913	24879.239443
HLA B*3901	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.479220	0.709300	-3.769920	30145.349447
HLA B*0801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.341259	0.571232	-3.770027	21941.108410
HLA B*3801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.492995	0.722962	-3.770034	31116.830428
HLA A*2501	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.450298	0.680074	-3.770224	28203.185392
HLA A*6802	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.173498	0.403047	-3.770451	14910.708696
HLA A*2403	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.407263	0.636741	-3.770522	25542.455501
HLA B*1502	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.600050	0.829510	-3.770540	39815.267445
HLA A*2301	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.445928	0.675193	-3.770735	27920.816868
HLA A*0202	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.567667	0.796898	-3.770768	36954.445110
HLA B*5801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.349428	0.578365	-3.771063	22357.730796
HLA B*1502	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.484030	0.712902	-3.771128	30481.035616
HLA B*4402	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.383368	0.612002	-3.771367	24175.105775
HLA B*4501	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.597909	0.826538	-3.771371	39619.524269
HLA A*1101	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.322404	0.550986	-3.771418	21008.930585
HLA B*4001	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.363501	0.592081	-3.771420	23094.105092
HLA A*2601	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.356058	0.584529	-3.771529	22701.678520
HLA A*3101	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.389491	0.617889	-3.771603	24518.344386
HLA B*7301	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.568524	0.796898	-3.771626	37027.487801
HLA A*8001	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.342929	0.571232	-3.771697	22025.665892
HLA B*4501	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.603593	0.831818	-3.771775	40141.413448
HLA A*6801	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.503862	0.732039	-3.771823	31905.218361
HLA B*7301	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.545593	0.773768	-3.771825	35123.135076
HLA B*4001	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.385701	0.613866	-3.771835	24305.324380
HLA B*3801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.536247	0.764363	-3.771884	34375.341598
HLA B*5301	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.518581	0.746693	-3.771888	33005.114585
HLA A*2602	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.563353	0.791452	-3.771901	36589.209860
HLA B*1503	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.429280	0.657361	-3.771918	26870.742639
HLA A*0101	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.384057	0.612002	-3.772055	24213.456062
HLA A*6801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.518755	0.746693	-3.772062	33018.330227
HLA B*7301	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.167206	0.395099	-3.772107	14696.244370
HLA B*5401	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-3.989064	0.216943	-3.772121	9751.326837
HLA B*4403	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.634979	0.862842	-3.772138	43149.863958
HLA A*8001	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.395560	0.623337	-3.772223	24863.362428
HLA A*0301	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.298117	0.525884	-3.772233	19866.315105
HLA B*1501	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.388838	0.616515	-3.772323	24481.497757
HLA A*0250	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.569809	0.797462	-3.772347	37137.222173
HLA B*5701	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.120813	0.348457	-3.772356	13207.281484
HLA B*4403	1:326-334	9	IGSVGRWVA	1.210483	-0.315892	-4.666984	0.894591	-3.772393	46449.828571
HLA B*5101	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.418364	0.645932	-3.772432	26203.781057
HLA A*8001	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.434907	0.662443	-3.772464	27221.163618
HLA A*0202	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.542591	0.770046	-3.772545	34881.136931
HLA A*3301	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.503230	0.730675	-3.772555	31858.821735
HLA B*4501	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.395952	0.623337	-3.772615	24885.835420
HLA B*1501	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.201246	0.428564	-3.772681	15894.457284
HLA B*2705	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.408705	0.635971	-3.772734	25627.440226
HLA B*2705	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.396074	0.623337	-3.772738	24892.837145

HLA B*3501	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.386326	0.613540	-3.772787	24340.325662
HLA B*4403	1:36-44	9	DVAVKVLRA	1.132205	-0.243830	-4.661204	0.888375	-3.772829	45835.754264
HLA B*4001	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.365355	0.592477	-3.772878	23192.890707
HLA A*2402	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.556890	0.783751	-3.773139	36048.699181
HLA A*2501	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.485061	0.711889	-3.773172	30553.512317
HLA A*2601	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.399117	0.625924	-3.773193	25067.843859
HLA B*1509	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.506246	0.732827	-3.773419	32080.892987
HLA A*2602	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.602808	0.829345	-3.773463	40068.947298
HLA A*2402	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.506293	0.732827	-3.773466	32084.364257
HLA B*4001	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.366922	0.593391	-3.773531	23276.731016
HLA B*4002	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.643539	0.869990	-3.773549	44008.706568
HLA A*0250	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.557040	0.783381	-3.773659	36061.182588
HLA A*2301	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.543765	0.770046	-3.773719	34975.616196
HLA B*5801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.347955	0.574191	-3.773763	22282.021838
HLA B*5801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.353694	0.579907	-3.773787	22578.463667
HLA B*4501	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.643825	0.869990	-3.773836	44037.762187
HLA B*5701	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.411269	0.637402	-3.773866	25779.145479
HLA A*3301	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.506712	0.732827	-3.773885	32115.275105
HLA A*2603	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.604608	0.830662	-3.773946	40235.336535
HLA B*3801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.572673	0.798696	-3.773977	37382.938653
HLA A*2601	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.390459	0.616392	-3.774067	24573.053642
HLA B*1503	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.134553	0.360485	-3.774068	13631.800520
HLA A*0101	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.392179	0.617889	-3.774290	24670.556820
HLA B*4601	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.410343	0.635971	-3.774371	25724.255845
HLA A*2603	1:20-28	9	GGMSEVHLA	1.317730	-0.442696	-4.649516	0.875034	-3.774482	44618.574854
HLA A*6801	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.622229	0.847664	-3.774565	41901.423344
HLA B*3501	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.388572	0.613866	-3.774706	24466.536363
HLA B*5301	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.561617	0.786863	-3.774753	36443.221580
HLA A*0203	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.295801	0.521039	-3.774762	19760.627315
HLA B*4002	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.568115	0.793337	-3.774779	36992.649460
HLA A*0250	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.591467	0.816673	-3.774794	39036.149140
HLA B*7301	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.507720	0.732827	-3.774892	32189.896157
HLA A*6901	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.391291	0.616392	-3.774899	24620.158607
HLA B*4002	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.548669	0.773768	-3.774900	35372.743899
HLA A*2602	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.622701	0.847787	-3.774914	41947.011219
HLA A*0219	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.412370	0.637402	-3.774968	25844.636355
HLA A*0202	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.571022	0.795837	-3.775185	37241.035663
HLA B*0802	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.472599	0.697387	-3.775212	29689.266894
HLA B*4501	1:459-467	9	STPELVGKV	0.780846	0.079303	-4.635374	0.860149	-3.775225	43189.099029
HLA B*5401	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.540380	0.765110	-3.775269	34704.018540
HLA A*6802	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.429818	0.654485	-3.775333	26904.052480
HLA B*3801	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.548053	0.772678	-3.775375	35322.642407
HLA B*0801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.367984	0.592477	-3.775507	23333.718552
HLA A*0101	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.355433	0.579907	-3.775526	22669.033606
HLA B*5401	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.522291	0.746693	-3.775598	33288.258986
HLA B*7301	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.522326	0.746693	-3.775634	33290.960383
HLA B*5801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.354463	0.578823	-3.775640	22618.441082
HLA A*2402	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.473083	0.697387	-3.775696	29722.372160
HLA A*2403	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.433112	0.657361	-3.775750	27108.886511
HLA A*6901	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.368249	0.592477	-3.775773	23347.987223
HLA B*1502	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.354601	0.578823	-3.775778	22625.661666
HLA A*2403	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.308657	0.532852	-3.775805	20354.343968
HLA B*4601	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.393694	0.617889	-3.775806	24756.792097
HLA B*3901	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.286393	0.510481	-3.775912	19337.191115
HLA A*3201	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.509080	0.733042	-3.776038	32290.883480
HLA B*1517	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.473441	0.697387	-3.776053	29746.823012
HLA A*2602	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-3.963008	0.186843	-3.776165	9183.493529
HLA B*0802	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.442714	0.666540	-3.776174	27714.945227
HLA A*3301	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.567183	0.790996	-3.776187	36913.284642
HLA A*6802	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.105650	0.329236	-3.776414	12754.101174
HLA A*0211	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.264755	0.488312	-3.776443	18397.322972
HLA A*0203	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.362472	0.586005	-3.776467	23039.447666
HLA B*5101	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.499529	0.722962	-3.776568	31588.519443
HLA B*4801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.431054	0.654485	-3.776569	26980.719728
HLA B*1503	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.414010	0.637402	-3.776608	25942.412844

HLA A*0301	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.298409	0.521798	-3.776610	19879.646422
HLA A*0101	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.380060	0.603309	-3.776752	23991.660549
HLA B*2705	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.467372	0.690572	-3.776800	29334.039316
HLA A*0216	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.413562	0.636741	-3.776821	25915.620684
HLA A*0212	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.431350	0.654485	-3.776865	26999.117298
HLA B*1503	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.185739	0.408739	-3.777000	15336.953559
HLA B*5301	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.600656	0.823629	-3.777027	39870.878461
HLA A*0219	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.446722	0.669685	-3.777038	27971.917975
HLA A*2301	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.541489	0.764421	-3.777068	34792.747365
HLA B*1501	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.243508	0.466242	-3.777266	17518.956722
HLA A*6901	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.380704	0.603309	-3.777395	24027.249989
HLA A*2902	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.371005	0.593391	-3.777614	23496.619978
HLA A*3001	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.052772	0.275124	-3.777649	11292.038451
HLA A*0250	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.356540	0.578823	-3.777717	22726.869266
HLA A*3101	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.391270	0.613540	-3.777730	24618.959905
HLA B*4002	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.533059	0.755176	-3.777882	34123.908709
HLA B*4001	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.415286	0.637402	-3.777884	26018.732535
HLA A*0301	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.349134	0.571232	-3.777902	22342.616802
HLA A*2603	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.651055	0.873123	-3.777932	44776.960217
HLA A*3201	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.468521	0.690572	-3.777949	29411.743369
HLA A*3301	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.625741	0.847787	-3.777954	42241.687152
HLA B*1517	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.318391	0.540402	-3.777989	20815.700269
HLA A*0201	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.391585	0.613540	-3.778045	24636.813278
HLA A*2501	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.163339	0.385288	-3.778051	14565.959984
HLA B*5301	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.597414	0.819348	-3.778066	39574.324915
HLA B*0802	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.487397	0.709300	-3.778096	30718.254232
HLA A*0201	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.396011	0.617889	-3.778122	24889.201388
HLA B*1801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.330531	0.552387	-3.778144	21405.768030
HLA A*2403	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.447857	0.669685	-3.778173	28045.103513
HLA A*2601	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.401614	0.623337	-3.778278	25212.417115
HLA A*3001	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.259574	0.481266	-3.778308	18179.168631
HLA B*3901	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.432860	0.654485	-3.778375	27093.198852
HLA B*3501	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.432865	0.654485	-3.778380	27093.491996
HLA B*0801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.440879	0.662443	-3.778436	27598.093194
HLA A*0206	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.364464	0.586005	-3.778460	23145.385928
HLA A*2602	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.560188	0.781690	-3.778498	36323.548999
HLA B*4501	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.641361	0.862842	-3.778519	43788.556830
HLA A*0250	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.574764	0.796188	-3.778577	37563.364084
HLA B*1517	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.453792	0.675193	-3.778599	28430.981086
HLA A*2403	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.421797	0.643088	-3.778709	26411.712407
HLA B*1509	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.491626	0.712902	-3.778723	31018.843627
HLA B*5701	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.421886	0.643088	-3.778798	26417.142574
HLA A*0203	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.392388	0.613540	-3.778848	24682.438063
HLA B*4001	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.396833	0.617889	-3.778945	24936.372770
HLA A*2601	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.384501	0.605498	-3.779002	24238.226233
HLA B*4501	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.560475	0.781429	-3.779046	36347.530690
HLA A*0206	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.488357	0.709300	-3.779057	30786.298064
HLA B*5801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.319462	0.540402	-3.779060	20867.114108
HLA A*0101	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.244020	0.464928	-3.779093	17539.629993
HLA B*5801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.353760	0.574537	-3.779223	22581.884042
HLA A*2402	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.576705	0.797462	-3.779243	37731.594141
HLA B*3801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.474629	0.695361	-3.779268	29828.363635
HLA B*4403	1:391-399	9	DSTIPPDHV	0.933339	-0.063349	-4.649281	0.869990	-3.779291	44594.443228
HLA B*5101	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.469928	0.690572	-3.779356	29507.207411
HLA A*8001	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.312238	0.532852	-3.779386	20522.852533
HLA B*4403	1:517-525	9	FTKFSQASV	0.794238	0.070907	-4.644737	0.865145	-3.779591	44130.296161
HLA A*2501	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.470468	0.690866	-3.779603	29543.945328
HLA A*2601	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.393511	0.613866	-3.779645	24746.347643
HLA A*0203	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.379381	0.599665	-3.779716	23954.179903
HLA A*2902	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.284730	0.505009	-3.779721	19263.267438
HLA A*2402	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.579748	0.799991	-3.779756	37996.862510
HLA A*3301	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.612939	0.833148	-3.779791	41014.640762
HLA B*5701	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.397813	0.617889	-3.779924	24992.690826
HLA B*0802	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.469242	0.689311	-3.779931	29460.632037
HLA A*3201	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.373425	0.593391	-3.780034	23627.912965

HLA A*0203	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.341165	0.561125	-3.780040	21936.360965
HLA B*1517	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.114230	0.334125	-3.780105	13008.588533
HLA A*3002	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.351486	0.571232	-3.780254	22463.936949
HLA A*3301	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.552989	0.772678	-3.780312	35726.416151
HLA B*5401	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.492201	0.711889	-3.780312	31059.983969
HLA A*3301	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.048910	0.268569	-3.780341	11192.053950
HLA A*2602	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.613656	0.833148	-3.780508	41082.371446
HLA A*6801	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.567446	0.786863	-3.780582	36935.657459
HLA B*2705	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.417340	0.636741	-3.780598	26142.046728
HLA A*0206	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.406555	0.625924	-3.780631	25500.896609
HLA A*0219	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.190447	0.409720	-3.780728	15504.132472
HLA B*1502	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.611433	0.830662	-3.780771	40872.659015
HLA B*7301	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.579579	0.798791	-3.780787	37982.065158
HLA B*1501	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.365338	0.584529	-3.780810	23192.012427
HLA A*0201	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.386322	0.605498	-3.780823	24340.062306
HLA A*0201	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.394712	0.613866	-3.780845	24814.852413
HLA A*0216	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.406936	0.625924	-3.781012	25523.255443
HLA A*2601	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.398953	0.617889	-3.781064	25058.352659
HLA B*5301	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.581136	0.799991	-3.781145	38118.542185
HLA A*2301	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.531569	0.750403	-3.781166	34007.068635
HLA A*2603	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.604817	0.823629	-3.781187	40254.713715
HLA A*2601	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.376132	0.594934	-3.781198	23775.626473
HLA B*1801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.476568	0.695361	-3.781206	29961.789881
HLA A*0212	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.427160	0.645932	-3.781229	26739.940337
HLA B*0803	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.478779	0.697387	-3.781391	30114.705429
HLA B*3801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.494309	0.712902	-3.781407	31211.074137
HLA A*2402	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.577443	0.795837	-3.781606	37795.743465
HLA B*4403	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.600992	0.819348	-3.781644	39901.735070
HLA A*0201	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.393685	0.612002	-3.781683	24756.256376
HLA A*3101	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.436234	0.654485	-3.781749	27304.494773
HLA A*2902	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.448334	0.666540	-3.781794	28075.919774
HLA B*0702	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.451670	0.669685	-3.781986	28292.430744
HLA B*1517	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.507971	0.725976	-3.781995	32208.534934
HLA B*4001	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.394200	0.612002	-3.782198	24785.604122
HLA B*0803	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.494196	0.711889	-3.782307	31202.970464
HLA B*4801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.400266	0.617889	-3.782377	25134.247024
HLA A*0201	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.398840	0.616392	-3.782448	25051.846484
HLA A*3002	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.480299	0.697848	-3.782450	30220.297558
HLA B*1509	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.394587	0.612002	-3.782586	24807.738416
HLA B*4001	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.396159	0.613540	-3.782619	24897.685646
HLA B*1801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.376038	0.593391	-3.782647	23770.482090
HLA A*0301	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.368654	0.586005	-3.782649	23369.722658
HLA B*5301	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.599352	0.816673	-3.782679	39751.346145
HLA A*2601	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.374765	0.592081	-3.782683	23700.885319
HLA B*5801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.343829	0.561125	-3.782704	22071.350109
HLA A*2902	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.396572	0.613866	-3.782706	24921.403030
HLA B*4403	1:173-181	9	TAAVIGTAQ	0.901087	-0.047671	-4.636283	0.853416	-3.782868	43279.615618
HLA A*3001	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.293360	0.510481	-3.782879	19649.866879
HLA B*4001	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.419898	0.636741	-3.783157	26296.513744
HLA B*4402	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.420563	0.637402	-3.783161	26336.804505
HLA A*0301	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.367716	0.584529	-3.783187	23319.332446
HLA B*5401	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.463338	0.680074	-3.783264	29062.823471
HLA B*4601	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.375350	0.592081	-3.783268	23732.833404
HLA A*6801	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.627492	0.844164	-3.783328	42412.280217
HLA A*3101	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.399730	0.616392	-3.783338	25103.264181
HLA A*6901	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.293884	0.510481	-3.783403	19673.586887
HLA A*3001	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.211973	0.428564	-3.783409	16291.964386
HLA A*2402	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.570305	0.786863	-3.783442	37179.638019
HLA B*3501	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.419433	0.635971	-3.783462	26268.361102
HLA A*8001	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.409539	0.625924	-3.783615	25676.705289
HLA A*2902	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.409614	0.625924	-3.783690	25681.150734
HLA B*1501	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.288806	0.505009	-3.783798	19444.926711
HLA A*0101	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.368341	0.584529	-3.783812	23352.913834
HLA B*1517	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.053623	0.269799	-3.783824	11314.174220
HLA B*3501	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.157423	0.373369	-3.784054	14368.886334

HLA A*0216	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.242625	0.458556	-3.784069	17483.357310
HLA B*4403	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.631892	0.847787	-3.784105	42844.216728
HLA A*2402	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.549249	0.765110	-3.784139	35420.042061
HLA B*0801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.335225	0.550986	-3.784240	21638.397062
HLA B*4601	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.398191	0.613866	-3.784325	25014.468747
HLA A*2501	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.400881	0.616515	-3.784366	25169.897338
HLA A*0219	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.464447	0.680074	-3.784373	29137.129280
HLA A*0101	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.379311	0.594934	-3.784376	23950.292535
HLA B*4601	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.397956	0.613540	-3.784416	25000.939856
HLA A*2501	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.493841	0.709300	-3.784541	31177.491376
HLA A*2402	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.535016	0.750403	-3.784613	34278.032991
HLA B*1509	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.327277	0.542619	-3.784658	21245.980475
HLA B*3501	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.427816	0.643088	-3.784728	26780.330983
HLA A*2601	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.370745	0.586005	-3.784740	23482.514547
HLA A*2402	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.324399	0.539629	-3.784770	21105.646454
HLA B*1502	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.608404	0.823629	-3.784775	40588.631239
HLA A*0212	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.390466	0.605498	-3.784968	24573.452458
HLA A*6901	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.017380	0.232368	-3.785011	10408.297718
HLA B*4501	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.632813	0.847664	-3.785149	42935.171862
HLA B*1801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.194940	0.409720	-3.785220	15665.334970
HLA B*1502	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.578622	0.793337	-3.785285	37898.527303
HLA B*5701	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.399197	0.613866	-3.785331	25072.455168
HLA B*4002	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.611900	0.826538	-3.785362	40916.684903
HLA B*1501	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.344076	0.558588	-3.785487	22083.891044
HLA A*2602	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.559291	0.773768	-3.785522	36248.561075
HLA A*3001	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.285190	0.499448	-3.785742	19283.703850
HLA A*0211	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.498660	0.712902	-3.785758	31525.353239
HLA B*0803	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.507825	0.722004	-3.785821	32197.733581
HLA A*6801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.309968	0.524138	-3.785830	20415.880830
HLA B*1517	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.399777	0.613866	-3.785911	25105.980445
HLA A*0202	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.550290	0.764363	-3.785927	35505.030857
HLA A*6901	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.244535	0.458556	-3.785979	17560.422661
HLA A*2301	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.475332	0.689311	-3.786021	29876.651753
HLA A*2402	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.584881	0.798696	-3.786185	38448.673599
HLA B*0702	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.422250	0.635971	-3.786279	26439.303505
HLA A*2902	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.134769	0.348457	-3.786312	13638.586890
HLA B*0801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.440816	0.654485	-3.786331	27594.062317
HLA B*2705	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.461604	0.675193	-3.786411	28947.021524
HLA A*0203	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.440950	0.654485	-3.786465	27602.572636
HLA A*0219	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.422497	0.635971	-3.786525	26454.326310
HLA B*0803	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.501550	0.714935	-3.786615	31735.827587
HLA B*4601	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.365508	0.578823	-3.786685	23201.047754
HLA B*1509	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.410030	0.623337	-3.786693	25705.753507
HLA A*6901	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.212909	0.426123	-3.786785	16327.080991
HLA B*4402	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.365719	0.578823	-3.786896	23212.346863
HLA A*0250	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.551418	0.764421	-3.786997	35597.348243
HLA A*1101	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.400910	0.613866	-3.787043	25171.531387
HLA A*8001	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.444469	0.657361	-3.787108	27827.173123
HLA A*0216	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.433159	0.645932	-3.787227	27111.819791
HLA A*3301	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.631427	0.844164	-3.787263	42798.348370
HLA A*0301	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.367274	0.579907	-3.787367	23295.627362
HLA A*8001	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.441913	0.654485	-3.787428	27663.864597
HLA A*3301	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.513441	0.725976	-3.787464	32616.741498
HLA B*2705	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.380908	0.593391	-3.787517	24038.561324
HLA A*6901	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.373616	0.586005	-3.787611	23638.269009
HLA A*8001	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.433577	0.645932	-3.787645	27137.939970
HLA B*1502	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.585114	0.797462	-3.787652	38469.271417
HLA A*6801	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.635463	0.847787	-3.787676	43197.978575
HLA B*2705	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.478600	0.690866	-3.787734	30102.326265
HLA B*1801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.445186	0.657361	-3.787824	27873.126310
HLA B*7301	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.542323	0.754459	-3.787864	34859.631412
HLA A*3201	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.442082	0.654207	-3.787875	27674.642104
HLA A*2902	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.190950	0.403047	-3.787903	15522.092253
HLA B*1501	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.405912	0.617889	-3.788023	25463.124386
HLA A*0301	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.366870	0.578823	-3.788047	23273.960841

HLA A*2403	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.366889	0.578823	-3.788066	23274.968140
HLA A*2402	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.560900	0.772678	-3.788222	36383.139257
HLA B*5301	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.584625	0.796188	-3.788438	38426.007948
HLA A*6801	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.587292	0.798791	-3.788501	38662.678112
HLA B*0702	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.388232	0.599665	-3.788567	24447.351508
HLA A*3002	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.563080	0.774481	-3.788599	36566.255609
HLA B*0702	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.406492	0.617889	-3.788603	25497.172041
HLA A*2403	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.406511	0.617889	-3.788622	25498.275560
HLA A*0219	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.455246	0.666540	-3.788706	28526.348109
HLA A*6802	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.425549	0.636741	-3.788808	26640.887415
HLA A*2601	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.367660	0.578823	-3.788837	23316.304923
HLA B*1502	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.580105	0.790996	-3.789109	38028.120300
HLA A*1101	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.472083	0.682948	-3.789135	29653.952472
HLA A*2603	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.487056	0.697848	-3.789207	30694.167240
HLA B*1801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.519885	0.730675	-3.789210	33104.360979
HLA A*8001	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.425210	0.635971	-3.789239	26620.141605
HLA A*0301	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.367624	0.578365	-3.789260	23314.412920
HLA B*4601	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.405818	0.616515	-3.789302	25457.614875
HLA B*1501	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.375500	0.586005	-3.789495	23741.051915
HLA A*0219	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.426244	0.636741	-3.789503	26683.582368
HLA B*0802	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.469656	0.680074	-3.789581	29488.696056
HLA A*2902	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.446981	0.657361	-3.789619	27988.568676
HLA B*4001	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.392971	0.603309	-3.789662	24715.575542
HLA A*0101	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.389430	0.599665	-3.789765	24514.895949
HLA A*0206	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.435781	0.645932	-3.789849	27276.000793
HLA A*3001	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.256123	0.466242	-3.789880	18035.269018
HLA A*6901	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.211875	0.421976	-3.789899	16288.263022
HLA B*4403	1:134-142	9	IIHRDVKPA	1.039325	-0.166069	-4.663166	0.873256	-3.789910	46043.274524
HLA B*5101	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.502901	0.712902	-3.789999	31834.701493
HLA B*1517	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.473051	0.682948	-3.790103	29720.121119
HLA A*0203	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.393502	0.603309	-3.790193	24745.812149
HLA B*1503	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.285907	0.495678	-3.790229	19315.548539
HLA B*0803	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.447688	0.657361	-3.790327	28034.181735
HLA A*2301	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.481213	0.690866	-3.790347	30283.961534
HLA B*2705	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.436305	0.645932	-3.790373	27308.926561
HLA B*3901	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.470640	0.680074	-3.790566	29555.615183
HLA B*5801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.349209	0.558588	-3.790621	22346.485011
HLA B*5701	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.416550	0.625924	-3.790626	26094.570897
HLA A*2403	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.396180	0.605498	-3.790682	24898.897919
HLA A*3101	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.382774	0.592081	-3.790693	24142.039895
HLA B*0801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.426846	0.635971	-3.790874	26720.562907
HLA A*1101	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.427722	0.636741	-3.790981	26774.536465
HLA A*0211	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.312113	0.521039	-3.791075	20516.968979
HLA B*7301	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.445872	0.654485	-3.791387	27917.191939
HLA B*5301	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.584820	0.793337	-3.791483	38443.265899
HLA B*4501	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.588415	0.796898	-3.791517	38762.786356
HLA B*3901	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.365712	0.574191	-3.791521	23211.970138
HLA A*8001	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.458075	0.666540	-3.791535	28712.761106
HLA B*4402	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.434683	0.643088	-3.791596	27207.177182
HLA B*4402	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.362965	0.571232	-3.791734	23065.637120
HLA A*0301	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.315889	0.524138	-3.791750	20696.114776
HLA A*0219	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.383834	0.592081	-3.791752	24201.015009
HLA B*3501	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.227842	0.436027	-3.791815	16898.255556
HLA B*3501	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.195701	0.403854	-3.791847	15692.817312
HLA B*0702	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.428594	0.636741	-3.791853	26828.328768
HLA B*4001	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.408372	0.616392	-3.791979	25607.760677
HLA A*0250	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.573411	0.781429	-3.791982	37446.495212
HLA B*1801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.224308	0.432298	-3.792010	16761.321188
HLA B*0803	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.482937	0.690866	-3.792071	30404.453935
HLA A*3101	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.406017	0.613866	-3.792151	25469.324012
HLA B*1509	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.538885	0.746693	-3.792193	34584.817972
HLA B*0801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.384292	0.592081	-3.792210	24226.558817
HLA B*5801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.325136	0.532852	-3.792285	21141.529194
HLA A*2602	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.525482	0.733042	-3.792440	33533.716027
HLA B*1509	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.459034	0.666540	-3.792493	28776.206905

HLA A*0206	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.280999	0.488312	-3.792687	19098.487376
HLA B*0801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.225041	0.432298	-3.792744	16789.636268
HLA B*5701	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.409271	0.616515	-3.792756	25660.874645
HLA A*2501	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.392449	0.599665	-3.792784	24685.910068
HLA B*4402	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.447023	0.654207	-3.792816	27991.294280
HLA A*2601	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.286866	0.494046	-3.792820	19358.229575
HLA B*5701	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.406407	0.613540	-3.792868	25492.206797
HLA B*2705	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.482310	0.689311	-3.792999	30360.568216
HLA A*0216	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.298033	0.505009	-3.793024	19862.446398
HLA A*6802	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.409466	0.616392	-3.793074	25672.399498
HLA B*5101	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.462795	0.669685	-3.793111	29026.526798
HLA B*4402	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.411048	0.617889	-3.793159	25766.039354
HLA B*4001	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.392825	0.599665	-3.793160	24707.287004
HLA B*3501	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.333634	0.540402	-3.793232	21559.291492
HLA A*0101	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.379287	0.586005	-3.793282	23948.996886
HLA A*0216	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.219558	0.426123	-3.793434	16578.971678
HLA A*2403	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.407328	0.613866	-3.793462	25546.324886
HLA B*1801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.491489	0.697848	-3.793641	31009.112260
HLA B*0803	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.484222	0.690572	-3.793651	30494.560336
HLA B*1501	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.344696	0.550986	-3.793710	22115.454029
HLA A*8001	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.405712	0.612002	-3.793710	25451.418100
HLA A*0216	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.393391	0.599665	-3.793726	24739.520960
HLA A*8001	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.430476	0.636741	-3.793734	26944.836785
HLA A*2403	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.344755	0.550986	-3.793769	22118.445285
HLA A*1101	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.519817	0.725976	-3.793841	33099.167750
HLA B*4801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.430584	0.636741	-3.793843	26951.542974
HLA B*3901	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.477007	0.682948	-3.794059	29992.116041
HLA B*0702	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.326964	0.532852	-3.794113	21230.699166
HLA A*3301	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.641870	0.847664	-3.794207	43839.992414
HLA A*0201	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.397672	0.603309	-3.794363	24984.579682
HLA A*2403	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.448632	0.654207	-3.794425	28095.216129
HLA A*3201	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.593304	0.798696	-3.794608	39201.642685
HLA A*2602	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.197665	0.403047	-3.794618	15763.951441
HLA A*3201	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.621195	0.826538	-3.794657	41801.801854
HLA A*3101	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.208872	0.414162	-3.794710	16176.037009
HLA A*8001	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.408616	0.613866	-3.794750	25622.172386
HLA A*2602	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.594761	0.799991	-3.794770	39333.350900
HLA B*5301	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.586286	0.791452	-3.794835	38573.260848
HLA A*2501	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.464649	0.669685	-3.794964	29150.688497
HLA A*2402	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.586632	0.791452	-3.795180	38603.948577
HLA A*6802	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.394874	0.599665	-3.795209	24824.117088
HLA B*0702	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.369427	0.574191	-3.795235	23411.354379
HLA A*0101	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.373639	0.578365	-3.795274	23639.547848
HLA B*0801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.213891	0.418508	-3.795383	16364.043746
HLA B*4801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.432849	0.637402	-3.795446	27092.466006
HLA B*2705	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.475576	0.680074	-3.795502	29893.465938
HLA B*4002	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.591949	0.796188	-3.795761	39079.465309
HLA A*0101	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.370373	0.574537	-3.795836	23462.451151
HLA B*4002	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.595856	0.799991	-3.795865	39432.635702
HLA A*2902	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.450369	0.654485	-3.795884	28207.763047
HLA A*2601	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.399218	0.603309	-3.795909	25073.675951
HLA B*5401	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.560299	0.764363	-3.795936	36332.785973
HLA A*2301	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.528985	0.733042	-3.795943	33805.297669
HLA A*2403	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.302560	0.506563	-3.795997	20070.592611
HLA B*4601	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.401647	0.605498	-3.796149	25214.326737
HLA A*1101	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.388627	0.592477	-3.796150	24469.580861
HLA A*2902	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.388413	0.592081	-3.796331	24457.537454
HLA A*2501	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.380869	0.584529	-3.796340	24036.350645
HLA A*1101	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.476502	0.680074	-3.796428	29957.251706
HLA B*4001	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.340420	0.543984	-3.796436	21898.773774
HLA A*0212	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.433908	0.637402	-3.796506	27158.648535
HLA A*2603	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.381254	0.584529	-3.796725	24057.685683
HLA A*0203	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.205531	0.408742	-3.796789	16052.074407
HLA B*4601	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.408830	0.612002	-3.796828	25634.789285
HLA A*2603	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.396561	0.599665	-3.796896	24920.728929

HLA B*1509	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.486311	0.689311	-3.797000	30641.573853
HLA A*0202	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.487977	0.690866	-3.797111	30759.328709
HLA A*0301	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.348164	0.550986	-3.797178	22292.752772
HLA B*1509	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.506505	0.709300	-3.797205	32099.989617
HLA A*3002	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-3.954475	0.157255	-3.797220	9004.810852
HLA B*3901	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.512285	0.714935	-3.797349	32530.042077
HLA A*0212	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.389503	0.592081	-3.797421	24519.007603
HLA B*4002	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.629315	0.831818	-3.797497	42590.704363
HLA A*6901	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.304083	0.506563	-3.797520	20141.075715
HLA A*2902	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.170890	0.373369	-3.797521	14821.438535
HLA A*0206	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.561929	0.764363	-3.797567	36469.452470
HLA B*0803	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.506925	0.709300	-3.797625	32131.089345
HLA B*4001	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.392705	0.594934	-3.797771	24700.471097
HLA A*3201	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.528583	0.730675	-3.797908	33774.039152
HLA B*4601	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.359056	0.561125	-3.797931	22858.930760
HLA B*5101	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.507428	0.709300	-3.798128	32168.309571
HLA B*4001	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.403630	0.605498	-3.798132	25329.717235
HLA A*2602	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.372328	0.574191	-3.798137	23568.294317
HLA B*4001	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.424066	0.625924	-3.798142	26550.100061
HLA B*5101	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.489008	0.690866	-3.798142	30832.467126
HLA B*3901	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.277952	0.479739	-3.798213	18964.949469
HLA B*3801	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.552764	0.754459	-3.798305	35707.866477
HLA B*4002	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.595278	0.796898	-3.798379	39380.192364
HLA A*3301	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.627903	0.829510	-3.798393	42452.452233
HLA A*3301	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.630226	0.831818	-3.798409	42680.197719
HLA B*4002	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.496294	0.697848	-3.798446	31354.077690
HLA B*1501	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.372699	0.574191	-3.798508	23588.448223
HLA A*6802	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.384531	0.586005	-3.798526	24239.930932
HLA A*1101	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.369901	0.571232	-3.798669	23436.952235
HLA A*0201	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.391298	0.592477	-3.798821	24620.558187
HLA A*6901	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.248351	0.449508	-3.798843	17715.382278
HLA A*6802	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.339666	0.540737	-3.798929	21860.777925
HLA A*0201	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.393868	0.594934	-3.798934	24766.705012
HLA A*0250	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.594784	0.795837	-3.798948	39335.478849
HLA B*0802	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.481906	0.682948	-3.798958	30332.330818
HLA B*1502	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.303455	0.504447	-3.799008	20112.004133
HLA B*5401	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.496397	0.697387	-3.799010	31361.541950
HLA A*3201	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.415538	0.616515	-3.799022	26033.798050
HLA B*1502	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.599136	0.799991	-3.799144	39731.566433
HLA A*0201	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.351643	0.552387	-3.799257	22472.080761
HLA A*6802	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.417180	0.617889	-3.799291	26132.431558
HLA A*3001	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.257469	0.458095	-3.799374	18091.262685
HLA B*1801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.479474	0.680074	-3.799400	30162.967557
HLA B*5301	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.596885	0.797462	-3.799423	39526.183361
HLA A*2602	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-3.809027	0.009579	-3.799448	6442.098727
HLA A*1101	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.490357	0.690866	-3.799491	30928.359266
HLA B*4601	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.415937	0.616392	-3.799545	26057.751857
HLA B*3501	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.416087	0.616515	-3.799572	26066.775470
HLA A*6802	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.413496	0.613866	-3.799630	25911.695363
HLA B*1509	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.514580	0.714935	-3.799645	32702.433551
HLA A*0203	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.258207	0.458556	-3.799651	18122.020524
HLA A*0212	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.436424	0.636741	-3.799683	27316.462252
HLA A*0219	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.425617	0.625924	-3.799693	26645.067346
HLA B*4501	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-3.940241	0.140490	-3.799751	8714.478738
HLA B*4801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.442857	0.643088	-3.799769	27724.092758
HLA A*0211	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.074937	0.275124	-3.799814	11883.308990
HLA A*0212	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.425812	0.625924	-3.799888	26657.034222
HLA A*3201	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.574398	0.774481	-3.799917	37531.676130
HLA A*0212	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.324183	0.524138	-3.800044	21095.144581
HLA B*5801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.354357	0.554273	-3.800084	22612.935405
HLA B*7301	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.574607	0.774481	-3.800126	37549.751237
HLA A*0219	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.454612	0.654485	-3.800127	28484.710943
HLA A*3201	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.483245	0.682948	-3.800297	30426.009071
HLA B*3901	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.393704	0.593391	-3.800313	24757.327828
HLA B*5701	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.403684	0.603309	-3.800376	25332.869143

HLA A*2602	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.619790	0.819348	-3.800442	41666.786784
HLA A*3201	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.375007	0.574537	-3.800469	23714.095573
HLA A*3201	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.624162	0.823629	-3.800533	42088.398605
HLA A*6901	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.017154	0.216497	-3.800657	10402.893578
HLA A*2301	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.523637	0.722962	-3.800676	33391.608246
HLA B*5101	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.480759	0.680074	-3.800685	30252.358291
HLA A*0206	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.226855	0.426123	-3.800732	16859.903714
HLA B*4601	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.386785	0.586005	-3.800780	24366.016511
HLA B*0803	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.467421	0.666540	-3.800881	29337.372078
HLA A*2902	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.414422	0.613540	-3.800882	25966.984950
HLA B*1503	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.437649	0.636741	-3.800907	27393.563734
HLA B*4601	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.394355	0.593391	-3.800964	24794.455469
HLA A*6901	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.296647	0.495678	-3.800969	19799.149824
HLA B*1801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.510393	0.709300	-3.801093	32388.683050
HLA B*1501	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.280860	0.479739	-3.801121	19092.392427
HLA B*3801	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.455347	0.654207	-3.801140	28532.984830
HLA A*3001	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.292030	0.490880	-3.801150	19589.791064
HLA A*2602	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.617863	0.816673	-3.801190	41482.357748
HLA B*5101	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.463700	0.662443	-3.801257	29087.046464
HLA B*4801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.424616	0.623337	-3.801279	26583.731489
HLA B*1509	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.381251	0.579907	-3.801345	24057.555534
HLA B*1517	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.437324	0.635971	-3.801353	27373.120299
HLA B*7301	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.533686	0.732333	-3.801353	34173.234276
HLA A*0212	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.353753	0.552387	-3.801367	22581.517548
HLA A*2403	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.393502	0.592081	-3.801420	24745.812149
HLA B*4402	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.393523	0.592081	-3.801441	24747.017027
HLA A*2301	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.498972	0.697387	-3.801585	31548.044374
HLA A*0203	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.419518	0.617889	-3.801629	26273.477521
HLA B*5801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.354030	0.552387	-3.801644	22595.937444
HLA A*0201	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.386183	0.584529	-3.801654	24332.294601
HLA A*0250	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.524664	0.722962	-3.801703	33470.643455
HLA B*4501	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.617006	0.815296	-3.801710	41400.527107
HLA B*5301	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.598614	0.796898	-3.801716	39683.877647
HLA A*3301	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.625377	0.823629	-3.801748	42206.280958
HLA A*2402	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.583462	0.781690	-3.801772	38323.244785
HLA A*2403	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.437768	0.635971	-3.801797	27401.122780
HLA B*2705	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.418324	0.616515	-3.801809	26201.371255
HLA A*2603	1:75-83	9	YDTGEAETP	0.941281	-0.093617	-4.649504	0.847664	-3.801840	44617.367963
HLA B*0801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.405179	0.603309	-3.801870	25420.181801
HLA A*2403	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.439357	0.637402	-3.801954	27501.514476
HLA A*0212	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.445087	0.643088	-3.801999	27866.793828
HLA A*6801	1:321-329	9	DRDRSIGSV	0.847521	0.015321	-4.664865	0.862842	-3.802023	46223.718539
HLA B*1517	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.468681	0.666540	-3.802140	29422.565130
HLA B*2705	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.464642	0.662443	-3.802199	29150.215394
HLA A*2603	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.595541	0.793337	-3.802204	39404.060352
HLA A*3002	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.598074	0.795837	-3.802237	39634.530717
HLA A*2501	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.459792	0.657361	-3.802431	28826.534240
HLA B*2705	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.472130	0.669685	-3.802445	29657.161138
HLA A*0212	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.420342	0.617889	-3.802454	26323.414865
HLA A*0216	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.342983	0.540402	-3.802581	22028.406660
HLA B*4501	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.477895	0.675193	-3.802702	30053.510815
HLA B*5401	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.345450	0.542619	-3.802831	22153.892526
HLA B*0803	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.528853	0.725976	-3.802877	33795.057778
HLA A*3001	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.183258	0.380356	-3.802902	15249.585749
HLA A*2603	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.629503	0.826538	-3.802965	42609.141232
HLA A*0301	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.364140	0.561125	-3.803016	23128.112848
HLA A*2902	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.347020	0.543984	-3.803035	22234.097230
HLA A*2601	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.395534	0.592477	-3.803057	24861.882884
HLA A*0101	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.381888	0.578823	-3.803065	24092.851701
HLA B*1501	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.374417	0.571232	-3.803185	23681.916478
HLA B*3801	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.549935	0.746693	-3.803242	35476.038880
HLA B*1517	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.492596	0.689311	-3.803285	31088.226021
HLA B*4601	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.327479	0.524138	-3.803340	21255.867477
HLA A*2602	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.599180	0.795837	-3.803343	39735.650567
HLA B*4002	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.382203	0.578823	-3.803380	24110.323547

HLA A*0203	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.291764	0.488312	-3.803452	19577.819142
HLA A*2403	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.449403	0.645932	-3.803471	28145.113764
HLA A*1101	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.518417	0.714935	-3.803482	32992.618170
HLA A*6801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.268500	0.464928	-3.803572	18556.655777
HLA A*6802	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.381961	0.578365	-3.803596	24096.892569
HLA B*2705	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.354639	0.550986	-3.803653	22627.620188
HLA B*4801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.409246	0.605498	-3.803747	25659.347643
HLA A*0203	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.409361	0.605498	-3.803862	25666.150441
HLA B*4403	1:375-383	9	ATLQNRGFK	0.529092	0.267806	-4.600839	0.796898	-3.803941	39887.706379
HLA B*0802	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.461369	0.657361	-3.804008	28931.365742
HLA A*0212	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.416146	0.612002	-3.804144	26070.301168
HLA A*0301	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.344564	0.540402	-3.804162	22108.755083
HLA B*7301	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.388702	0.584529	-3.804173	24473.817315
HLA A*2501	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.450127	0.645932	-3.804195	28192.049535
HLA B*4501	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.461583	0.657361	-3.804221	28945.612157
HLA A*3301	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.633603	0.829345	-3.804257	43013.287075
HLA B*5801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.309284	0.505009	-3.804276	20383.765849
HLA A*2601	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.375596	0.571232	-3.804364	23746.318393
HLA B*0802	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.466883	0.662443	-3.804441	29301.049549
HLA B*4801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.396533	0.592081	-3.804451	24919.111161
HLA A*0203	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.418359	0.613866	-3.804493	26203.497539
HLA A*0202	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.535190	0.730675	-3.804515	34291.758324
HLA A*0202	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.356913	0.552387	-3.804527	22746.426701
HLA B*5701	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.309604	0.505009	-3.804595	20398.768619
HLA A*3301	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.624127	0.819348	-3.804779	42084.983340
HLA A*3301	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.631321	0.826538	-3.804783	42787.930594
HLA B*4002	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.638069	0.833148	-3.804921	43457.926753
HLA A*6901	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.384865	0.579907	-3.804958	24258.559304
HLA B*0702	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.417100	0.612002	-3.805098	26127.625299
HLA B*0702	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.309743	0.504447	-3.805295	20405.280608
HLA B*5301	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.589052	0.783751	-3.805301	38819.657378
HLA B*0702	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.448430	0.643088	-3.805342	28082.147857
HLA A*2403	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.431296	0.625924	-3.805371	26995.758075
HLA A*0250	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.418968	0.613540	-3.805428	26240.238600
HLA A*3201	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.605458	0.799991	-3.805467	40314.209815
HLA B*1509	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.384322	0.578823	-3.805499	24228.262696
HLA A*0202	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.209422	0.403854	-3.805568	16196.527448
HLA B*4601	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.405298	0.599665	-3.805634	25427.196308
HLA A*0301	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-3.902607	0.096922	-3.805685	7991.114692
HLA B*5701	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.397782	0.592081	-3.805701	24990.933188
HLA A*0203	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.390283	0.584529	-3.805754	24563.085352
HLA A*3002	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.503185	0.697387	-3.805798	31855.547202
HLA A*1101	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.463225	0.657361	-3.805864	29055.277571
HLA A*2902	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.442608	0.636741	-3.805867	27708.198983
HLA A*1101	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.495194	0.689311	-3.805883	31274.794962
HLA B*0801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.422302	0.616392	-3.805909	26442.450433
HLA A*2602	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.518861	0.712902	-3.805959	33026.369353
HLA B*1509	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.449058	0.643088	-3.805970	28122.740155
HLA B*5701	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.418014	0.612002	-3.806012	26182.667395
HLA A*2603	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.580558	0.774481	-3.806077	38067.846523
HLA A*2301	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.528144	0.722004	-3.806139	33739.888947
HLA B*1801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.429482	0.623337	-3.806145	26883.247173
HLA A*2501	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.472893	0.666540	-3.806353	29709.350640
HLA B*3501	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.130897	0.324517	-3.806381	13517.532537
HLA A*2902	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.310866	0.504447	-3.806418	20458.115458
HLA B*5801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.349038	0.542619	-3.806418	22337.661637
HLA B*1517	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.380958	0.574537	-3.806421	24041.292445
HLA B*4402	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.442449	0.635971	-3.806477	27698.007774
HLA A*3001	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.311044	0.504447	-3.806597	20466.528574
HLA A*0212	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.384999	0.578365	-3.806634	24266.040917
HLA A*0216	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.420225	0.613540	-3.806685	26316.295490
HLA B*0803	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.481885	0.675193	-3.806692	30330.854003
HLA A*2603	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.623462	0.816673	-3.806789	42020.600586
HLA A*2902	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.347294	0.540402	-3.806892	22248.174913
HLA B*5101	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.464301	0.657361	-3.806940	29127.357943

HLA A*2402	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.496463	0.689311	-3.807152	31366.292859
HLA A*2603	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.647051	0.839877	-3.807174	44366.082736
HLA A*2403	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.349860	0.542619	-3.807241	22379.997200
HLA A*1101	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.473873	0.666540	-3.807333	29776.448325
HLA B*3801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.473894	0.666540	-3.807354	29777.898146
HLA B*5101	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.461759	0.654207	-3.807552	28957.358981
HLA A*0211	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.272487	0.464928	-3.807559	18727.801079
HLA B*1502	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.350048	0.542449	-3.807599	22389.685161
HLA B*0803	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.490632	0.682948	-3.807684	30947.941785
HLA A*6901	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.350400	0.542619	-3.807781	22407.861392
HLA A*0201	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.393791	0.586005	-3.807786	24762.283897
HLA B*3501	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.413317	0.605498	-3.807819	25901.043919
HLA A*2603	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.637343	0.829510	-3.807834	43385.340746
HLA B*1801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.076497	0.268569	-3.807929	11926.072575
HLA A*0219	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.387893	0.579907	-3.807987	24428.313850
HLA B*0803	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.503350	0.695361	-3.807988	31867.612935
HLA B*3501	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.424557	0.616392	-3.808165	26580.136356
HLA B*4801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.420218	0.612002	-3.808216	26315.868389
HLA A*6801	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.503617	0.695361	-3.808256	31887.272626
HLA A*2603	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.606997	0.798696	-3.808301	40457.315703
HLA A*2603	1:367-375	9	GQSSADAIA	1.065394	-0.221230	-4.652483	0.844164	-3.808319	44924.483644
HLA A*3002	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.483595	0.675193	-3.808402	30450.544557
HLA B*5701	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.413961	0.605498	-3.808463	25939.465755
HLA B*0702	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.332641	0.524138	-3.808502	21510.011981
HLA B*3501	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.104428	0.295880	-3.808548	12718.272491
HLA B*3901	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.471030	0.662443	-3.808587	29582.169277
HLA A*3301	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.639263	0.830662	-3.808601	43577.523120
HLA B*4501	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.637975	0.829345	-3.808630	43448.523668
HLA B*4402	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.394637	0.586005	-3.808632	24810.556925
HLA B*4501	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.582424	0.773768	-3.808655	38231.716826
HLA A*2603	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.599768	0.790996	-3.808772	39789.428291
HLA B*1501	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-3.964060	0.155271	-3.808789	9205.777916
HLA A*8001	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.451898	0.643088	-3.808810	28307.281355
HLA B*1517	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.488914	0.680074	-3.808840	30825.795838
HLA A*8001	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.383044	0.574191	-3.808853	24157.064230
HLA B*4501	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.638478	0.829510	-3.808968	43498.853859
HLA B*5701	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.425422	0.616392	-3.809030	26633.105843
HLA A*2301	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.541367	0.732333	-3.809033	34782.961046
HLA A*2603	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.555764	0.746693	-3.809071	35955.405786
HLA B*5301	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.607805	0.798696	-3.809109	40532.676945
HLA A*2602	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.590802	0.781429	-3.809373	38976.430575
HLA A*2601	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.333529	0.524138	-3.809390	21554.043629
HLA B*4002	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.617523	0.807959	-3.809564	41449.830339
HLA B*0801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.383798	0.574191	-3.809607	24199.051216
HLA B*0803	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.507539	0.697848	-3.809690	32176.489879
HLA B*4501	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.435642	0.625924	-3.809718	27267.296134
HLA B*4801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.435656	0.625924	-3.809732	27268.181226
HLA B*4601	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.380965	0.571232	-3.809733	24041.682630
HLA B*3501	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.384271	0.574537	-3.809733	24225.379279
HLA B*1502	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.605991	0.796188	-3.809804	40363.747884
HLA B*0802	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.479495	0.669685	-3.809811	30164.436197
HLA A*2403	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.395823	0.586005	-3.809818	24878.431893
HLA B*5301	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.591288	0.781429	-3.809859	39020.102664
HLA A*2403	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.268676	0.458556	-3.810120	18564.186513
HLA B*5101	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.381428	0.571232	-3.810196	24067.318667
HLA A*0301	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.368816	0.558588	-3.810227	23378.447791
HLA A*2601	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.362632	0.552387	-3.810245	23047.924803
HLA B*3501	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.371377	0.561125	-3.810252	23516.712593
HLA B*2705	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.467637	0.657361	-3.810276	29351.977209
HLA B*4601	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.361286	0.550986	-3.810300	22976.589935
HLA B*1801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.501197	0.690866	-3.810331	31710.084937
HLA B*0803	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.405273	0.594934	-3.810338	25425.683211
HLA A*2602	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.519667	0.709300	-3.810366	33087.709712
HLA A*1101	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.403769	0.593391	-3.810378	25337.803352
HLA A*3002	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.361375	0.550986	-3.810389	22981.313851

HLA A*2402	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.580518	0.770046	-3.810472	38064.345656
HLA A*0201	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.390400	0.579907	-3.810493	24569.730429
HLA B*1502	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.565000	0.754459	-3.810541	36728.231744
HLA A*2902	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.428565	0.617889	-3.810677	26826.587165
HLA A*0212	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.353309	0.542619	-3.810690	22558.440445
HLA A*0301	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.276192	0.465424	-3.810768	18888.258842
HLA A*0203	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.422788	0.612002	-3.810786	26472.078520
HLA A*6901	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.304910	0.494046	-3.810864	20179.466524
HLA B*4002	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.594618	0.783751	-3.810867	39320.372909
HLA A*2402	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.594369	0.783381	-3.810987	39297.831174
HLA B*1517	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.436988	0.625924	-3.811064	27351.952254
HLA A*2601	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.390971	0.579907	-3.811064	24602.051112
HLA B*4002	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.640715	0.829510	-3.811205	43723.460174
HLA A*0212	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.425081	0.613866	-3.811215	26612.222123
HLA A*0250	1:41-49	9	VLRADLARD	0.810769	-0.688323	-3.933663	0.122446	-3.811217	8583.469270
HLA B*5801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.350870	0.539629	-3.811242	22432.119322
HLA B*1509	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.473697	0.662443	-3.811254	29764.369229
HLA A*2501	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.473807	0.662443	-3.811364	29771.938223
HLA B*4403	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.486631	0.675193	-3.811438	30664.126530
HLA B*5801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.352191	0.540737	-3.811454	22500.424773
HLA B*4801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.425389	0.613866	-3.811523	26631.088769
HLA A*0211	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.362575	0.550986	-3.811590	23044.932516
HLA A*2602	1:121-129	9	DACQALNFS	1.030074	-1.020224	-3.821451	0.009850	-3.811602	6629.052415
HLA A*3101	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.396171	0.584529	-3.811642	24898.359124
HLA A*2301	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.509587	0.697848	-3.811739	32328.638596
HLA B*1502	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.481431	0.669685	-3.811747	30299.201825
HLA A*3101	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.305802	0.494046	-3.811757	20220.993291
HLA B*1501	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.277228	0.465424	-3.811804	18933.375513
HLA A*2402	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.576292	0.764421	-3.811871	37695.685460
HLA A*0203	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.220934	0.409024	-3.811910	16631.613650
HLA B*5101	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.455035	0.643088	-3.811947	28512.462296
HLA B*5101	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.501329	0.689311	-3.812018	31719.693083
HLA A*2603	1:167-175	9	GNSVTQTAA	1.201720	-0.353933	-4.659912	0.847787	-3.812125	45699.575469
HLA A*2602	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.544646	0.732333	-3.812313	35046.643546
HLA B*0702	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.396899	0.584529	-3.812370	24940.150340
HLA A*0211	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.482131	0.669685	-3.812447	30348.087986
HLA A*3001	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.274902	0.462438	-3.812464	18832.243388
HLA B*5301	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.503049	0.690572	-3.812477	31845.553341
HLA B*4002	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.611271	0.798696	-3.812575	40857.404820
HLA A*3201	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.192994	0.380356	-3.812638	15595.320781
HLA B*4403	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.130122	0.317460	-3.812662	13493.421709
HLA A*0250	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.577206	0.764363	-3.812843	37775.097557
HLA A*0211	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.449708	0.636741	-3.812967	28164.914779
HLA A*2603	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.646151	0.833148	-3.813004	44274.251934
HLA A*2403	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.391479	0.578365	-3.813114	24630.816299
HLA A*6802	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.425128	0.612002	-3.813127	26615.101662
HLA B*1509	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.488369	0.675193	-3.813176	30787.130828
HLA B*5701	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.408179	0.594934	-3.813244	25596.403314
HLA A*3101	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.387480	0.574191	-3.813289	24405.065732
HLA B*4402	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.408287	0.594934	-3.813353	25602.773897
HLA B*5301	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.587846	0.774481	-3.813365	38712.071585
HLA B*5801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.357353	0.543984	-3.813368	22769.449751
HLA A*3301	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.413200	0.599665	-3.813535	25894.038777
HLA B*0702	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.419043	0.605498	-3.813545	26244.781610
HLA B*5301	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.242644	0.429083	-3.813560	17484.113990
HLA A*0219	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.456686	0.643088	-3.813598	28621.105989
HLA B*4403	1:341-349	9	VLTVVVTIA	0.984284	-0.144407	-4.653505	0.839877	-3.813628	45030.329005
HLA A*3002	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.539644	0.725976	-3.813668	34645.304113
HLA A*2902	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.451130	0.637402	-3.813728	28257.249086
HLA A*2603	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.605202	0.791452	-3.813750	40290.444424
HLA A*0101	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.385011	0.571232	-3.813779	24266.697308
HLA A*2602	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.496731	0.682948	-3.813783	31385.643276
HLA A*3101	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.393807	0.579907	-3.813900	24763.221643
HLA B*0803	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.476363	0.662443	-3.813921	29947.691373
HLA B*0802	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.459919	0.645932	-3.813988	28834.956681

HLA A*3101	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.392355	0.578365	-3.813990	24680.568724
HLA A*0250	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.584038	0.770046	-3.813992	38374.072966
HLA A*0301	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.366555	0.552387	-3.814169	23257.095076
HLA B*5301	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.597601	0.783381	-3.814220	39591.456039
HLA A*2403	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.409199	0.594934	-3.814264	25656.571508
HLA A*0201	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-3.911225	0.096922	-3.814303	8151.269926
HLA B*7301	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.597695	0.783381	-3.814314	39600.024381
HLA A*3001	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.243407	0.429083	-3.814324	17514.881844
HLA A*3001	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.302109	0.487735	-3.814374	20049.756136
HLA A*6801	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.643797	0.829345	-3.814452	44034.903407
HLA B*4403	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.631169	0.816673	-3.814496	42772.887172
HLA A*0301	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.368816	0.554273	-3.814543	23378.447791
HLA B*5701	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.385842	0.571232	-3.814611	24313.215008
HLA A*0101	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.367011	0.552387	-3.814625	23281.516640
HLA B*5301	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.584780	0.770046	-3.814734	38439.730507
HLA A*8001	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.452150	0.637402	-3.814747	28323.671998
HLA A*0201	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.347689	0.532852	-3.814837	22268.404611
HLA A*0101	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.373451	0.558588	-3.814863	23629.319075
HLA B*1801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.319392	0.504447	-3.814945	20863.727719
HLA A*0206	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.495023	0.680074	-3.814949	31262.446298
HLA B*3901	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.357609	0.542619	-3.814989	22782.880352
HLA A*6801	1:424-432	9	PEQREIPDV	1.032518	-0.159395	-4.688172	0.873123	-3.815049	48772.135451
HLA A*3002	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.585140	0.770046	-3.815094	38471.560745
HLA A*0206	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.407596	0.592477	-3.815119	25562.084862
HLA B*4402	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.420624	0.605498	-3.815126	26340.509224
HLA B*1502	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.580286	0.765110	-3.815175	38043.964649
HLA A*3201	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.611214	0.795837	-3.815378	40852.100347
HLA A*6801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.389938	0.574537	-3.815400	24543.559233
HLA B*4001	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.389982	0.574537	-3.815445	24546.082143
HLA B*4601	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.393814	0.578365	-3.815449	24763.623546
HLA A*0201	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.393873	0.578365	-3.815508	24766.972984
HLA A*3001	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.284612	0.469073	-3.815539	19258.057535
HLA B*1517	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.458653	0.643088	-3.815565	28750.998426
HLA B*4801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.431984	0.616392	-3.815592	27038.582916
HLA A*0101	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.366584	0.550986	-3.815598	23258.604945
HLA A*0201	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.415279	0.599665	-3.815614	26018.310263
HLA B*3501	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.441553	0.625924	-3.815629	27640.976330
HLA A*0206	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.485411	0.669685	-3.815727	30578.150622
HLA A*2403	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.409213	0.593391	-3.815822	25657.404317
HLA A*0212	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.366887	0.550986	-3.815901	23274.842225
HLA A*3101	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.355560	0.539629	-3.815931	22675.656969
HLA B*5701	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.409340	0.593391	-3.815949	25664.900813
HLA A*0216	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.482585	0.666540	-3.816044	30379.791234
HLA B*4601	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.411001	0.594934	-3.816066	25763.251676
HLA A*2403	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.432590	0.616515	-3.816075	27076.348406
HLA B*2705	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-3.878957	0.062590	-3.816367	7567.587442
HLA B*1801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.453801	0.637402	-3.816399	28431.596326
HLA A*0212	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.375004	0.558588	-3.816416	23713.967283
HLA B*4601	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.390612	0.574191	-3.816421	24581.696099
HLA A*3001	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.296238	0.479739	-3.816499	19780.521244
HLA A*2902	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.395337	0.578823	-3.816514	24850.587448
HLA A*8001	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.434458	0.617889	-3.816569	27193.050821
HLA A*2602	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.609943	0.793337	-3.816606	40732.711258
HLA A*0212	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.401194	0.584529	-3.816665	25188.013980
HLA B*0702	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.471183	0.654485	-3.816698	29592.573463
HLA A*1101	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.471270	0.654485	-3.816785	29598.497479
HLA A*6901	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.326358	0.509478	-3.816880	21201.087058
HLA B*4402	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.433459	0.616515	-3.816944	27130.600301
HLA A*2402	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.539088	0.722004	-3.817083	34600.912318
HLA A*2403	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.358100	0.540737	-3.817363	22808.654768
HLA B*3801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.388650	0.571232	-3.817418	24470.904674
HLA B*4001	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.403466	0.586005	-3.817461	25320.126883
HLA B*1517	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.474846	0.657361	-3.817484	29843.213199
HLA A*2602	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.608496	0.790996	-3.817500	40597.195763
HLA B*4501	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.650705	0.833148	-3.817557	44740.881240

HLA A*3301	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.599260	0.781690	-3.817570	39742.960065
HLA B*5101	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.440917	0.623337	-3.817580	27600.482139
HLA A*0202	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.497704	0.680074	-3.817630	31456.016294
HLA A*3002	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.409981	0.592081	-3.817900	25702.833302
HLA A*3002	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.582325	0.764421	-3.817905	38223.030980
HLA B*3901	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.507250	0.689311	-3.817939	32155.086238
HLA B*1503	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.191350	0.373369	-3.817980	15536.374195
HLA A*8001	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.417664	0.599665	-3.817999	26161.570745
HLA A*1101	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.430039	0.612002	-3.818037	26917.737466
HLA B*1503	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.508920	0.690866	-3.818054	32279.006738
HLA A*6901	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.376675	0.558588	-3.818086	23805.357076
HLA A*2301	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.530021	0.711889	-3.818132	33886.045318
HLA A*2902	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.434528	0.616392	-3.818136	27197.464521
HLA A*3101	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.221306	0.403047	-3.818259	16645.835807
HLA B*5301	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.583476	0.765110	-3.818366	38324.488752
HLA A*0206	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.515778	0.697387	-3.818391	32792.785572
HLA B*5101	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.444335	0.625924	-3.818411	27818.593556
HLA A*3101	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.362416	0.543984	-3.818431	23036.456479
HLA A*8001	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.434874	0.616392	-3.818482	27219.102008
HLA B*5801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.342642	0.524138	-3.818504	22011.133606
HLA A*0219	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.403130	0.584529	-3.818601	25300.546450
HLA B*5801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.361060	0.542449	-3.818611	22964.660156
HLA A*0219	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.369810	0.550986	-3.818824	23432.007896
HLA A*0219	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.436803	0.617889	-3.818914	27340.265041
HLA B*5401	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.398945	0.579907	-3.819039	25057.945973
HLA B*4601	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.403673	0.584529	-3.819144	25332.183912
HLA B*4501	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.635959	0.816673	-3.819286	43247.316643
HLA A*6801	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.602747	0.783381	-3.819366	40063.311712
HLA B*7301	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.534351	0.714935	-3.819416	34225.593522
HLA B*3501	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.315156	0.495678	-3.819478	20661.211571
HLA A*2402	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.363482	0.543984	-3.819498	23093.105621
HLA B*5701	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.405740	0.586005	-3.819735	25453.070426
HLA A*2402	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.494945	0.675193	-3.819753	31256.865626
HLA A*2602	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.574278	0.754459	-3.819819	37521.322406
HLA A*0219	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.419503	0.599665	-3.819839	26272.624715
HLA B*4601	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.412366	0.592477	-3.819889	25844.356723
HLA A*6802	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.423324	0.603309	-3.820015	26504.750776
HLA A*2603	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.552933	0.732827	-3.820106	35721.777829
HLA B*1517	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.413498	0.593391	-3.820107	25911.835543
HLA A*2602	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.550910	0.730675	-3.820235	35555.775752
HLA A*6802	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.415258	0.594934	-3.820323	26017.043489
HLA B*7301	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.593015	0.772678	-3.820337	39175.565947
HLA A*0216	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.463434	0.643088	-3.820346	29069.270479
HLA A*6802	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.391589	0.571232	-3.820357	24637.079845
HLA B*5301	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.552402	0.732039	-3.820363	35678.129823
HLA B*5301	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.584733	0.764363	-3.820371	38435.571639
HLA A*2301	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.533317	0.712902	-3.820415	34144.221474
HLA B*3501	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.286694	0.466242	-3.820452	19350.586096
HLA A*2501	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.463655	0.643088	-3.820567	29084.056822
HLA A*6802	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.399415	0.578823	-3.820592	25085.072788
HLA A*2402	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.553652	0.733042	-3.820610	35780.961565
HLA B*2705	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.458075	0.637402	-3.820673	28712.761106
HLA A*2603	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.602122	0.781429	-3.820693	40005.700846
HLA B*1502	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.546688	0.725976	-3.820712	35211.792499
HLA A*0212	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.279394	0.458556	-3.820838	19028.049550
HLA B*4601	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.361279	0.540402	-3.820876	22976.217036
HLA A*2902	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.316620	0.495678	-3.820942	20730.964792
HLA A*2403	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.392177	0.571232	-3.820945	24670.423355
HLA A*0206	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.533893	0.712902	-3.820991	34189.507010
HLA A*3301	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.239571	0.418508	-3.821063	17360.830738
HLA A*0203	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.156018	0.334871	-3.821147	14322.476464
HLA B*1503	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.447103	0.625924	-3.821179	27996.443367
HLA A*0301	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.273983	0.452683	-3.821301	18792.450273
HLA A*2902	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.395893	0.574537	-3.821356	24882.469907
HLA A*0206	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.235525	0.414162	-3.821362	17199.851199

HLA B*4002	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.644993	0.823629	-3.821364	44156.326496
HLA B*4501	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.458141	0.636741	-3.821400	28717.110756
HLA A*6901	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.362150	0.540737	-3.821413	23022.378195
HLA B*4601	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.380034	0.558588	-3.821446	23990.232877
HLA B*4403	1:299-307	9	SAAGNLSGP	0.711648	0.120170	-4.653270	0.831818	-3.821453	45005.974684
HLA B*7301	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.586564	0.765110	-3.821453	38597.892603
HLA A*0203	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.264515	0.442960	-3.821555	18387.173970
HLA A*6802	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.414187	0.592477	-3.821710	25952.940898
HLA B*5401	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.552491	0.730675	-3.821816	35685.465137
HLA B*0801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.406360	0.584529	-3.821832	25489.448746
HLA A*2602	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.097008	0.275124	-3.821885	12502.833621
HLA A*6801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.501982	0.680074	-3.821908	31767.433780
HLA A*0301	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.365947	0.543984	-3.821963	23224.530954
HLA B*4403	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.603416	0.781429	-3.821987	40125.129707
HLA A*0101	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.354853	0.532852	-3.822001	22638.762506
HLA B*3801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.519911	0.697848	-3.822063	33106.331038
HLA A*6801	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.620765	0.798696	-3.822069	41760.438143
HLA A*2301	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.548095	0.725976	-3.822119	35326.082223
HLA B*1503	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.511444	0.689311	-3.822132	32467.100803
HLA B*1517	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.440134	0.617889	-3.822246	27550.804822
HLA A*0206	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.459081	0.636741	-3.822339	28779.320595
HLA A*2501	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.476836	0.654485	-3.822351	29980.273836
HLA B*5801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.037111	0.214737	-3.822373	10892.076459
HLA B*0702	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.417361	0.594934	-3.822426	26143.319589
HLA A*0212	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.435997	0.613540	-3.822457	27289.579704
HLA B*4801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.439004	0.616515	-3.822489	27479.206506
HLA B*0702	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.414607	0.592081	-3.822526	25978.085124
HLA B*5101	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.327028	0.504447	-3.822580	21233.800497
HLA B*1503	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.316690	0.494046	-3.822644	20734.329631
HLA A*3002	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.537617	0.714935	-3.822682	34483.931389
HLA B*4403	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.652196	0.829510	-3.822687	44894.842976
HLA B*3801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.553459	0.730675	-3.822784	35765.092260
HLA B*4001	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.401269	0.578365	-3.822904	25192.374817
HLA B*4601	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.365555	0.542619	-3.822935	23203.558192
HLA B*4601	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.277104	0.454147	-3.822957	18927.947635
HLA A*0101	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.365649	0.542619	-3.823029	23208.579882
HLA A*6901	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.348944	0.525884	-3.823060	22332.828389
HLA A*2403	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.426399	0.603309	-3.823091	26693.111514
HLA A*6801	1:492-500	9	PATKDIPDV	0.908769	-0.079259	-4.652610	0.829510	-3.823100	44937.609530
HLA B*4001	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.381738	0.558588	-3.823149	24084.511407
HLA B*3901	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.415629	0.592477	-3.823152	26039.291388
HLA B*3801	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.556225	0.733042	-3.823183	35993.550899
HLA B*4001	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.375777	0.552387	-3.823391	23756.212255
HLA A*0203	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.418531	0.594934	-3.823596	26213.847918
HLA B*0702	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.461026	0.637402	-3.823624	28908.523503
HLA B*4403	1:515-523	9	YGFTKFSQA	1.102156	-0.286860	-4.639028	0.815296	-3.823731	43553.954539
HLA A*0301	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.328776	0.505009	-3.823767	21319.437870
HLA B*4501	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.622483	0.798696	-3.823786	41925.912159
HLA A*8001	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.427102	0.603309	-3.823793	26736.324079
HLA B*3801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.535716	0.711889	-3.823827	34333.338786
HLA B*1501	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.376219	0.552387	-3.823832	23780.386019
HLA B*4002	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.556951	0.733042	-3.823909	36053.770044
HLA A*0211	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.459922	0.635971	-3.823950	28835.112675
HLA A*3301	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.640628	0.816673	-3.823955	43714.709105
HLA B*5701	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.423629	0.599665	-3.823964	26523.397741
HLA A*2602	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.546084	0.722004	-3.824080	35162.870100
HLA A*6901	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.105702	0.281512	-3.824190	12755.619226
HLA A*0201	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.395461	0.571232	-3.824229	24857.713733
HLA B*4002	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.623075	0.798791	-3.824283	41983.108401
HLA B*4403	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.615326	0.790996	-3.824330	41240.696258
HLA B*4801	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.395565	0.571232	-3.824333	24863.631446
HLA A*6801	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.647977	0.823629	-3.824348	44460.749733
HLA A*3201	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.621815	0.797462	-3.824353	41861.546290
HLA B*5401	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.499616	0.675193	-3.824423	31594.843020
HLA B*0803	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.504717	0.680074	-3.824643	31968.108006

HLA A*0211	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.365103	0.540402	-3.824701	23179.469199
HLA B*3901	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.494386	0.669685	-3.824702	31216.646634
HLA B*5301	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.004298	0.179592	-3.824706	10099.451170
HLA B*4801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.398964	0.574191	-3.824773	25059.030482
HLA A*3002	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.318913	0.494046	-3.824867	20840.714848
HLA A*3101	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.430466	0.605498	-3.824968	26944.253717
HLA A*3301	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.625072	0.799991	-3.825080	42176.608324
HLA A*0212	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.346890	0.521798	-3.825092	22227.482594
HLA A*3001	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.290035	0.464928	-3.825107	19500.021547
HLA B*5801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.351032	0.525884	-3.825148	22440.494399
HLA B*0702	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.471093	0.645932	-3.825162	29586.490571
HLA A*0219	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.283868	0.458556	-3.825312	19225.059524
HLA A*2902	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.468439	0.643088	-3.825351	29406.174897
HLA A*3101	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.418773	0.593391	-3.825382	26228.458832
HLA A*0202	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.290324	0.464928	-3.825396	19513.001499
HLA B*4403	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.621677	0.796188	-3.825489	41848.186909
HLA A*0301	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.367953	0.542449	-3.825504	23332.077583
HLA A*3101	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.386641	0.561125	-3.825517	24357.976973
HLA A*2402	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.538446	0.712902	-3.825544	34549.847958
HLA B*1503	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.278248	0.452683	-3.825565	18977.881258
HLA B*4801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.428925	0.603309	-3.825616	26848.801073
HLA B*3801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.547635	0.722004	-3.825631	35288.644478
HLA B*0803	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.495418	0.669685	-3.825733	31290.872444
HLA A*2601	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.404119	0.578365	-3.825754	25358.235717
HLA A*2602	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.622130	0.796188	-3.825942	41891.903779
HLA B*0702	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.442477	0.616515	-3.825961	27699.805951
HLA A*2301	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.540904	0.714935	-3.825968	34745.910916
HLA A*2602	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.590391	0.764421	-3.825970	38939.547857
HLA B*1517	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.442496	0.616515	-3.825980	27701.004800
HLA A*0201	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.321739	0.495678	-3.826061	20976.790550
HLA A*6801	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.659219	0.833148	-3.826072	45626.700892
HLA A*0201	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.387250	0.561125	-3.826125	24392.130349
HLA B*4501	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.609889	0.783751	-3.826138	40727.643306
HLA A*1101	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.439678	0.613540	-3.826139	27521.904911
HLA A*0216	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.347955	0.521798	-3.826156	22282.021838
HLA B*7301	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.617196	0.790996	-3.826201	41418.672836
HLA A*0301	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.368830	0.542619	-3.826211	23379.206652
HLA B*1509	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.552200	0.725976	-3.826224	35661.534418
HLA A*0202	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.252415	0.426183	-3.826232	17881.960754
HLA A*0216	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.387360	0.561125	-3.826236	24398.333197
HLA B*1501	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.387374	0.561125	-3.826250	24399.125164
HLA A*2602	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.598934	0.772678	-3.826256	39713.085602
HLA B*2705	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.469449	0.643088	-3.826361	29474.660706
HLA B*1509	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.496054	0.669685	-3.826370	31336.781010
HLA A*0216	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.244946	0.418508	-3.826439	17577.055522
HLA A*0206	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.493002	0.666540	-3.826462	31117.335447
HLA A*3201	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.599154	0.772678	-3.826477	39733.286017
HLA B*4402	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.440437	0.613866	-3.826571	27570.038569
HLA A*3002	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.420030	0.593391	-3.826639	26304.481579
HLA A*3201	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.379083	0.552387	-3.826696	23937.727695
HLA A*0211	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.506775	0.680074	-3.826701	32119.966430
HLA A*6801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.331205	0.504447	-3.826758	21439.029257
HLA B*1503	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.405136	0.578365	-3.826772	25417.706555
HLA B*4601	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.401328	0.574537	-3.826791	25195.782246
HLA A*0250	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.559852	0.733042	-3.826810	36295.459454
HLA B*5101	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.493425	0.666540	-3.826885	31147.651646
HLA A*0250	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.095608	0.268569	-3.827040	12462.585731
HLA A*0203	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.443447	0.616392	-3.827055	27761.764380
HLA A*0301	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.367883	0.540737	-3.827146	23328.291172
HLA B*1502	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.542194	0.714935	-3.827258	34849.260684
HLA B*0803	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.516589	0.689311	-3.827278	32854.047565
HLA B*4601	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.379743	0.552387	-3.827357	23974.144995
HLA B*4801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.407317	0.579907	-3.827410	25545.633881
HLA B*4801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.441027	0.613540	-3.827487	27607.500862
HLA B*0803	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.427182	0.599665	-3.827517	26741.242310

HLA A*2501	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.450902	0.623337	-3.827565	28242.424723
HLA B*1501	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.368355	0.540737	-3.827618	23353.671866
HLA A*2602	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.625119	0.797462	-3.827657	42181.171986
HLA B*1517	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.253790	0.426123	-3.827666	17938.642964
HLA B*4501	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.651299	0.823629	-3.827670	44802.160098
HLA A*0301	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.323419	0.495678	-3.827741	21058.087390
HLA B*1503	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.553718	0.725976	-3.827742	35786.381965
HLA A*2902	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.427433	0.599665	-3.827768	26756.726177
HLA A*6901	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.173968	0.346054	-3.827914	14926.850483
HLA A*3201	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.550981	0.722962	-3.828019	35561.546804
HLA B*4601	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.407928	0.579907	-3.828021	25581.590915
HLA A*6801	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.609713	0.781690	-3.828023	40711.121755
HLA B*0802	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.465434	0.637402	-3.828031	29203.408578
HLA B*1503	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.510985	0.682948	-3.828037	32432.868397
HLA B*1502	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.525999	0.697848	-3.828150	33573.650798
HLA A*0211	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.237874	0.409720	-3.828155	17293.152635
HLA A*6801	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.654715	0.826538	-3.828177	45155.962617
HLA B*3901	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.414208	0.586005	-3.828203	25954.204552
HLA A*0301	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.367866	0.539629	-3.828238	23327.407764
HLA B*4403	1:257-265	9	KNPENRYQT	1.095309	-0.265964	-4.657626	0.829345	-3.828281	45459.653040
HLA A*0219	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.389432	0.561125	-3.828308	24515.028572
HLA A*2301	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.440369	0.612002	-3.828368	27565.713534
HLA B*4001	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.407277	0.578823	-3.828454	25543.284605
HLA B*2705	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.382732	0.554273	-3.828459	24139.689106
HLA A*3201	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.583660	0.755176	-3.828483	38340.664001
HLA A*0206	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.369227	0.540737	-3.828490	23400.591363
HLA A*2403	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.319538	0.490880	-3.828658	20870.726861
HLA B*4801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.407105	0.578365	-3.828740	25533.198994
HLA A*6802	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.264818	0.436027	-3.828791	18400.010410
HLA B*1501	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.282944	0.454147	-3.828797	19184.228806
HLA A*0250	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-3.984073	0.155271	-3.828802	9639.919491
HLA A*3101	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.403384	0.574537	-3.828846	25315.333069
HLA B*4801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.423874	0.594934	-3.828939	26538.324759
HLA B*4402	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.445395	0.616392	-3.829003	27886.549898
HLA B*4403	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.526882	0.697848	-3.829034	33642.013081
HLA A*0206	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.001657	0.172544	-3.829113	10038.225618
HLA A*2602	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.466613	0.637402	-3.829211	29282.825944
HLA B*0702	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.403828	0.574537	-3.829290	25341.230451
HLA A*0216	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.317778	0.488312	-3.829466	20786.329635
HLA B*4403	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.613338	0.783751	-3.829588	41052.378504
HLA A*2902	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.362557	0.532852	-3.829705	23043.935174
HLA A*6801	1:101-109	9	RDIVHTEGP	0.763109	0.067553	-4.660422	0.830662	-3.829760	45753.255803
HLA B*5101	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.391039	0.561125	-3.829915	24605.911151
HLA B*4801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.423314	0.593391	-3.829923	26504.177231
HLA B*4403	1:117-125	9	EVIADACQA	1.033905	-0.225946	-4.637926	0.807959	-3.829967	43443.587863
HLA B*4402	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.429634	0.599665	-3.829970	26892.702136
HLA B*7301	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.527822	0.697848	-3.829973	33714.891730
HLA A*2603	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.628826	0.798791	-3.830035	42542.805832
HLA A*2501	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.416148	0.586005	-3.830143	26070.442206
HLA A*2603	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.630142	0.799991	-3.830151	42671.886303
HLA B*4002	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.562982	0.732827	-3.830155	36557.948138
HLA B*5401	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.562542	0.732333	-3.830209	36520.983018
HLA B*4001	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.381223	0.550986	-3.830238	24055.993800
HLA A*0206	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.443966	0.613540	-3.830426	27794.975793
HLA B*1503	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.414971	0.584529	-3.830443	25999.877737
HLA B*0802	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.442604	0.612002	-3.830602	27707.899188
HLA B*4403	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.563452	0.732827	-3.830625	36597.524434
HLA B*4001	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.401941	0.571232	-3.830709	25231.383342
HLA A*0212	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.447143	0.616392	-3.830751	27999.018265
HLA A*3301	1:171-179	9	TQTAAVIGT	1.065940	-0.279077	-4.617758	0.786863	-3.830894	41472.260304
HLA B*4403	1:251-259	9	VLKALAKNP	0.734176	0.098972	-4.664045	0.833148	-3.830897	46136.528123
HLA A*3001	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.280421	0.449508	-3.830913	19073.087389
HLA A*2601	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.381916	0.550986	-3.830931	24094.415827
HLA B*5701	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.405571	0.574537	-3.831034	25443.158080
HLA B*2705	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.373667	0.542619	-3.831048	23641.082546

HLA B*1501	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.234963	0.403854	-3.831109	17177.626790
HLA A*0301	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.337730	0.506563	-3.831167	21763.544953
HLA A*0206	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.415754	0.584529	-3.831225	26046.758552
HLA B*0803	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.443273	0.612002	-3.831272	27750.652688
HLA A*3201	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.614696	0.783381	-3.831315	41180.946747
HLA B*5401	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.520661	0.689311	-3.831349	33163.513770
HLA B*0702	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.411259	0.579907	-3.831352	25778.587636
HLA A*2601	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.373820	0.542449	-3.831371	23649.397224
HLA B*5701	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.338068	0.506563	-3.831505	21780.505883
HLA A*0202	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.488891	0.657361	-3.831529	30824.128242
HLA B*1509	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.355675	0.524138	-3.831537	22681.668732
HLA A*8001	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.416108	0.584529	-3.831580	26068.044667
HLA A*3002	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.290183	0.458556	-3.831627	19506.668736
HLA A*2403	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.390283	0.558588	-3.831694	24563.085352
HLA B*4403	1:307-315	9	PRTDPLPRQ	1.018548	-0.194919	-4.655347	0.823629	-3.831718	45221.724130
HLA B*5401	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.554770	0.722962	-3.831809	35873.220115
HLA A*1101	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.448252	0.616392	-3.831860	28070.604211
HLA B*0803	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.486069	0.654207	-3.831862	30624.504554
HLA B*4801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.431556	0.599665	-3.831891	27011.973834
HLA A*0201	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.390541	0.558588	-3.831953	24577.706895
HLA A*0201	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.382981	0.550986	-3.831995	24153.535938
HLA A*2501	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.445543	0.613540	-3.832003	27896.055896
HLA A*2403	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.327697	0.495678	-3.832019	21266.564413
HLA B*4801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.372798	0.540737	-3.832061	23593.808490
HLA B*0803	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.411003	0.578823	-3.832180	25763.391053
HLA B*4801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.418185	0.586005	-3.832180	26193.009546
HLA A*6802	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.353255	0.521039	-3.832216	22555.633731
HLA A*8001	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.411092	0.578823	-3.832269	25768.687927
HLA B*4402	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.425673	0.593391	-3.832282	26648.527096
HLA A*0211	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.521640	0.689311	-3.832329	33238.412580
HLA A*6801	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.606118	0.773768	-3.832350	40375.541230
HLA B*1501	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.258672	0.426183	-3.832488	18141.442472
HLA B*5701	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.411351	0.578823	-3.832528	25784.027122
HLA B*4402	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.425027	0.592477	-3.832550	26608.911038
HLA A*8001	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.446102	0.613540	-3.832562	27931.996697
HLA A*2602	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.547687	0.714935	-3.832751	35292.844696
HLA B*4801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.417314	0.584529	-3.832785	26140.491093
HLA B*4402	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.411160	0.578365	-3.832796	25772.731010
HLA A*0101	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.375253	0.542449	-3.832804	23727.569916
HLA B*1501	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.167751	0.334871	-3.832880	14714.701122
HLA B*4801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.425389	0.592477	-3.832912	26631.088769
HLA B*4002	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.547861	0.714935	-3.832925	35306.976372
HLA B*1501	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.328639	0.495678	-3.832962	21312.749443
HLA B*3801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.523828	0.690866	-3.832962	33406.243689
HLA A*2301	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.542266	0.709300	-3.832966	34855.105624
HLA B*5401	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.269010	0.436027	-3.832983	18578.453079
HLA A*8001	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.385398	0.552387	-3.833012	24288.368203
HLA B*4501	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.555978	0.722962	-3.833016	35973.110987
HLA A*0212	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.436450	0.603309	-3.833142	27318.087870
HLA A*0216	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.451149	0.617889	-3.833260	28258.472061
HLA A*0101	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.394392	0.561125	-3.833268	24796.601726
HLA B*1517	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.404596	0.571232	-3.833364	25386.099619
HLA A*0216	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.247596	0.414162	-3.833434	17684.644895
HLA B*4501	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.632226	0.798791	-3.833435	42877.142483
HLA A*2602	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.607930	0.774481	-3.833448	40544.300307
HLA A*3002	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.449864	0.616392	-3.833471	28174.972933
HLA B*4001	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.355318	0.521798	-3.833520	22663.025191
HLA B*1801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.459522	0.625924	-3.833598	28808.605757
HLA A*0212	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.387983	0.554273	-3.833710	24433.336236
HLA B*4403	1:527-535	9	SPRPAGEVT	1.281976	-0.455438	-4.660349	0.826538	-3.833811	45745.583325
HLA A*0301	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.342304	0.508438	-3.833867	21993.993081
HLA B*1517	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.488360	0.654485	-3.833875	30786.464615
HLA B*0702	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.447432	0.613540	-3.833892	28017.655470
HLA A*2603	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.629832	0.795837	-3.833995	42641.424958
HLA A*0216	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.445999	0.612002	-3.833997	27925.348692

HLA A*3201	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.604044	0.770046	-3.833998	40183.129944
HLA A*2902	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.388274	0.554273	-3.834001	24449.732258
HLA B*5301	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.584625	0.750403	-3.834222	38426.007948
HLA A*0212	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.426702	0.592477	-3.834225	26711.746489
HLA A*0201	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.408451	0.574191	-3.834260	25612.471305
HLA B*1503	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.229395	0.395099	-3.834296	16958.790819
HLA B*1801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.270410	0.436027	-3.834383	18638.452148
HLA B*5701	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.418947	0.584529	-3.834418	26238.961020
HLA B*5701	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.386860	0.552387	-3.834473	24370.235034
HLA A*6801	1:450-458	9	GRFKQANSP	0.757924	0.058749	-4.651313	0.816673	-3.834640	44803.614370
HLA A*3201	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.556648	0.722004	-3.834643	36028.617771
HLA A*0216	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.448604	0.613866	-3.834738	28093.392284
HLA B*1502	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.497215	0.662443	-3.834772	31420.640100
HLA B*5401	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.413597	0.578823	-3.834774	25917.723778
HLA B*1509	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.480724	0.645932	-3.834792	30249.903462
HLA A*8001	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.429806	0.594934	-3.834871	26903.324750
HLA A*3001	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-3.983073	0.148101	-3.834972	9617.728790
HLA A*0216	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.451426	0.616392	-3.835034	28276.517094
HLA A*0216	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.489650	0.654485	-3.835165	30878.037231
HLA A*2601	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.375904	0.540737	-3.835167	23763.153267
HLA A*8001	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.428572	0.593391	-3.835181	26827.022556
HLA B*4501	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.626289	0.790996	-3.835293	42294.966547
HLA A*2602	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.599685	0.764363	-3.835323	39781.895030
HLA B*5101	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.489892	0.654485	-3.835407	30895.247842
HLA B*0803	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.458808	0.623337	-3.835471	28761.265881
HLA A*2301	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.505222	0.669685	-3.835538	32005.312582
HLA B*2705	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.449405	0.613866	-3.835539	28145.266026
HLA B*2705	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.451997	0.616392	-3.835605	28313.713934
HLA A*2501	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.414537	0.578823	-3.835714	25973.869310
HLA A*2602	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.619496	0.783751	-3.835746	41638.619722
HLA A*2602	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.257779	0.421976	-3.835803	18104.186367
HLA B*4403	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.629228	0.793337	-3.835891	42582.180010
HLA A*0206	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.490416	0.654485	-3.835931	30932.542524
HLA A*6901	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.390349	0.554273	-3.836076	24566.806374
HLA A*6901	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.380070	0.543984	-3.836085	23992.179723
HLA B*7301	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.431082	0.594934	-3.836147	26982.471337
HLA A*0206	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.450171	0.613866	-3.836305	28194.947486
HLA A*2403	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.346801	0.510481	-3.836320	22222.913631
HLA B*1501	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.342943	0.506563	-3.836380	22026.380842
HLA A*0212	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.416299	0.579907	-3.836392	26079.470213
HLA A*3301	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.632240	0.795837	-3.836403	42878.534269
HLA A*0212	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.431375	0.594934	-3.836441	27000.724030
HLA B*5401	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.265539	0.429083	-3.836456	18430.595201
HLA B*5401	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.562500	0.725976	-3.836524	36517.426850
HLA B*4601	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.358447	0.521798	-3.836649	22826.924140
HLA A*0219	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.450557	0.613866	-3.836690	28219.973758
HLA A*3201	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.546033	0.709300	-3.836732	35158.685350
HLA B*5101	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.450599	0.613866	-3.836733	28222.721897
HLA A*8001	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.442258	0.605498	-3.836760	27685.873138
HLA B*0802	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.454689	0.617889	-3.836801	28489.796668
HLA A*2301	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.516925	0.680074	-3.836851	32879.473754
HLA A*3101	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.422913	0.586005	-3.836908	26479.669792
HLA B*3801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.546230	0.709300	-3.836930	35174.666166
HLA B*3901	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.472961	0.635971	-3.836990	29714.012010
HLA A*3301	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.633208	0.796188	-3.837020	42974.211720
HLA A*6801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.506839	0.669685	-3.837154	32124.658440
HLA B*4001	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.127641	0.290447	-3.837194	13416.555681
HLA B*0702	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.451149	0.613866	-3.837282	28258.472061
HLA B*5401	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.473283	0.635971	-3.837312	29736.042856
HLA A*0212	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.378303	0.540737	-3.837566	23894.772132
HLA A*3101	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.416421	0.578823	-3.837598	26086.807772
HLA A*0211	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.475034	0.637402	-3.837631	29856.131873
HLA B*5301	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.512825	0.675193	-3.837632	32570.543571
HLA B*7301	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.570702	0.733042	-3.837660	37213.645837
HLA A*2603	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.568360	0.730675	-3.837685	37013.468433

HLA A*0211	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.398842	0.561125	-3.837717	25051.982012
HLA B*4801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.388779	0.550986	-3.837794	24478.186926
HLA B*7301	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.563832	0.725976	-3.837856	36629.612638
HLA A*8001	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.429989	0.592081	-3.837908	26914.679578
HLA A*6802	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.380589	0.542619	-3.837970	24020.881580
HLA B*3901	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.483931	0.645932	-3.837999	30474.110644
HLA A*0212	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.264167	0.426123	-3.838044	18372.457921
HLA B*0802	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.492690	0.654485	-3.838205	31094.954103
HLA A*0206	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.481387	0.643088	-3.838299	30296.087594
HLA A*2902	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.424320	0.586005	-3.838315	26565.616968
HLA A*0101	1:62-70 9		NAAALNHPA	0.615967	-0.206247	-4.248059	0.409720	-3.838340	17703.502319
HLA A*0206	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.527789	0.689311	-3.838478	33712.338314
HLA B*7301	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.513725	0.675193	-3.838532	32638.099295
HLA B*0802	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.430638	0.592081	-3.838556	26954.896695
HLA A*6901	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.304094	0.465424	-3.838670	20141.620528
HLA B*5801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.359716	0.521039	-3.838678	22893.706850
HLA B*4001	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.371558	0.532852	-3.838706	23526.510790
HLA A*0212	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.410009	0.571232	-3.838777	25704.501950
HLA B*4402	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.442164	0.603309	-3.838856	27679.882686
HLA A*2601	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.400043	0.561125	-3.838918	25121.332862
HLA B*0702	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.343993	0.505009	-3.838985	22079.709941
HLA A*2301	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.534391	0.695361	-3.839029	34228.741330
HLA B*4501	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.248062	0.409024	-3.839037	17703.598093
HLA B*4402	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.379588	0.540402	-3.839186	23965.586490
HLA A*0101	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.393589	0.554273	-3.839316	24750.765913
HLA A*0203	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.431850	0.592477	-3.839373	27030.246485
HLA A*0212	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.338871	0.499448	-3.839423	21820.841087
HLA A*8001	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.380065	0.540402	-3.839663	23991.920134
HLA B*0801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.382227	0.542449	-3.839777	24111.627924
HLA A*2601	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.398367	0.558588	-3.839779	25024.620219
HLA B*0802	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.439479	0.599665	-3.839814	27509.252131
HLA B*4001	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-3.980573	0.140490	-3.840082	9562.526995
HLA B*1509	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.414295	0.574191	-3.840104	25959.400219
HLA A*0203	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.382788	0.542619	-3.840169	24142.823542
HLA A*2603	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.553090	0.712902	-3.840188	35734.727983
HLA B*0702	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.432675	0.592477	-3.840198	27081.622201
HLA B*1502	1:42-50 9		LRADLARDP	0.607027	0.163019	-4.610317	0.770046	-3.840271	40767.763484
HLA A*6801	1:131-139	9	QNGIIHRDV	0.825242	-0.005894	-4.659673	0.819348	-3.840325	45674.365002
HLA B*0802	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.392752	0.552387	-3.840366	24703.143777
HLA B*4601	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.381108	0.540737	-3.840371	24049.617772
HLA B*2705	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.466331	0.625924	-3.840407	29263.822093
HLA B*4001	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.366525	0.525884	-3.840641	23255.459495
HLA A*3001	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.294826	0.454147	-3.840679	19716.312416
HLA A*1101	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.457201	0.616515	-3.840685	28655.035390
HLA A*0201	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.395034	0.554273	-3.840761	24833.250877
HLA A*0216	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.414964	0.574191	-3.840773	25999.455771
HLA A*2603	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.636993	0.796188	-3.840805	43350.383065
HLA A*6801	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.563788	0.722962	-3.840826	36625.847751
HLA B*2705	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.329154	0.488312	-3.840842	21338.015022
HLA A*0212	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.440557	0.599665	-3.840892	27577.646312
HLA B*2705	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.495394	0.654485	-3.840909	31289.179688
HLA A*6901	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.373898	0.532852	-3.841046	23653.619641
HLA B*5801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.329420	0.488312	-3.841108	21351.063311
HLA A*2402	1:60-68 9		AQNAAALNH	0.981888	-0.249555	-4.573468	0.732333	-3.841134	37451.357481
HLA B*7301	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.467120	0.625924	-3.841196	29317.063983
HLA A*2402	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.524255	0.682948	-3.841307	33439.151669
HLA A*0206	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.221221	0.379878	-3.841343	16642.594246
HLA B*3901	1:54-62 9		LRFRREAQN	1.069423	-0.451534	-4.459346	0.617889	-3.841457	28796.919275
HLA B*4002	1:370-378	9	SADAIATLQ	0.845543	-0.054547	-4.632456	0.790996	-3.841461	42899.880647
HLA B*7301	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.434853	0.593391	-3.841462	27217.776769
HLA A*6801	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.637301	0.795837	-3.841464	43381.116174
HLA B*5401	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.554401	0.712902	-3.841499	35842.764038
HLA B*0802	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.458054	0.616515	-3.841538	28711.363145
HLA B*5301	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.539029	0.697387	-3.841641	34596.232957
HLA B*5301	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.487655	0.645932	-3.841723	30736.539731

HLA B*3501	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.459708	0.617889	-3.841819	28820.920646
HLA B*5701	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.421761	0.579907	-3.841854	26409.569227
HLA A*0206	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.348417	0.506563	-3.841854	22305.781520
HLA A*2902	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.260373	0.418508	-3.841865	18212.637480
HLA A*3002	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.551197	0.709300	-3.841897	35579.250540
HLA B*0802	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.465278	0.623337	-3.841942	29192.983284
HLA A*2501	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.478696	0.636741	-3.841955	30109.003866
HLA A*0216	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.428046	0.586005	-3.842041	26794.532852
HLA B*4002	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.382513	0.540402	-3.842111	24127.547007
HLA B*2705	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.455693	0.613540	-3.842153	28555.684817
HLA B*3501	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.422069	0.579907	-3.842162	26428.292203
HLA A*0301	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.363219	0.521039	-3.842181	23079.117572
HLA A*0216	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.434406	0.592081	-3.842325	27189.814563
HLA B*0802	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.479105	0.636741	-3.842364	30137.359439
HLA A*2902	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.307320	0.464928	-3.842392	20291.785013
HLA B*4403	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.642425	0.799991	-3.842434	43896.000162
HLA A*2402	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.565444	0.722962	-3.842483	36765.804429
HLA A*2603	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.568510	0.725976	-3.842534	37026.285933
HLA A*3001	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.268864	0.426183	-3.842680	18572.222667
HLA B*1503	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.268822	0.426123	-3.842698	18570.414229
HLA A*8001	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.428812	0.586005	-3.842807	26841.830025
HLA B*3501	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.421197	0.578365	-3.842833	26375.301996
HLA A*2603	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.607232	0.764363	-3.842869	40479.208583
HLA A*3101	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.395332	0.552387	-3.842945	24850.318572
HLA B*4002	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.624689	0.781690	-3.842999	42139.432881
HLA B*2705	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.238835	0.395731	-3.843104	17331.458600
HLA A*6801	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.607467	0.764363	-3.843104	40501.113311
HLA A*3301	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.607512	0.764363	-3.843149	40505.276549
HLA A*3001	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.286318	0.442960	-3.843358	19333.843819
HLA B*4001	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.397768	0.554273	-3.843496	24990.122012
HLA B*3801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.518715	0.675193	-3.843522	33015.293733
HLA A*3301	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.641029	0.797462	-3.843567	43755.167902
HLA A*1101	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.246671	0.403047	-3.843624	17646.990284
HLA B*3901	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.460211	0.616515	-3.843695	28854.306417
HLA A*6802	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.423704	0.579907	-3.843797	26527.989775
HLA B*2705	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.435879	0.592081	-3.843798	27282.199023
HLA A*0202	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.332204	0.488312	-3.843892	21488.378646
HLA B*5101	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.480682	0.636741	-3.843941	30246.957930
HLA B*5301	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.576357	0.732333	-3.844024	37701.395918
HLA B*5701	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.422400	0.578365	-3.844036	26448.459246
HLA A*0206	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.449539	0.605498	-3.844041	28153.946342
HLA A*0250	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.576411	0.732333	-3.844078	37706.087298
HLA B*1509	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.527049	0.682948	-3.844101	33654.937532
HLA B*5401	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.513835	0.669685	-3.844151	32646.399069
HLA B*4601	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.388213	0.543984	-3.844229	24446.293471
HLA B*3801	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.534920	0.690572	-3.844348	34270.430779
HLA B*5701	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.405486	0.561125	-3.844362	25438.203354
HLA B*7301	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.566478	0.722004	-3.844473	36853.424198
HLA A*2902	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.312971	0.468482	-3.844489	20557.522007
HLA A*2501	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.396887	0.552387	-3.844501	24939.475732
HLA B*5801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.355008	0.510481	-3.844527	22646.847180
HLA B*1502	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.437930	0.593391	-3.844539	27411.353045
HLA A*1101	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.418763	0.574191	-3.844572	26227.891266
HLA A*0212	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.248430	0.403854	-3.844576	17718.641078
HLA B*5801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.349031	0.504447	-3.844583	22337.299107
HLA B*0801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.365714	0.521039	-3.844676	23212.095712
HLA B*2705	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.419226	0.574537	-3.844689	26255.858493
HLA A*6901	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.309768	0.464928	-3.844841	20406.494937
HLA B*4001	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.353304	0.508438	-3.844867	22558.196369
HLA A*2402	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.267560	0.422686	-3.844874	18516.543413
HLA A*6901	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.353347	0.508438	-3.844909	22560.393149
HLA A*2402	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.570921	0.725976	-3.844945	37232.373466
HLA B*4403	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.609386	0.764363	-3.845024	40680.519533
HLA A*0202	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.288087	0.442960	-3.845127	19412.763701
HLA A*0212	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.419337	0.574191	-3.845146	26262.535282

HLA B*4501	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.558093	0.712902	-3.845190	36148.687561
HLA B*1801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.450700	0.605498	-3.845202	28229.287978
HLA A*0211	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.491142	0.645932	-3.845210	30984.294330
HLA A*0101	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.367077	0.521798	-3.845279	23285.043519
HLA A*2601	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.399580	0.554273	-3.845307	25094.574109
HLA A*3101	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.367117	0.521798	-3.845319	23287.185099
HLA A*2403	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.445214	0.599665	-3.845549	27874.935855
HLA B*4002	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.641398	0.795837	-3.845561	43792.347254
HLA A*2403	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.333923	0.488312	-3.845612	21573.642172
HLA A*2603	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.643290	0.797462	-3.845828	43983.477087
HLA A*0211	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.367627	0.521798	-3.845829	23314.539049
HLA B*4001	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.386291	0.540402	-3.845889	24338.350565
HLA B*3801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.561013	0.714935	-3.846078	36392.588264
HLA A*2602	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.298782	0.452683	-3.846099	19896.753701
HLA B*0801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.424534	0.578365	-3.846169	26578.698439
HLA A*3301	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.637641	0.791452	-3.846190	43415.159144
HLA A*0101	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.370329	0.524138	-3.846190	23460.039619
HLA A*6802	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.248929	0.402654	-3.846274	17738.974183
HLA B*3501	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.438772	0.592477	-3.846295	27464.493160
HLA B*4402	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.459884	0.613540	-3.846344	28832.616867
HLA A*0219	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.420594	0.574191	-3.846402	26338.656799
HLA A*0219	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.460051	0.613540	-3.846511	28843.693664
HLA A*0211	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.460060	0.613540	-3.846520	28844.317835
HLA A*0202	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.432536	0.586005	-3.846531	27072.979574
HLA A*1101	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.492471	0.645932	-3.846540	31079.313554
HLA B*2705	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.458683	0.612002	-3.846682	28753.020514
HLA B*1502	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.593490	0.746693	-3.846797	39218.400312
HLA B*4801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.372817	0.525884	-3.846933	23594.829631
HLA B*1801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.058491	0.211378	-3.847113	11441.711549
HLA B*1502	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.569156	0.722004	-3.847152	37081.411657
HLA A*3201	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.562157	0.714935	-3.847222	36488.595174
HLA A*0212	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.326976	0.479739	-3.847237	21231.273452
HLA A*8001	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.427151	0.579907	-3.847244	26739.361703
HLA A*3201	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.611745	0.764421	-3.847325	40902.078099
HLA B*5801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.356843	0.509478	-3.847365	22742.735332
HLA B*4002	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.309818	0.462438	-3.847380	20408.813404
HLA B*1502	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.602568	0.755176	-3.847392	40046.843004
HLA B*3501	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.459482	0.612002	-3.847481	28805.956405
HLA A*0203	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.406086	0.558588	-3.847497	25473.320125
HLA B*4801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.390118	0.542619	-3.847499	24553.785263
HLA B*0801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.357057	0.509478	-3.847579	22753.934335
HLA B*1503	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.490688	0.643088	-3.847600	30951.960244
HLA B*5701	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.421806	0.574191	-3.847615	26412.283951
HLA A*0101	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.388377	0.540737	-3.847641	24455.552846
HLA A*0203	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.021454	0.173777	-3.847677	10506.394726
HLA A*2902	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.400080	0.552387	-3.847694	25123.507414
HLA B*1503	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.327474	0.479739	-3.847735	21255.637494
HLA B*1509	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.419017	0.571232	-3.847785	26243.219862
HLA B*1517	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.313264	0.465424	-3.847840	20571.428448
HLA B*5801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.311188	0.463212	-3.847975	20473.283709
HLA B*0801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.306564	0.458556	-3.848008	20256.467812
HLA B*1801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.514575	0.666540	-3.848035	32702.079720
HLA A*0219	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.419285	0.571232	-3.848053	26259.409765
HLA B*0802	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.474042	0.625924	-3.848118	29788.048869
HLA A*0206	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.484119	0.635971	-3.848148	30487.302423
HLA A*0219	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.426524	0.578365	-3.848159	26700.766170
HLA A*2501	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.474150	0.625924	-3.848226	29795.462693
HLA A*0301	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.358765	0.510481	-3.848284	22843.601532
HLA A*0211	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.448031	0.599665	-3.848366	28056.333107
HLA A*2902	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.453867	0.605498	-3.848369	28435.903382
HLA B*4801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.400813	0.552387	-3.848427	25165.948824
HLA A*2602	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.603621	0.755176	-3.848444	40144.019460
HLA A*0219	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.453961	0.605498	-3.848463	28442.057451
HLA B*5101	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.434500	0.586005	-3.848495	27195.698955
HLA A*0219	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.451814	0.603309	-3.848505	28301.768878

HLA A*0206	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.369669	0.521039	-3.848630	23424.403256
HLA B*1501	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.307205	0.458556	-3.848649	20286.406687
HLA A*2501	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.465138	0.616392	-3.848745	29183.508973
HLA B*2705	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.443769	0.594934	-3.848834	27782.347772
HLA A*2403	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.423375	0.574537	-3.848838	26507.905494
HLA A*0250	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.373064	0.524138	-3.848925	23608.236207
HLA B*1502	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.022779	0.173777	-3.849002	10538.500556
HLA A*3201	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.575014	0.725976	-3.849037	37584.910907
HLA B*4501	1:380-388	9	RGFKIRTLQ	0.740005	0.053332	-4.642432	0.793337	-3.849095	43896.712585
HLA B*0702	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.465495	0.616392	-3.849102	29207.516534
HLA B*0803	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.452439	0.603309	-3.849130	28342.525305
HLA A*0201	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.391758	0.542619	-3.849139	24646.678153
HLA B*1501	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.388953	0.539629	-3.849324	24487.988285
HLA B*1503	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.495357	0.645932	-3.849425	31286.471470
HLA A*0212	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.410618	0.561125	-3.849493	25740.543347
HLA A*0201	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.390417	0.540737	-3.849680	24570.660884
HLA A*0219	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.466075	0.616392	-3.849683	29246.570950
HLA B*4501	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.614064	0.764363	-3.849702	41121.061340
HLA A*6802	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.373858	0.524138	-3.849719	23651.444363
HLA A*2902	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.410853	0.561125	-3.849728	25754.472463
HLA A*0250	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.562634	0.712902	-3.849732	36528.689235
HLA A*8001	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.442218	0.592477	-3.849741	27683.327038
HLA B*5101	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.428624	0.578823	-3.849801	26830.215632
HLA B*5401	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.559103	0.709300	-3.849803	36232.876414
HLA A*0203	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.358243	0.508438	-3.849805	22816.182940
HLA A*2501	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.467760	0.617889	-3.849871	29360.235500
HLA A*0219	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.435978	0.586005	-3.849973	27288.398661
HLA A*8001	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.401037	0.550986	-3.850051	25178.885922
HLA A*1101	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.487575	0.637402	-3.850173	30730.886687
HLA A*0203	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.421430	0.571232	-3.850198	26389.431838
HLA B*5401	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.232083	0.381799	-3.850284	17064.072758
HLA B*1509	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.434824	0.584529	-3.850296	27216.009884
HLA A*6801	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.565343	0.714935	-3.850408	36757.252770
HLA B*3501	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.450098	0.599665	-3.850434	28190.219404
HLA A*0201	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.394439	0.543984	-3.850455	24799.284808
HLA A*2603	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.520195	0.669685	-3.850511	33128.009424
HLA A*0206	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.079354	0.228841	-3.850514	12004.785972
HLA A*0203	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.428890	0.578365	-3.850525	26846.622426
HLA B*5801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.346251	0.495678	-3.850573	22194.799131
HLA B*0802	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.435231	0.584529	-3.850702	27241.493566
HLA A*0202	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.540081	0.689311	-3.850770	34680.183128
HLA B*3801	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.576757	0.725976	-3.850781	37736.085130
HLA B*1501	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.323746	0.472905	-3.850840	21073.928492
HLA B*4501	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.605348	0.754459	-3.850889	40303.960634
HLA A*0212	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.265126	0.414162	-3.850963	18413.055036
HLA A*8001	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.339301	0.488312	-3.850990	21842.454629
HLA A*0201	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.393448	0.542449	-3.850998	24742.733282
HLA B*4001	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.375140	0.524138	-3.851002	23721.409267
HLA A*1101	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.253672	0.402654	-3.851018	17933.791317
HLA A*6802	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.314333	0.463212	-3.851121	20622.127382
HLA B*4001	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.412258	0.561125	-3.851133	25837.926028
HLA A*1101	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.494238	0.643088	-3.851150	31206.009095
HLA A*0216	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.402164	0.550986	-3.851179	25244.354079
HLA B*2705	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.425459	0.574191	-3.851268	26635.411257
HLA B*2705	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.450935	0.599665	-3.851270	28244.563841
HLA B*0802	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.443774	0.592477	-3.851297	27782.648373
HLA B*3901	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.464954	0.613540	-3.851414	29171.196966
HLA B*5801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.350915	0.499448	-3.851467	22434.425191
HLA A*2601	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.394176	0.542619	-3.851557	24784.263285
HLA B*1503	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.444970	0.593391	-3.851578	27859.257034
HLA B*5101	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.487606	0.635971	-3.851634	30733.048022
HLA B*5801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.317252	0.465424	-3.851827	20761.155702
HLA B*2705	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.455279	0.603309	-3.851970	28528.508733
HLA B*4601	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.406299	0.554273	-3.852027	25485.863726
HLA A*0301	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.320649	0.468482	-3.852167	20924.200883

HLA A*0212	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.357197	0.505009	-3.852189	22761.321309
HLA A*2301	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.542811	0.690572	-3.852240	34898.879532
HLA A*2902	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.444779	0.592477	-3.852302	27847.051753
HLA B*4002	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.616703	0.764363	-3.852340	41371.644765
HLA B*1801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.522098	0.669685	-3.852414	33273.495226
HLA B*0803	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.478346	0.625924	-3.852422	30084.743576
HLA B*5801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.360907	0.508438	-3.852470	22956.586219
HLA A*2403	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.426716	0.574191	-3.852525	26712.613549
HLA A*0211	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.495615	0.643088	-3.852527	31305.095208
HLA B*3901	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.351984	0.499448	-3.852536	22489.715539
HLA A*6802	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.395104	0.542449	-3.852655	24837.281558
HLA B*1801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.095326	0.242669	-3.852657	12454.497812
HLA A*3001	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.076009	0.223225	-3.852784	11912.660226
HLA B*4002	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.617222	0.764421	-3.852801	41421.137684
HLA A*6802	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.385661	0.532852	-3.852810	24303.089168
HLA A*0219	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.393232	0.540402	-3.852829	24730.421646
HLA B*3901	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.403830	0.550986	-3.852844	25341.367545
HLA A*3301	1:591-599	9	ADVDAGGSQ	0.880767	-0.097386	-4.636251	0.783381	-3.852869	43276.337812
HLA A*6901	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.392750	0.539629	-3.853121	24703.010136
HLA B*5701	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.374929	0.521798	-3.853131	23709.862360
HLA A*0206	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.433121	0.579907	-3.853214	27109.473141
HLA A*2402	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.568200	0.714935	-3.853265	36999.854702
HLA B*5701	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.411901	0.558588	-3.853312	25816.688153
HLA B*1517	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.453007	0.599665	-3.853342	28379.655446
HLA A*1101	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.507656	0.654207	-3.853449	32185.194619
HLA B*1501	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.352950	0.499448	-3.853501	22539.776256
HLA B*1502	1:114-122	9	RAIEVIADA	0.761430	-0.028603	-4.586366	0.732827	-3.853539	38580.356521
HLA A*3002	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.536501	0.682948	-3.853553	34395.431879
HLA A*0216	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.285858	0.432298	-3.853560	19313.354269
HLA B*0802	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.496693	0.643088	-3.853605	31382.926708
HLA A*0219	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.386561	0.532852	-3.853710	24353.497071
HLA A*0201	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.360358	0.506563	-3.853795	22927.543540
HLA A*2403	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.374847	0.521039	-3.853808	23705.373415
HLA B*5401	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.496921	0.643088	-3.853833	31399.399511
HLA B*5701	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.408334	0.554273	-3.854061	25605.544210
HLA B*1517	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.457600	0.603309	-3.854292	28681.401008
HLA A*0216	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.378472	0.524138	-3.854334	23904.081245
HLA B*0802	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.490380	0.635971	-3.854409	30930.032501
HLA A*0206	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.364953	0.510481	-3.854472	23171.445093
HLA A*2402	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.549865	0.695361	-3.854503	35470.281704
HLA B*4501	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.145023	0.290447	-3.854575	13964.407944
HLA A*0219	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.466622	0.612002	-3.854621	29283.459619
HLA B*3501	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.397254	0.542619	-3.854635	24960.532105
HLA A*1101	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.457943	0.603309	-3.854635	28704.063784
HLA B*1502	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.425899	0.571232	-3.854667	26662.370586
HLA A*0216	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.261717	0.407006	-3.854711	18269.082985
HLA A*0219	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.273234	0.418508	-3.854726	18760.047083
HLA A*0201	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.376630	0.521798	-3.854832	23802.910299
HLA B*0802	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.429075	0.574191	-3.854884	26858.098621
HLA B*1502	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.387736	0.532852	-3.854884	24419.461105
HLA B*7301	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.124953	0.269799	-3.855155	13333.778198
HLA B*4403	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.610411	0.755176	-3.855234	40776.586402
HLA B*4002	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.627983	0.772678	-3.855305	42460.261495
HLA A*0301	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.364817	0.509478	-3.855339	23164.175646
HLA B*2705	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.426573	0.571232	-3.855341	26703.799754
HLA B*0801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.365959	0.510481	-3.855478	23225.159173
HLA B*3901	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.512844	0.657361	-3.855482	32571.953226
HLA B*5301	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.568404	0.712902	-3.855502	37017.273165
HLA B*4601	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.388422	0.532852	-3.855571	24458.066710
HLA B*5101	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.493016	0.637402	-3.855614	31118.345512
HLA B*4501	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.606111	0.750403	-3.855708	40374.885954
HLA A*6802	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.429923	0.574191	-3.855732	26910.602935
HLA A*1101	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.491715	0.635971	-3.855743	31025.221005
HLA A*0219	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.229181	0.373369	-3.855812	16950.444063
HLA A*6801	1:556-564	9	SKGNQFVMP	0.758469	0.037719	-4.652051	0.796188	-3.855863	44879.787182

HLA B*1501	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.410143	0.554273	-3.855870	25712.429507
HLA A*0250	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.510081	0.654207	-3.855874	32365.387280
HLA A*0201	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.376980	0.521039	-3.855942	23822.104929
HLA A*2501	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.467952	0.612002	-3.855951	29373.262910
HLA B*4801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.414647	0.558588	-3.856059	25980.474390
HLA A*6802	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.274568	0.418508	-3.856061	18817.781934
HLA B*1509	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.414711	0.558588	-3.856122	25984.269557
HLA B*7301	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.223763	0.367626	-3.856137	16740.297346
HLA A*0201	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.380399	0.524138	-3.856260	24010.357911
HLA B*1501	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.324852	0.468482	-3.856370	21127.694550
HLA A*0202	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.553854	0.697387	-3.856467	35797.612547
HLA B*1503	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.492488	0.635971	-3.856516	31080.490526
HLA B*4801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.356002	0.499448	-3.856553	22698.731185
HLA A*0211	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.513922	0.657361	-3.856561	32652.934419
HLA A*0201	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.315139	0.458556	-3.856583	20660.429161
HLA B*3901	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.482542	0.625924	-3.856618	30376.833055
HLA B*4403	1:209-217	9	VLTGEPPFT	1.158367	-0.359576	-4.655413	0.798791	-3.856622	45228.574695
HLA A*0219	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.449107	0.592477	-3.856630	28125.935296
HLA A*0212	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.397056	0.540402	-3.856654	24949.191850
HLA A*2601	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.137269	0.280603	-3.856666	13717.318638
HLA B*4402	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.325759	0.469073	-3.856686	21171.859862
HLA A*3301	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.638196	0.781429	-3.856767	43470.624146
HLA B*4501	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.652697	0.795837	-3.856860	44946.605408
HLA A*0201	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.396549	0.539629	-3.856920	24920.054847
HLA B*1517	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.367404	0.510481	-3.856923	23302.559866
HLA B*1801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.469068	0.612002	-3.857067	29448.840370
HLA A*2403	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.437017	0.579907	-3.857110	27353.727964
HLA B*1502	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.409542	0.552387	-3.857155	25676.844198
HLA A*3301	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.570061	0.712902	-3.857159	37158.725579
HLA A*2902	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.460565	0.603309	-3.857257	28877.886935
HLA B*0802	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.462809	0.605498	-3.857311	29027.468995
HLA B*3801	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.527023	0.669685	-3.857338	33652.934827
HLA A*2402	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.566652	0.709300	-3.857351	36868.180749
HLA B*1801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.452399	0.594934	-3.857464	28339.918816
HLA B*3901	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.293672	0.436027	-3.857645	19664.010346
HLA A*8001	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.400379	0.542619	-3.857759	25140.774600
HLA B*3901	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.494515	0.636741	-3.857774	31225.936339
HLA A*2601	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.366248	0.508438	-3.857810	23240.618717
HLA B*2705	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.410211	0.552387	-3.857825	25716.463764
HLA B*5701	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.400623	0.542619	-3.858004	25154.923495
HLA A*2602	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.520503	0.662443	-3.858060	33151.495415
HLA A*6802	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.416860	0.558588	-3.858272	26113.211825
HLA A*2403	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.346054	0.487735	-3.858319	22184.715425
HLA B*4402	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.432945	0.574537	-3.858408	27098.475929
HLA A*2902	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.280440	0.421976	-3.858464	19073.912873
HLA A*0301	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.362916	0.504447	-3.858469	23063.016835
HLA B*4403	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.628572	0.770046	-3.858526	42517.956690
HLA B*3901	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.501660	0.643088	-3.858572	31743.897917
HLA A*2301	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.541644	0.682948	-3.858696	34805.172427
HLA A*3101	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.363724	0.505009	-3.858716	23105.977115
HLA A*6801	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.623232	0.764421	-3.858811	41998.328465
HLA B*1503	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.470835	0.612002	-3.858833	29568.889249
HLA B*4601	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.401283	0.542449	-3.858834	25193.192558
HLA B*4801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.433372	0.574537	-3.858835	27125.170223
HLA A*2501	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.382990	0.524138	-3.858852	24154.058615
HLA A*0250	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.482319	0.623337	-3.858982	30361.225212
HLA B*4402	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.409981	0.550986	-3.858995	25702.833302
HLA A*2501	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.438917	0.579907	-3.859010	27473.706657
HLA A*0216	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.451593	0.592477	-3.859116	28287.380250
HLA B*1502	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.556516	0.697387	-3.859129	36017.704418
HLA B*4403	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.650674	0.791452	-3.859222	44737.734789
HLA A*3101	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.401678	0.542449	-3.859229	25216.100086
HLA A*3001	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.294452	0.435191	-3.859261	19699.360281
HLA A*0219	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.454318	0.594934	-3.859384	28465.455064
HLA A*3201	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.556782	0.697387	-3.859394	36039.729402

HLA A*6802	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.263317	0.403854	-3.859462	18336.512878
HLA A*0202	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.473065	0.613540	-3.859525	29721.085830
HLA A*3001	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.291854	0.432298	-3.859556	19581.844281
HLA B*5401	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.550203	0.690572	-3.859631	35497.924672
HLA A*3201	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.322860	0.463212	-3.859647	21030.991421
HLA A*0211	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-3.941745	0.082090	-3.859656	8744.703425
HLA B*1801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.473619	0.613866	-3.859753	29759.055980
HLA A*6802	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.370345	0.510481	-3.859864	23460.928049
HLA A*0301	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.286001	0.426123	-3.859878	19319.728790
HLA B*1503	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.459659	0.599665	-3.859994	28817.646554
HLA A*6801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.001347	0.141319	-3.860028	10031.059826
HLA A*0216	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.402796	0.542619	-3.860177	25281.117926
HLA A*0250	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.549557	0.689311	-3.860246	35445.152981
HLA A*2603	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.522714	0.662443	-3.860271	33320.690217
HLA A*2403	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.444845	0.584529	-3.860316	27851.270258
HLA A*0206	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.418933	0.558588	-3.860344	26238.109335
HLA A*3301	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.624823	0.764421	-3.860402	42152.429155
HLA B*0802	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.386355	0.525884	-3.860470	24341.905855
HLA A*3301	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.454031	0.593391	-3.860640	28446.673877
HLA A*2603	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.615152	0.754459	-3.860693	41224.189600
HLA A*0201	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.365844	0.505009	-3.860835	23219.003358
HLA B*1503	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.474423	0.613540	-3.860883	29814.166619
HLA B*4002	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.630931	0.770046	-3.860885	42749.522501
HLA B*0802	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.432193	0.571232	-3.860961	27051.604592
HLA B*1502	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.543911	0.682948	-3.860963	34987.349445
HLA A*2902	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.400670	0.539629	-3.861041	25157.645349
HLA B*3901	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.498463	0.637402	-3.861060	31511.030406
HLA A*3101	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.370561	0.509478	-3.861084	23472.607689
HLA A*3101	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.415617	0.554273	-3.861345	26038.587050
HLA B*4001	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.401130	0.539629	-3.861502	25184.335111
HLA A*0206	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.366687	0.505009	-3.861678	23264.141968
HLA A*2601	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.405764	0.543984	-3.861779	25454.447446
HLA B*5101	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.479758	0.617889	-3.861870	30182.718596
HLA B*4402	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.422995	0.561125	-3.861870	26484.684089
HLA B*1801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.394742	0.532852	-3.861891	24816.597667
HLA B*3901	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.402641	0.540737	-3.861904	25272.092846
HLA A*3301	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.552844	0.690866	-3.861978	35714.435051
HLA B*4002	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.498754	0.636741	-3.862013	31532.175924
HLA A*2603	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.626448	0.764421	-3.862028	42310.528563
HLA A*2602	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.632214	0.770046	-3.862168	42875.982695
HLA B*0801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.265488	0.403047	-3.862441	18428.401767
HLA A*3301	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.636922	0.774481	-3.862441	43343.348013
HLA A*0101	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.383498	0.521039	-3.862459	24182.300001
HLA B*4001	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.403266	0.540737	-3.862529	25308.486338
HLA A*2902	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.384348	0.521798	-3.862550	24229.704533
HLA B*4501	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.372154	0.509478	-3.862677	23558.861068
HLA B*0803	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.508655	0.645932	-3.862723	32259.280047
HLA B*3501	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.395626	0.532852	-3.862774	24867.128938
HLA B*5401	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.525233	0.662443	-3.862790	33514.491689
HLA A*0101	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.371236	0.508438	-3.862798	23509.080463
HLA A*3001	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.313950	0.451064	-3.862887	20603.950559
HLA B*0802	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.476643	0.613540	-3.863103	29966.977209
HLA A*8001	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.437700	0.574537	-3.863163	27396.824243
HLA A*2601	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.396018	0.532852	-3.863166	24889.605335
HLA A*2601	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.384332	0.521039	-3.863293	24228.786991
HLA B*3901	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.421905	0.558588	-3.863316	26418.285909
HLA A*0301	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.351639	0.488312	-3.863327	22471.837619
HLA B*4501	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.610061	0.746693	-3.863368	40743.730721
HLA B*0702	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.403771	0.540402	-3.863369	25337.940427
HLA B*1503	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.126776	0.263371	-3.863405	13389.872046
HLA A*2301	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.518067	0.654485	-3.863582	32966.034411
HLA A*0203	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.404399	0.540737	-3.863662	25374.566017
HLA A*3101	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.404460	0.540737	-3.863723	25378.135382
HLA A*3201	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.249025	0.385288	-3.863737	17742.909221
HLA B*4501	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.628168	0.764421	-3.863748	42478.412093

HLA B*3901	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.487115	0.623337	-3.863778	30698.318822
HLA A*2902	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.443814	0.579907	-3.863907	27785.203608
HLA B*0802	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.442777	0.578823	-3.863954	27718.993762
HLA A*3301	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.595994	0.732039	-3.863956	39445.223956
HLA B*5101	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.414962	0.550986	-3.863976	25999.315117
HLA B*5401	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.546942	0.682948	-3.863994	35232.371635
HLA A*0203	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.438236	0.574191	-3.864045	27430.637835
HLA A*3002	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.244086	0.379878	-3.864208	17542.287043
HLA B*4801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.273253	0.409024	-3.864228	18760.859018
HLA B*5101	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.404634	0.540402	-3.864232	25388.297090
HLA A*0203	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.415432	0.550986	-3.864446	26027.461024
HLA B*4501	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.637129	0.772678	-3.864451	43363.987404
HLA B*0702	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.467785	0.603309	-3.864477	29361.982744
HLA B*7301	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.595273	0.730675	-3.864598	39379.766282
HLA A*3001	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.249986	0.385288	-3.864698	17782.211439
HLA A*0202	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.425981	0.561125	-3.864856	26667.419480
HLA A*0203	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.317580	0.452683	-3.864898	20776.885835
HLA A*0216	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.371489	0.506563	-3.864926	23522.820081
HLA A*1101	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.482857	0.617889	-3.864969	30398.861968
HLA A*0211	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.531555	0.666540	-3.865015	34005.964806
HLA A*6801	1:80-88	9	AETPAGPLP	0.838045	-0.040583	-4.662539	0.797462	-3.865077	45976.815768
HLA A*6801	1:112-120	9	PKRAIEVIA	1.193397	-0.393406	-4.665121	0.799991	-3.865130	46250.983683
HLA B*1501	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.409133	0.543984	-3.865149	25652.685425
HLA A*2601	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.405592	0.540402	-3.865190	25444.396912
HLA A*8001	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.387074	0.521798	-3.865275	24382.235452
HLA A*0219	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.314808	0.449508	-3.865300	20644.675511
HLA B*1501	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.407770	0.542449	-3.865321	25572.320226
HLA A*0250	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.491323	0.625924	-3.865398	30997.203881
HLA B*5401	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.491416	0.625924	-3.865492	31003.912265
HLA B*3901	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.247303	0.381799	-3.865504	17672.689941
HLA B*7301	1:18-26	9	GFGGMSEVH	1.050622	-0.286259	-4.629869	0.764363	-3.865507	42645.116084
HLA A*3001	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.301543	0.436027	-3.865516	20023.632632
HLA B*5801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.353257	0.487735	-3.865522	22555.755755
HLA B*1501	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.376064	0.510481	-3.865583	23771.896684
HLA A*6801	1:453-461	9	KQANSPSTP	0.696748	0.084681	-4.647053	0.781429	-3.865624	44366.322752
HLA A*2501	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.501698	0.635971	-3.865726	31746.645731
HLA B*3501	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.469127	0.603309	-3.865818	29452.823513
HLA A*3101	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.324387	0.458556	-3.865831	21105.075566
HLA B*7301	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.555184	0.689311	-3.865873	35907.392726
HLA B*4601	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.386958	0.521039	-3.865920	24375.772955
HLA A*0101	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.391805	0.525884	-3.865921	24649.345013
HLA A*0301	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.359986	0.494046	-3.865940	22907.954309
HLA A*3002	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.511925	0.645932	-3.865993	32503.127677
HLA A*0250	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.535685	0.669685	-3.866001	34330.924257
HLA B*1801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.458145	0.592081	-3.866064	28717.421470
HLA A*0201	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.376611	0.510481	-3.866130	23801.880152
HLA A*0250	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.563576	0.697387	-3.866189	36608.019332
HLA B*4001	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.408698	0.542449	-3.866249	25627.024304
HLA B*0702	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.248158	0.381799	-3.866359	17707.525284
HLA B*1501	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.354688	0.488312	-3.866376	22630.191005
HLA B*1517	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.478656	0.612002	-3.866655	30106.234925
HLA A*3201	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.480209	0.613540	-3.866670	30214.085635
HLA A*2902	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.292829	0.426123	-3.866705	19625.856946
HLA A*0211	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.458817	0.592081	-3.866736	28761.888268
HLA B*4002	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.631869	0.765110	-3.866758	42841.898966
HLA A*3101	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.375293	0.508438	-3.866856	23729.752196
HLA A*2403	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.419252	0.552387	-3.866865	26257.420994
HLA A*2601	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.392769	0.525884	-3.866885	24704.079284
HLA B*1801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.529344	0.662443	-3.866902	33833.290338
HLA B*4501	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.632036	0.765110	-3.866925	42858.357791
HLA B*3501	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.461872	0.594934	-3.866937	28964.879451
HLA B*7301	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.589937	0.722962	-3.866976	38898.911958
HLA B*3501	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.139929	0.272858	-3.867070	13801.581170
HLA A*6802	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.376560	0.509478	-3.867082	23799.047479
HLA B*4002	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.617614	0.750403	-3.867211	41458.576582

HLA B*7301	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.617661	0.750403	-3.867258	41463.062551
HLA A*8001	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.445681	0.578365	-3.867317	27904.961277
HLA A*2902	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.445768	0.578365	-3.867404	27910.547458
HLA A*1101	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.407810	0.540402	-3.867408	25574.672173
HLA B*4403	1:187-195	9	QARGDSVDA	1.036329	-0.254639	-4.649170	0.781690	-3.867480	44583.105873
HLA B*1503	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.375951	0.508438	-3.867513	23765.724526
HLA A*0219	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.391671	0.524138	-3.867533	24641.745222
HLA A*2501	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.389343	0.521798	-3.867545	24509.989394
HLA B*2705	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.367014	0.499448	-3.867565	23281.642591
HLA B*4801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.407975	0.540402	-3.867572	25584.358937
HLA B*5801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.361622	0.494046	-3.867576	22994.371828
HLA B*5301	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.590710	0.722962	-3.867749	38968.207974
HLA B*4402	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.441946	0.574191	-3.867755	27665.959895
HLA A*0216	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.452309	0.584529	-3.867781	28334.093414
HLA B*5801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.293959	0.426123	-3.867835	19676.993004
HLA A*3002	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.411844	0.543984	-3.867860	25813.336401
HLA B*5101	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.461425	0.593391	-3.868034	28935.122357
HLA A*2402	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.580149	0.711889	-3.868260	38032.029331
HLA B*3901	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.372798	0.504447	-3.868351	23593.808490
HLA B*5101	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.411055	0.542449	-3.868605	25766.457531
HLA B*0803	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.523196	0.654485	-3.868711	33357.664270
HLA A*2601	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.364518	0.495678	-3.868841	23148.266028
HLA A*0301	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.368388	0.499448	-3.868940	23355.440704
HLA B*5301	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.583918	0.714935	-3.868983	38363.486853
HLA A*8001	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.427666	0.558588	-3.869077	26771.060356
HLA B*0801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.427734	0.558588	-3.869145	26775.260711
HLA A*2902	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.453700	0.584529	-3.869171	28424.983189
HLA A*0203	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.411644	0.542449	-3.869195	25801.469110
HLA A*2601	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.408837	0.539629	-3.869208	25635.205332
HLA B*3801	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.549310	0.680074	-3.869236	35425.024492
HLA A*2601	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.374250	0.505009	-3.869241	23672.821950
HLA A*0216	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.142250	0.272858	-3.869392	13875.547712
HLA B*5301	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.600127	0.730675	-3.869452	39822.376153
HLA A*1101	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.291485	0.421976	-3.869509	19565.219452
HLA A*0206	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.043299	0.173777	-3.869522	11048.395817
HLA A*2403	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.430649	0.561125	-3.869525	26955.625820
HLA B*0702	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.379083	0.509478	-3.869605	23937.727695
HLA B*5101	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.486149	0.616515	-3.869633	30630.138028
HLA B*4001	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.380124	0.510481	-3.869643	23995.165195
HLA A*3101	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.249657	0.379878	-3.869779	17768.748567
HLA B*0702	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.455827	0.586005	-3.869822	28564.491710
HLA B*4403	1:618-626	9	GIITLRFGQ	0.864686	-0.099576	-4.635050	0.765110	-3.869940	43156.867606
HLA A*3002	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.481979	0.612002	-3.869977	30337.418176
HLA A*2602	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.581876	0.711889	-3.869987	38183.555948
HLA B*1801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.524565	0.654485	-3.870081	33463.039275
HLA B*5401	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.484004	0.613866	-3.870138	30479.221781
HLA B*5401	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.561107	0.690866	-3.870241	36400.464310
HLA B*4601	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.378709	0.508438	-3.870272	23917.145976
HLA B*4801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.431451	0.561125	-3.870326	27005.398704
HLA A*0216	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.450284	0.579907	-3.870377	28202.269950
HLA A*2501	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.462617	0.592081	-3.870535	29014.594949
HLA A*0216	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.473908	0.603309	-3.870600	29778.864732
HLA A*2902	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.465598	0.594934	-3.870664	29214.469776
HLA B*1501	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.396681	0.525884	-3.870796	24927.605615
HLA B*3501	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.456844	0.586005	-3.870839	28631.481949
HLA B*5301	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.582795	0.711889	-3.870906	38264.409834
HLA A*0206	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.508321	0.637402	-3.870919	32234.507847
HLA A*3101	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.293658	0.422686	-3.870972	19663.372075
HLA B*0801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.320585	0.449508	-3.871077	20921.144771
HLA A*0211	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.457105	0.586005	-3.871100	28648.680251
HLA A*0203	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.425403	0.554273	-3.871130	26631.953210
HLA A*0201	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.359554	0.488312	-3.871242	22885.162628
HLA B*5801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.351152	0.479739	-3.871413	22446.686684
HLA B*4402	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.412206	0.540737	-3.871469	25834.851044
HLA B*1502	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.580774	0.709300	-3.871474	38086.797979

HLA A*2301	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.494891	0.623337	-3.871555	31252.976656
HLA A*0101	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.411238	0.539629	-3.871609	25777.332533
HLA A*0201	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.397517	0.525884	-3.871633	24975.660463
HLA B*5801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.352959	0.481266	-3.871693	22540.264012
HLA A*8001	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.432921	0.561125	-3.871797	27097.009971
HLA A*6802	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.360139	0.488312	-3.871827	22916.011143
HLA B*0702	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.450211	0.578365	-3.871846	28197.540641
HLA B*5101	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.475217	0.603309	-3.871908	29868.732964
HLA A*0101	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.415899	0.543984	-3.871915	26055.496442
HLA B*4402	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.396164	0.524138	-3.872025	24897.955035
HLA A*3301	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.642117	0.770046	-3.872071	43864.902286
HLA B*1517	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.485700	0.613540	-3.872160	30598.504595
HLA A*0202	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.542067	0.669685	-3.872382	34839.081516
HLA A*3002	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.527021	0.654485	-3.872536	33652.752769
HLA B*0702	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.331104	0.458556	-3.872548	21434.042578
HLA A*0101	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.382144	0.509478	-3.872667	24107.062913
HLA A*0211	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.379351	0.506563	-3.872788	23952.495300
HLA B*3801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.562159	0.689311	-3.872848	36488.792574
HLA A*2402	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.570723	0.697848	-3.872875	37215.457777
HLA A*6901	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.308932	0.436027	-3.872905	20367.231471
HLA B*4002	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.594956	0.722004	-3.872952	39351.016359
HLA A*3301	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.148082	0.275124	-3.872958	14063.115930
HLA B*0803	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.491015	0.617889	-3.873126	30975.244085
HLA A*0219	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.379706	0.506563	-3.873143	23972.069926
HLA B*0802	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.487098	0.613866	-3.873232	30697.156322
HLA A*6801	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.562554	0.689311	-3.873243	36521.970903
HLA B*2705	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.453176	0.579907	-3.873269	28390.711816
HLA B*4001	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.372735	0.499448	-3.873286	23590.362464
HLA B*5801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.339581	0.466242	-3.873339	21856.520822
HLA A*6801	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.595426	0.722004	-3.873421	39393.616328
HLA A*0201	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.287700	0.414162	-3.873537	19395.442984
HLA B*4601	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.378547	0.505009	-3.873538	23908.219793
HLA A*0250	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.519481	0.645932	-3.873549	33073.571667
HLA A*0216	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.384038	0.510481	-3.873557	24212.408148
HLA B*5701	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.417542	0.543984	-3.873557	26154.212157
HLA A*1101	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.434740	0.561125	-3.873615	27210.709919
HLA B*1501	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.367702	0.494046	-3.873656	23318.575529
HLA B*4402	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.426068	0.552387	-3.873681	26672.757922
HLA A*2603	1:568-576	9	GMFWVDAEP	0.693247	0.090504	-4.657600	0.783751	-3.873849	45456.947872
HLA B*4501	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.643976	0.770046	-3.873930	44053.012149
HLA B*0801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.300126	0.426123	-3.874003	19958.418703
HLA B*1801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.510786	0.636741	-3.874045	32417.957876
HLA A*6802	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.220164	0.346054	-3.874109	16602.127958
HLA A*2501	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.487982	0.613866	-3.874115	30759.661520
HLA B*1509	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.510908	0.636741	-3.874167	32427.078792
HLA B*3801	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.536618	0.662443	-3.874176	34404.736911
HLA A*0202	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.500159	0.625924	-3.874235	31634.351284
HLA B*1801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.448914	0.574537	-3.874377	28113.461091
HLA B*5101	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.487989	0.613540	-3.874449	30760.160743
HLA B*4002	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.621181	0.746693	-3.874488	41800.445017
HLA B*5701	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.414250	0.539629	-3.874621	25956.732044
HLA B*2705	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.415375	0.540737	-3.874639	26024.081907
HLA B*1501	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.384139	0.509478	-3.874661	24218.041220
HLA B*5101	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.469688	0.594934	-3.874754	29490.929569
HLA B*4402	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.317780	0.442960	-3.874820	20786.442087
HLA A*0206	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.491372	0.616392	-3.874980	31000.725602
HLA B*3501	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.188878	0.313851	-3.875027	15448.204663
HLA B*1503	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.491616	0.616515	-3.875101	31018.172400
HLA A*2601	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.385654	0.510481	-3.875173	24302.694741
HLA B*0803	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.518281	0.643088	-3.875193	32982.267582
HLA B*4601	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.401112	0.525884	-3.875228	25183.245179
HLA B*1801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.511528	0.635971	-3.875557	32473.424582
HLA B*1502	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.555644	0.680074	-3.875570	35945.486902
HLA B*3901	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.489443	0.613866	-3.875577	30863.340615
HLA A*0216	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.285315	0.409720	-3.875595	19289.233746

HLA A*3101	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.418289	0.542619	-3.875670	26199.245144
HLA A*2501	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.481236	0.605498	-3.875738	30285.599907
HLA A*8001	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.419792	0.543984	-3.875808	26290.112768
HLA B*5401	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.530296	0.654485	-3.875811	33907.500518
HLA B*0803	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.512672	0.636741	-3.875931	32559.092388
HLA B*0702	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.401889	0.525884	-3.876005	25228.380543
HLA A*0101	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.382826	0.506563	-3.876263	24144.913392
HLA B*4403	1:30-38	9	DLRLHRDVA	1.080145	-0.281449	-4.675022	0.798696	-3.876326	47317.490511
HLA B*1502	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.542903	0.666540	-3.876363	34906.243472
HLA A*2603	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.650167	0.773768	-3.876398	44685.487665
HLA A*3001	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.272134	0.395731	-3.876403	18712.609944
HLA B*1503	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.334967	0.458556	-3.876411	21625.524147
HLA B*4402	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.416050	0.539629	-3.876421	26064.519274
HLA A*2603	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.609464	0.733042	-3.876422	40687.782726
HLA B*7301	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.559638	0.682948	-3.876691	36277.595600
HLA A*3001	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.285580	0.408739	-3.876841	19301.029197
HLA B*0802	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.451386	0.574537	-3.876849	28273.916675
HLA B*0801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.417650	0.540737	-3.876913	26160.721571
HLA A*0101	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.387445	0.510481	-3.876964	24403.085382
HLA A*6802	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.326473	0.449508	-3.876965	21206.707884
HLA B*1517	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.455801	0.578823	-3.876978	28562.791923
HLA A*0301	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.367881	0.490880	-3.877001	23328.164969
HLA A*1101	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.476793	0.599665	-3.877128	29977.354559
HLA B*1502	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.600268	0.722962	-3.877307	39835.304330
HLA B*5101	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.493872	0.616392	-3.877479	31179.684121
HLA A*0203	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.309799	0.432298	-3.877501	20407.930147
HLA B*4002	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.631993	0.754459	-3.877534	42854.184533
HLA B*1509	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.303824	0.426123	-3.877701	20129.093572
HLA B*0702	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.438851	0.561125	-3.877727	27469.545340
HLA A*2301	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.544299	0.666540	-3.877758	35018.594205
HLA B*5801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.368722	0.490880	-3.877842	23373.389346
HLA A*0250	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.557930	0.680074	-3.877856	36135.196412
HLA B*5101	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.489868	0.612002	-3.877867	30893.576488
HLA A*2501	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.449182	0.571232	-3.877950	28130.804779
HLA B*0803	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.491837	0.613866	-3.877971	31033.950069
HLA B*2705	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.462551	0.584529	-3.878022	29010.200241
HLA A*0101	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.373846	0.495678	-3.878168	23650.804613
HLA B*5101	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.470297	0.592081	-3.878216	29532.280080
HLA A*0216	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.346761	0.468482	-3.878279	22220.869926
HLA A*0202	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.432562	0.554273	-3.878289	27074.590702
HLA B*0802	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.481657	0.603309	-3.878348	30314.941783
HLA B*4403	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.651033	0.772678	-3.878356	44774.780125
HLA A*0216	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.483891	0.605498	-3.878393	30471.308126
HLA B*3501	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.419153	0.540737	-3.878417	26251.455582
HLA A*6801	1:57-65	9	RREAQNAAA	0.935255	-0.143803	-4.669876	0.791452	-3.878425	46760.196934
HLA A*0202	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.343864	0.465424	-3.878440	22073.141235
HLA A*2301	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.535808	0.657361	-3.878446	34340.583393
HLA A*2301	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.515908	0.637402	-3.878505	32802.544317
HLA A*8001	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.402709	0.524138	-3.878571	25276.058015
HLA B*1517	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.241539	0.362756	-3.878783	17439.714515
HLA B*3801	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.561786	0.682948	-3.878838	36457.419418
HLA B*4001	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.374523	0.495678	-3.878845	23687.682425
HLA B*1517	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.484361	0.605498	-3.878863	30504.295248
HLA A*2403	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.383897	0.505009	-3.878888	24204.550237
HLA B*3901	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.495291	0.616392	-3.878899	31281.732651
HLA A*0212	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.423018	0.543984	-3.879034	26486.116920
HLA A*2301	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.533242	0.654207	-3.879035	34138.311059
HLA B*5301	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.605174	0.725976	-3.879198	40287.828907
HLA B*0801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.433683	0.554273	-3.879410	27144.547371
HLA B*4801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.433734	0.554273	-3.879462	27147.778241
HLA A*0101	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.367798	0.488312	-3.879486	23323.748289
HLA A*3201	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.308105	0.428564	-3.879541	20328.483445
HLA A*0301	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.301536	0.421976	-3.879560	20023.307658
HLA A*6802	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.423603	0.543984	-3.879619	26521.819413
HLA A*2603	1:437-445	9	YAEAVKKLT	1.123900	-0.351222	-4.652309	0.772678	-3.879631	44906.502544

HLA A*0219	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.401466	0.521798	-3.879668	25203.825607
HLA B*5801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.352616	0.472905	-3.879711	22522.467752
HLA A*3002	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.305849	0.426123	-3.879726	20223.181276
HLA B*4601	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.419355	0.539629	-3.879727	26263.671926
HLA A*3101	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.400783	0.521039	-3.879744	25164.179001
HLA B*5801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.344736	0.464928	-3.879808	22117.488039
HLA A*2403	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.401654	0.521798	-3.879856	25214.735960
HLA A*0219	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.375592	0.495678	-3.879914	23746.061465
HLA A*3201	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.575298	0.695361	-3.879936	37609.521915
HLA A*0301	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.367700	0.487735	-3.879964	23318.449378
HLA A*0203	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.345396	0.465424	-3.879972	22151.136145
HLA A*0101	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.370904	0.490880	-3.880025	23491.154707
HLA B*1517	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.496444	0.616392	-3.880052	31364.935383
HLA A*3101	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.438720	0.558588	-3.880131	27461.224598
HLA B*4403	1:538-546	9	NPPAGTTVP	0.869816	-0.073979	-4.675980	0.795837	-3.880143	47422.046669
HLA A*2603	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.650249	0.770046	-3.880203	44693.949490
HLA B*4402	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.438842	0.558588	-3.880254	27468.950918
HLA B*1801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.431390	0.550986	-3.880404	27001.600470
HLA A*1101	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.458770	0.578365	-3.880406	28758.776464
HLA A*0101	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.343646	0.463212	-3.880433	22062.038597
HLA A*3001	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.284406	0.403854	-3.880551	19248.891529
HLA A*2402	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.503932	0.623337	-3.880595	31910.396892
HLA B*3501	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.402411	0.521798	-3.880613	25258.697914
HLA B*0801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.441753	0.561125	-3.880628	27653.689695
HLA B*5701	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.390128	0.509478	-3.880650	24554.316602
HLA B*1801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.423145	0.542449	-3.880696	26493.855546
HLA A*2501	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.484034	0.603309	-3.880726	30481.365416
HLA B*5701	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.302795	0.421976	-3.880819	20081.453517
HLA B*5701	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.421557	0.540737	-3.880820	26397.142215
HLA A*2602	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.472947	0.592081	-3.880866	29713.047528
HLA A*3101	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.385401	0.504447	-3.880953	24288.499600
HLA B*0802	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.475891	0.594934	-3.880957	29915.144320
HLA B*1517	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.385424	0.504447	-3.880977	24289.813617
HLA B*1517	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.254469	0.373369	-3.881099	17966.711215
HLA A*3301	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.636391	0.755176	-3.881215	43290.387303
HLA B*1503	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.473708	0.592477	-3.881232	29765.174350
HLA B*4601	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.380718	0.499448	-3.881270	24028.029910
HLA B*1517	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.299835	0.418508	-3.881327	19945.034561
HLA B*5401	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.499299	0.617889	-3.881410	31571.776624
HLA A*3301	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.614755	0.733042	-3.881713	41186.516732
HLA B*3501	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.440357	0.558588	-3.881769	27564.967907
HLA B*1509	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.481441	0.599665	-3.881776	30299.857493
HLA B*7301	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.539158	0.657361	-3.881797	34606.528387
HLA B*0802	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.498303	0.616392	-3.881911	31499.440497
HLA A*6901	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.354846	0.472905	-3.881940	22638.395089
HLA B*5401	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.487563	0.605498	-3.882065	30730.055445
HLA A*2601	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.391570	0.509478	-3.882093	24636.013597
HLA B*5301	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.572972	0.690866	-3.882106	37408.631648
HLA B*5701	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.392595	0.510481	-3.882114	24694.191435
HLA A*2301	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.544599	0.662443	-3.882157	35042.851782
HLA A*0219	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.392670	0.510481	-3.882189	24698.466776
HLA B*2705	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.355266	0.472905	-3.882361	22660.328054
HLA B*4001	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.370686	0.488312	-3.882374	23479.338817
HLA A*0202	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.056235	0.173777	-3.882459	11382.443132
HLA A*0203	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.351547	0.469073	-3.882474	22467.096884
HLA A*2601	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.381992	0.499448	-3.882543	24098.587328
HLA B*2705	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.393058	0.510481	-3.882577	24720.523253
HLA B*4403	1:98-106	9	VTLRDIVHT	1.041183	-0.294490	-4.629453	0.746693	-3.882761	42604.300781
HLA B*5701	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.376846	0.494046	-3.882800	23814.760189
HLA B*0802	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.476192	0.593391	-3.882801	29935.866708
HLA A*0206	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.494896	0.612002	-3.882894	31253.314808
HLA B*4801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.426954	0.543984	-3.882969	26727.213277
HLA A*2403	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.407246	0.524138	-3.883108	25541.488246
HLA B*4002	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.596018	0.712902	-3.883116	39447.357957
HLA A*1101	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.462003	0.578823	-3.883180	28973.655800

HLA A*2603	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.520592	0.637402	-3.883190	33158.311261
HLA B*5701	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.425664	0.542449	-3.883214	26647.950440
HLA B*0803	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.519274	0.635971	-3.883303	33057.830071
HLA B*0803	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.499849	0.616515	-3.883333	31611.769088
HLA A*2402	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.553025	0.669685	-3.883340	35729.315408
HLA B*1801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.336092	0.452683	-3.883409	21681.635836
HLA B*1503	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.423054	0.539629	-3.883425	26488.266311
HLA B*3801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.540819	0.657361	-3.883458	34739.144600
HLA A*3301	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.305452	0.421976	-3.883477	20204.700253
HLA B*0801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.390121	0.506563	-3.883558	24553.918097
HLA A*0250	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.540922	0.657361	-3.883561	34747.414721
HLA A*2301	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.526666	0.643088	-3.883578	33625.273288
HLA A*3002	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.423230	0.539629	-3.883601	26499.015886
HLA A*6801	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.615965	0.732333	-3.883632	41301.426194
HLA A*6901	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.302217	0.418508	-3.883710	20054.746236
HLA B*4501	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.616813	0.733042	-3.883771	41382.165455
HLA A*0201	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.393255	0.509478	-3.883777	24731.759570
HLA B*1501	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.286852	0.403047	-3.883805	19357.601230
HLA A*3201	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.389047	0.505009	-3.884038	24493.287950
HLA B*4801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.408179	0.524138	-3.884040	25596.403314
HLA B*3901	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.462419	0.578365	-3.884054	29001.412822
HLA B*4601	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.336853	0.452683	-3.884171	21719.672822
HLA B*4001	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.388641	0.504447	-3.884193	24470.375141
HLA B*5401	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.003330	0.119119	-3.884211	10076.965830
HLA A*0101	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.378263	0.494046	-3.884217	23892.574675
HLA B*1503	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.458449	0.574191	-3.884257	28737.469655
HLA A*0219	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.442928	0.558588	-3.884339	27728.592651
HLA A*2902	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.319542	0.435191	-3.884351	20870.952679
HLA B*5401	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.435391	0.550986	-3.884405	27251.516805
HLA B*5701	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.408642	0.524138	-3.884503	25623.697176
HLA A*2602	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.484194	0.599665	-3.884529	30492.580733
HLA A*0219	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.427229	0.542619	-3.884609	26744.135810
HLA A*0301	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.365876	0.481266	-3.884611	23220.761995
HLA A*6901	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.287270	0.402654	-3.884616	19376.250809
HLA B*0801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.427259	0.542619	-3.884640	26746.016752
HLA A*0301	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.303171	0.418508	-3.884664	20098.843192
HLA B*5301	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.564746	0.680074	-3.884672	36706.778880
HLA A*3301	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.599620	0.714935	-3.884684	39775.869449
HLA A*2402	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.575359	0.690572	-3.884787	37614.812334
HLA B*0702	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.337535	0.452683	-3.884852	21753.774862
HLA A*1101	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.490373	0.605498	-3.884875	30929.530521
HLA B*3501	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.389888	0.505009	-3.884879	24540.771055
HLA A*6801	1:42-50	9	LRADLARDP	0.607027	0.163019	-4.654929	0.770046	-3.884883	45178.198367
HLA A*6802	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.439352	0.554273	-3.885079	27501.216917
HLA B*1509	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.522503	0.637402	-3.885100	33304.470654
HLA A*0212	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.427642	0.542449	-3.885193	26769.612111
HLA B*0802	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.465116	0.579907	-3.885209	29182.088092
HLA B*1503	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.358241	0.472905	-3.885335	22816.059507
HLA A*2902	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.299583	0.414162	-3.885421	19933.492556
HLA B*1509	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.542828	0.657361	-3.885467	34900.201150
HLA B*1509	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.499062	0.613540	-3.885522	31554.530555
HLA A*3101	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.348772	0.463212	-3.885560	22324.010407
HLA B*5401	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.552125	0.666540	-3.885584	35655.361354
HLA A*3101	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.350607	0.464928	-3.885679	22418.531648
HLA B*1517	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.265629	0.379878	-3.885751	18434.384474
HLA A*0219	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.406847	0.521039	-3.885808	25518.009019
HLA B*4403	1:154-162	9	VMDFGIARA	0.958305	-0.184537	-4.659698	0.773768	-3.885930	45677.083108
HLA A*2603	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.598135	0.711889	-3.886246	39640.105988
HLA A*6901	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.234709	0.348457	-3.886252	17167.593383
HLA B*5801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.354834	0.468482	-3.886352	22637.782742
HLA A*2902	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.428974	0.542619	-3.886355	26851.851477
HLA A*6802	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.390847	0.504447	-3.886399	24594.998122
HLA A*0250	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.447671	0.561125	-3.886547	28033.120123
HLA B*4402	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.321866	0.435191	-3.886675	20982.919480
HLA B*1501	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.249452	0.362756	-3.886696	17760.387489

HLA A*6802	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.382412	0.495678	-3.886734	24121.934984
HLA A*0203	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.386204	0.499448	-3.886756	24333.479345
HLA A*0101	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.374516	0.487735	-3.886780	23687.297984
HLA B*4501	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.617466	0.730675	-3.886791	41444.448953
HLA A*3301	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.582165	0.695361	-3.886804	38208.972366
HLA B*1503	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.235269	0.348457	-3.886811	17189.711817
HLA A*2601	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.339522	0.452683	-3.886840	21853.564988
HLA B*1801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.490155	0.603309	-3.886846	30913.973179
HLA B*5801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.296567	0.409720	-3.886847	19795.508378
HLA B*5801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.355922	0.469073	-3.886849	22694.556450
HLA B*4601	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.393422	0.506563	-3.886859	24741.260916
HLA B*5301	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.584736	0.697848	-3.886887	38435.779571
HLA B*0702	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.429512	0.542619	-3.886893	26885.137900
HLA B*0801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.411088	0.524138	-3.886949	25768.409117
HLA B*1509	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.319333	0.432298	-3.887035	20860.906149
HLA A*0211	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.466984	0.579907	-3.887077	29307.866506
HLA A*2603	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.609088	0.722004	-3.887084	40652.579341
HLA A*0201	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.395522	0.508438	-3.887085	24861.210393
HLA B*7301	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.596401	0.709300	-3.887101	39482.158449
HLA B*3501	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.393828	0.506563	-3.887265	24764.427369
HLA B*3501	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.222175	0.334871	-3.887304	16679.188463
HLA A*6901	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.349820	0.462438	-3.887382	22377.939049
HLA B*4601	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.221564	0.334125	-3.887439	16655.744489
HLA A*0206	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.319775	0.432298	-3.887477	20882.133717
HLA A*6802	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.413407	0.525884	-3.887522	25906.369093
HLA A*0216	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.408576	0.521039	-3.887537	25619.816071
HLA B*1503	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.330521	0.442960	-3.887561	21405.304824
HLA B*3901	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.487263	0.599665	-3.887598	30708.783298
HLA A*2601	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.394402	0.506563	-3.887839	24797.138319
HLA A*3201	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.472386	0.584529	-3.887857	29674.654468
HLA A*1101	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.482796	0.594934	-3.887862	30394.586453
HLA B*1801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.531024	0.643088	-3.887936	33964.413332
HLA A*0301	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.367676	0.479739	-3.887937	23317.187910
HLA A*0202	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.102741	0.214737	-3.888004	12668.966721
HLA B*2705	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.397510	0.509478	-3.888032	24975.255120
HLA A*1101	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.468049	0.579907	-3.888142	29379.778783
HLA A*0212	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.414034	0.525884	-3.888150	25943.816338
HLA A*0301	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.351382	0.463212	-3.888170	22458.590379
HLA A*0202	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.525573	0.637402	-3.888171	33540.791908
HLA A*0301	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.290897	0.402654	-3.888243	19538.775921
HLA B*1502	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.563445	0.675193	-3.888252	36596.930473
HLA A*0212	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.409434	0.521039	-3.888395	25670.455184
HLA B*4002	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.106886	0.218420	-3.888466	12790.445952
HLA A*2501	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.439483	0.550986	-3.888498	27509.549777
HLA A*3101	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.237012	0.348457	-3.888554	17258.852365
HLA A*2301	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.534548	0.645932	-3.888617	34241.150216
HLA A*0301	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.361551	0.472905	-3.888646	22990.640220
HLA A*2501	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.393140	0.504447	-3.888693	24725.204431
HLA A*2501	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.483630	0.594934	-3.888696	30453.015669
HLA A*0211	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.506653	0.617889	-3.888764	32110.931897
HLA B*7301	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.534739	0.645932	-3.888807	34256.158011
HLA A*0206	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.439986	0.550986	-3.889001	27541.416473
HLA B*1502	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.579983	0.690866	-3.889117	38017.423953
HLA B*0802	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.475217	0.586005	-3.889212	29868.732964
HLA A*0216	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.484201	0.594934	-3.889267	30493.075622
HLA A*0216	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.354216	0.464928	-3.889288	22605.596588
HLA A*0301	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.347865	0.458556	-3.889309	22277.441664
HLA B*1517	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.484248	0.594934	-3.889314	30496.375084
HLA B*7301	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.469226	0.579907	-3.889319	29459.516407
HLA B*4403	1:335-343	9	VVAVLAVLT	0.900027	-0.145568	-4.643823	0.754459	-3.889364	44037.523948
HLA A*0202	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.526109	0.636741	-3.889368	33582.188481
HLA A*0219	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.430130	0.540737	-3.889393	26923.417322
HLA B*1503	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.505809	0.616392	-3.889417	32048.628165
HLA A*0212	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.429080	0.539629	-3.889451	26858.389222
HLA B*4601	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.385187	0.495678	-3.889509	24276.545317

HLA A*0101	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.394521	0.505009	-3.889513	24803.980901
HLA A*6901	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.389056	0.499448	-3.889608	24493.817980
HLA B*1501	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.130559	0.240938	-3.889621	13507.006155
HLA B*4501	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.601751	0.711889	-3.889862	39971.520084
HLA B*1501	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.410928	0.521039	-3.889889	25758.931372
HLA A*2402	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.544184	0.654207	-3.889976	35009.312546
HLA A*0212	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.396603	0.506563	-3.890040	24923.155778
HLA B*5101	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.495547	0.605498	-3.890048	31300.184238
HLA B*5801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.352487	0.462438	-3.890049	22515.767326
HLA A*3201	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.527472	0.637402	-3.890070	33687.726001
HLA B*1509	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.355579	0.465424	-3.890155	22676.638372
HLA B*4601	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.394653	0.504447	-3.890206	24811.496499
HLA A*0202	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.533364	0.643088	-3.890276	34147.916003
HLA A*6901	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-3.941214	0.050897	-3.890317	8734.018378
HLA B*1801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.469148	0.578823	-3.890325	29454.257577
HLA A*3001	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.176289	0.285730	-3.890559	15006.847659
HLA A*3001	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.297579	0.407006	-3.890574	19841.718670
HLA B*3901	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.363489	0.472905	-3.890584	23093.480418
HLA A*2902	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.449224	0.558588	-3.890636	28133.544234
HLA B*4402	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.434686	0.543984	-3.890702	27207.324370
HLA B*1509	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.482914	0.592081	-3.890832	30402.809132
HLA B*4001	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.397449	0.506563	-3.890886	24971.742419
HLA A*0216	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.469303	0.578365	-3.890938	29464.776176
HLA A*0203	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.370686	0.479739	-3.890947	23479.338817
HLA B*1517	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.399404	0.508438	-3.890966	25084.394260
HLA B*5101	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.475534	0.584529	-3.891005	29890.555114
HLA A*0101	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.395640	0.504447	-3.891192	24867.936122
HLA B*4402	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.364110	0.472905	-3.891204	23126.486339
HLA A*3101	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.401802	0.510481	-3.891321	25223.331187
HLA A*0201	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.390795	0.499448	-3.891347	24592.071059
HLA B*3501	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.254156	0.362756	-3.891400	17953.788541
HLA B*4801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.159058	0.267585	-3.891473	14423.091239
HLA B*3901	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.503523	0.612002	-3.891522	31880.373108
HLA A*3201	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.344285	0.452683	-3.891602	22094.526559
HLA B*0801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.435637	0.543984	-3.891653	27267.001109
HLA B*4002	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.032191	0.140490	-3.891701	10769.383925
HLA A*6901	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.354921	0.463212	-3.891708	22642.314507
HLA B*2705	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.432132	0.540402	-3.891730	27047.799858
HLA A*0101	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.360329	0.468482	-3.891847	22926.055163
HLA A*0201	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.396328	0.504447	-3.891881	24907.385483
HLA B*1501	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.373209	0.481266	-3.891943	23616.156047
HLA A*6901	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.334924	0.442960	-3.891964	21623.418399
HLA B*1501	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.110396	0.218420	-3.891976	12894.242019
HLA B*3501	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.357425	0.465424	-3.892001	22773.268657
HLA A*8001	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.434453	0.542449	-3.892004	27192.756600
HLA B*1801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.505579	0.613540	-3.892039	32031.641475
HLA A*0301	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.357085	0.464928	-3.892157	22755.411538
HLA B*5301	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.575192	0.682948	-3.892244	37600.367179
HLA B*1502	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.581590	0.689311	-3.892279	38158.362868
HLA A*3002	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.416454	0.524138	-3.892315	26088.783621
HLA B*7301	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.587677	0.695361	-3.892316	38696.995705
HLA B*1503	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.361509	0.469073	-3.892436	22988.401547
HLA B*5301	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.601753	0.709300	-3.892453	39971.736326
HLA A*2403	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.346667	0.454147	-3.892520	22216.061948
HLA A*3101	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.345253	0.452683	-3.892570	22143.827405
HLA A*2601	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.314559	0.421976	-3.892583	20632.840252
HLA A*2601	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.381296	0.488312	-3.892984	24060.028486
HLA B*0803	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.479023	0.586005	-3.893018	30131.653587
HLA A*3001	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.243553	0.350532	-3.893021	17520.757551
HLA B*2705	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.351599	0.458556	-3.893043	22469.771022
HLA B*1801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.417187	0.524138	-3.893048	26132.855682
HLA B*4801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.398074	0.505009	-3.893065	25007.703387
HLA A*3201	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.583946	0.690866	-3.893080	38365.977440
HLA A*2501	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.351681	0.458556	-3.893125	22474.025989
HLA A*2403	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.356523	0.463212	-3.893311	22726.008634

HLA B*4601	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.402801	0.509478	-3.893323	25281.391463
HLA A*2603	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.648750	0.755176	-3.893573	44539.953820
HLA A*0201	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.315565	0.421976	-3.893589	20680.669554
HLA B*7301	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.605566	0.711889	-3.893677	40324.243452
HLA A*3301	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.531085	0.637402	-3.893683	33969.191004
HLA A*2403	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.402160	0.508438	-3.893722	25244.080942
HLA B*4402	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.448017	0.554273	-3.893744	28055.422432
HLA B*1517	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-3.944696	0.050897	-3.893799	8804.324445
HLA A*0206	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.359237	0.465424	-3.893813	22868.454894
HLA B*5301	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.563499	0.669685	-3.893814	36601.484419
HLA A*1101	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.400459	0.506563	-3.893896	25145.399324
HLA B*0801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.360296	0.466242	-3.894054	22924.318845
HLA B*5701	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.389973	0.495678	-3.894295	24545.550983
HLA B*4001	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.415340	0.521039	-3.894302	26021.970181
HLA A*0211	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.472679	0.578365	-3.894315	29694.728328
HLA A*0206	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.512327	0.617889	-3.894438	32533.209942
HLA B*1509	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.510955	0.616515	-3.894439	32430.587520
HLA B*4001	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.399594	0.505009	-3.894585	25095.388675
HLA B*4801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.437127	0.542449	-3.894678	27360.683939
HLA A*2603	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.569875	0.675193	-3.894682	37142.848030
HLA B*4601	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.374469	0.479739	-3.894730	23684.735210
HLA A*0203	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.438765	0.543984	-3.894780	27464.047424
HLA B*4801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.416614	0.521798	-3.894815	26098.382731
HLA A*0216	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.453493	0.558588	-3.894905	28411.454121
HLA A*6802	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.434559	0.539629	-3.894930	27199.377346
HLA A*0203	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.434867	0.539629	-3.895238	27218.660254
HLA B*4601	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.405797	0.510481	-3.895316	25456.375400
HLA B*5401	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.321532	0.426123	-3.895409	20966.806501
HLA A*0216	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.299414	0.403854	-3.895560	19925.729733
HLA A*3201	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.607671	0.711889	-3.895782	40520.180066
HLA A*6801	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.593758	0.697848	-3.895909	39242.594833
HLA B*0803	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.501470	0.605498	-3.895972	31729.990755
HLA B*4801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.405576	0.509478	-3.896098	25443.433371
HLA B*0801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.435896	0.539629	-3.896267	27283.232198
HLA A*2602	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.591700	0.695361	-3.896338	39057.061682
HLA B*5401	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.533179	0.636741	-3.896437	34133.324942
HLA A*0101	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.377781	0.481266	-3.896516	23866.091846
HLA A*0211	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.551129	0.654485	-3.896644	35573.669064
HLA B*5801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.349334	0.452683	-3.896651	22352.893206
HLA A*2501	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.439277	0.542619	-3.896658	27496.456416
HLA B*5801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.350910	0.454147	-3.896763	22434.182457
HLA A*0201	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.300692	0.403854	-3.896838	19984.457126
HLA A*0202	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.476767	0.579907	-3.896861	29975.570696
HLA A*0301	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.359336	0.462438	-3.896898	22873.651548
HLA B*4801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.376658	0.479739	-3.896919	23804.455602
HLA B*0803	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.490345	0.593391	-3.896954	30927.522682
HLA B*5401	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.551197	0.654207	-3.896990	35579.250540
HLA A*0202	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.510873	0.613866	-3.897006	32424.447495
HLA B*4501	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.612048	0.714935	-3.897113	40930.632628
HLA B*1501	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.401575	0.504447	-3.897127	25210.098483
HLA A*2601	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.377048	0.479739	-3.897309	23825.842596
HLA A*6801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.520670	0.623337	-3.897333	33164.231421
HLA B*1501	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.346850	0.449508	-3.897342	22225.438468
HLA A*0301	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.363663	0.466242	-3.897421	23102.727323
HLA B*7301	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.588342	0.690866	-3.897476	38756.286127
HLA A*2301	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.533559	0.635971	-3.897588	34163.252570
HLA A*3002	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.476462	0.578823	-3.897639	29954.496721
HLA B*5701	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.423577	0.525884	-3.897693	26520.241179
HLA A*6901	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.377497	0.479739	-3.897758	23850.474296
HLA A*6802	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.223345	0.325463	-3.897882	16724.184864
HLA B*4402	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.404500	0.506563	-3.897937	25380.469468
HLA A*2403	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.397414	0.499448	-3.897965	24969.716086
HLA A*6901	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.352139	0.454147	-3.897992	22497.746986
HLA A*6901	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.388908	0.490880	-3.898029	24485.471345
HLA A*0206	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.232919	0.334871	-3.898048	17096.968473

HLA B*5801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.347637	0.449508	-3.898129	22265.754437
HLA A*0212	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.386481	0.488312	-3.898170	24349.017992
HLA A*0301	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.301219	0.403047	-3.898172	20008.689273
HLA A*0201	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.392224	0.494046	-3.898178	24673.092785
HLA B*0801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.367265	0.469073	-3.898192	23295.123261
HLA A*0216	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.040203	0.141914	-3.898289	10969.898356
HLA A*3001	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.157503	0.259153	-3.898350	14371.529536
HLA B*4002	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.610242	0.711889	-3.898353	40760.706524
HLA B*4402	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.403363	0.505009	-3.898354	25314.100521
HLA B*5701	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.139356	0.240938	-3.898418	13783.374923
HLA A*0101	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.397907	0.499448	-3.898459	24998.099719
HLA B*5301	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.552686	0.654207	-3.898479	35701.492251
HLA B*3801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.516460	0.617889	-3.898571	32844.273497
HLA B*1502	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.449626	0.550986	-3.898641	28159.582366
HLA B*4001	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.380112	0.481266	-3.898846	23994.516147
HLA B*4801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.405425	0.506563	-3.898862	25434.625542
HLA B*1801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.477247	0.578365	-3.898882	30008.670519
HLA B*4601	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.325158	0.426123	-3.899034	21142.558579
HLA A*2902	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.110419	0.211378	-3.899041	12894.939602
HLA A*0301	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.368148	0.469073	-3.899075	23342.556524
HLA A*6901	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.386820	0.487735	-3.899084	24367.993853
HLA B*0702	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.457772	0.558588	-3.899183	28692.730158
HLA B*1503	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.408691	0.509478	-3.899213	25626.608390
HLA B*7301	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.589829	0.690572	-3.899258	38889.232978
HLA A*3002	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.565820	0.666540	-3.899280	36797.642034
HLA A*0250	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.536104	0.636741	-3.899363	34363.999495
HLA B*1502	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.515903	0.616515	-3.899387	32802.189403
HLA B*0801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.421212	0.521798	-3.899413	26376.158135
HLA A*2501	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.440231	0.540737	-3.899494	27556.916418
HLA B*3901	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.474094	0.574537	-3.899556	29791.594381
HLA A*0203	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.409069	0.509478	-3.899592	25648.938688
HLA A*2602	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.554124	0.654485	-3.899639	35819.890505
HLA B*0702	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.439286	0.539629	-3.899658	27497.051433
HLA A*3201	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.574863	0.675193	-3.899670	37571.900026
HLA B*4601	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.273048	0.373369	-3.899679	18752.031103
HLA B*0803	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.537105	0.637402	-3.899702	34443.286535
HLA A*1101	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.485811	0.586005	-3.899806	30606.285707
HLA A*6801	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.612821	0.712902	-3.899919	41003.548029
HLA B*7301	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.511998	0.612002	-3.899996	32508.579122
HLA B*4801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.439697	0.539629	-3.900069	27523.096060
HLA A*0216	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.471331	0.571232	-3.900099	29602.661012
HLA B*5701	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.421209	0.521039	-3.900171	26376.015443
HLA A*0101	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.322221	0.421976	-3.900245	21000.067288
HLA B*2705	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.478642	0.578365	-3.900278	30105.257713
HLA B*3901	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.433170	0.532852	-3.900319	27112.553160
HLA A*0203	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.394380	0.494046	-3.900335	24795.931000
HLA A*0212	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.396034	0.495678	-3.900357	24890.547903
HLA B*1501	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.391305	0.490880	-3.900425	24620.957774
HLA A*2501	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.492948	0.592477	-3.900472	31113.463838
HLA A*6801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.492582	0.592081	-3.900500	31087.216934
HLA A*6801	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.612391	0.711889	-3.900502	40962.974206
HLA A*0206	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.380272	0.479739	-3.900533	24003.344693
HLA A*3301	1:60-68	9	AQNAAALNH	0.981888	-0.249555	-4.632919	0.732333	-3.900586	42945.625488
HLA A*2902	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.366062	0.465424	-3.900638	23230.688234
HLA B*5801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.351726	0.451064	-3.900662	22476.336165
HLA B*4001	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.391577	0.490880	-3.900698	24636.413434
HLA A*3002	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.504139	0.603309	-3.900830	31925.592099
HLA A*0250	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.536891	0.635971	-3.900919	34426.334282
HLA B*3501	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.409434	0.508438	-3.900996	25670.455184
HLA B*3901	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.504310	0.603309	-3.901002	31938.202705
HLA B*3801	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.494440	0.593391	-3.901049	31220.531083
HLA A*2402	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.581362	0.680074	-3.901288	38138.344167
HLA A*2902	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.286593	0.385288	-3.901305	19346.085185
HLA A*3002	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.493832	0.592477	-3.901355	31176.816716
HLA B*0802	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.479834	0.578365	-3.901469	30187.944174

HLA B*0803	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.494078	0.592477	-3.901602	31194.531375
HLA B*4403	1:471-479	9	NPPANQTSA	1.113775	-0.349354	-4.666089	0.764421	-3.901668	46354.186283
HLA B*4501	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.591021	0.689311	-3.901709	38996.045319
HLA B*4402	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.434578	0.532852	-3.901726	27200.554537
HLA A*3201	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.494243	0.592477	-3.901766	31206.346739
HLA B*0803	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.493919	0.592081	-3.901837	31183.057876
HLA A*0250	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.310614	0.408742	-3.901872	20446.276539
HLA B*4403	1:466-474	9	KVIGTNPPA	0.839996	-0.107957	-4.633922	0.732039	-3.901883	43044.945528
HLA B*1517	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-3.891067	-0.010996	-3.902062	7781.560414
HLA B*3901	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.360174	0.458095	-3.902080	22917.870814
HLA B*3801	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.476295	0.574191	-3.902104	29942.993344
HLA B*0801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.406567	0.504447	-3.902120	25501.586403
HLA B*4801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.406621	0.504447	-3.902174	25504.759698
HLA A*1101	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.423996	0.521798	-3.902197	26545.791418
HLA A*2602	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.591552	0.689311	-3.902240	39043.752405
HLA A*0101	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.371355	0.469073	-3.902282	23515.567616
HLA A*0212	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.412789	0.510481	-3.902308	25869.535699
HLA A*0216	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.311216	0.408742	-3.902474	20474.612851
HLA B*7301	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.582551	0.680074	-3.902477	38242.887243
HLA A*2602	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.593356	0.690866	-3.902490	39206.308647
HLA B*4001	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.331116	0.428564	-3.902552	21434.622365
HLA A*3301	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.525923	0.623337	-3.902587	33567.839150
HLA B*1801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.502313	0.599665	-3.902649	31791.675044
HLA A*2403	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.382469	0.479739	-3.902730	24125.067115
HLA B*0801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.428636	0.525884	-3.902752	26830.941385
HLA A*3101	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.393645	0.490880	-3.902765	24753.979695
HLA B*4402	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.424639	0.521798	-3.902841	26585.169678
HLA A*1101	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.477407	0.574537	-3.902869	30019.711913
HLA A*8001	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.407378	0.504447	-3.902930	25549.227309
HLA A*6801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.487493	0.584529	-3.902964	30725.068464
HLA B*3901	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.497988	0.594934	-3.903054	31476.614036
HLA B*0803	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.516603	0.613540	-3.903063	32855.114002
HLA B*2705	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.409753	0.506563	-3.903190	25689.349041
HLA A*2301	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.489206	0.586005	-3.903201	30846.481529
HLA A*2403	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.443619	0.540402	-3.903217	27772.730274
HLA A*8001	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.408242	0.505009	-3.903234	25600.142377
HLA B*4402	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.312313	0.409024	-3.903289	20526.405684
HLA A*0206	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.506660	0.603309	-3.903351	32111.453051
HLA B*4001	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.391093	0.487735	-3.903358	24608.972993
HLA B*7301	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.616266	0.712902	-3.903364	41330.035924
HLA A*2603	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.592698	0.689311	-3.903387	39146.965104
HLA B*3901	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.310558	0.407006	-3.903552	20443.622021
HLA B*0801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.366854	0.463212	-3.903641	23273.079491
HLA A*0211	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.515727	0.612002	-3.903725	32788.882887
HLA A*1101	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.408766	0.505009	-3.903758	25631.045161
HLA A*2601	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.376670	0.472905	-3.903765	23805.099509
HLA B*1502	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.515788	0.612002	-3.903786	32793.495201
HLA A*6802	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.391530	0.487735	-3.903795	24633.747973
HLA A*2402	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.558297	0.654485	-3.903812	36165.705319
HLA B*0801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.399526	0.495678	-3.903848	25091.451849
HLA A*0219	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.408874	0.505009	-3.903866	25637.424366
HLA A*0202	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.570425	0.666540	-3.903885	37189.897458
HLA A*0212	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.312672	0.408742	-3.903930	20543.402691
HLA B*7301	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.527394	0.623337	-3.904057	33681.712391
HLA A*6901	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.372629	0.468482	-3.904147	23584.620207
HLA A*0212	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.372631	0.468482	-3.904149	23584.747798
HLA A*2902	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.366612	0.462438	-3.904174	23260.114911
HLA A*0250	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.409187	0.505009	-3.904178	25655.877522
HLA B*1509	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.430243	0.525884	-3.904359	26930.409560
HLA B*5701	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.412897	0.508438	-3.904459	25875.974261
HLA B*5801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.362573	0.458095	-3.904479	23044.807846
HLA A*1101	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.370000	0.465424	-3.904576	23442.278076
HLA A*2602	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.457020	0.552387	-3.904633	28643.101292
HLA B*0801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.392964	0.488312	-3.904652	24715.174420
HLA B*1503	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.465878	0.561125	-3.904753	29233.283430

HLA B*5701	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.393123	0.488312	-3.904812	24724.268125
HLA A*3301	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.174626	0.269799	-3.904828	14949.478346
HLA A*0211	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.326837	0.421976	-3.904862	21224.497862
HLA A*2501	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.483273	0.578365	-3.904908	30427.984351
HLA B*0802	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.437761	0.532852	-3.904910	27400.678073
HLA B*5401	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.426728	0.521798	-3.904930	26713.336120
HLA B*4402	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.426061	0.521039	-3.905022	26672.325036
HLA A*1101	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.457441	0.552387	-3.905054	28670.851851
HLA A*0219	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.393466	0.488312	-3.905155	24743.804149
HLA A*0203	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.431150	0.525884	-3.905266	26986.704862
HLA A*2301	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.531221	0.625924	-3.905297	33979.851311
HLA B*4601	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.399394	0.494046	-3.905348	25083.851450
HLA B*4801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.393676	0.488312	-3.905364	24755.720668
HLA A*6802	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.358161	0.452683	-3.905478	22811.863193
HLA A*0101	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.378470	0.472905	-3.905564	23903.951927
HLA A*0101	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.355076	0.449508	-3.905568	22650.400450
HLA B*4501	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.572121	0.666540	-3.905581	37335.443025
HLA B*5701	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.371057	0.465424	-3.905633	23499.416654
HLA B*1517	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.490371	0.584529	-3.905842	30929.363196
HLA A*3301	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.186510	0.280603	-3.905907	15364.192279
HLA B*5101	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.505572	0.599665	-3.905907	32031.121616
HLA A*2403	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.320139	0.414162	-3.905977	20899.651415
HLA A*2501	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.467172	0.561125	-3.906048	29320.553436
HLA A*0301	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.279434	0.373369	-3.906065	19029.799605
HLA A*8001	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.416595	0.510481	-3.906114	26097.253241
HLA A*2402	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.519686	0.613540	-3.906146	33089.141750
HLA A*1101	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.379052	0.472905	-3.906147	23936.044248
HLA B*1801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.524161	0.617889	-3.906273	33431.916368
HLA A*0301	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.360482	0.454147	-3.906335	22934.118362
HLA B*3501	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.460612	0.554273	-3.906340	28881.011627
HLA A*2602	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.490925	0.584529	-3.906397	30968.876980
HLA A*2301	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.543178	0.636741	-3.906437	34928.344618
HLA B*3901	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.486351	0.579907	-3.906444	30644.392030
HLA B*0801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.241347	0.334871	-3.906475	17431.979783
HLA A*3301	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.628554	0.722004	-3.906549	42516.116591
HLA B*0702	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.460836	0.554273	-3.906563	28895.858534
HLA A*0101	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.386305	0.479739	-3.906566	24339.140584
HLA B*4403	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.563966	0.657361	-3.906605	36640.909622
HLA A*8001	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.413193	0.506563	-3.906630	25893.618529
HLA B*4402	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.449086	0.542449	-3.906636	28124.565905
HLA B*0702	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.450632	0.543984	-3.906648	28224.859523
HLA B*5701	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.370047	0.463212	-3.906834	23444.814615
HLA B*5701	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.411405	0.504447	-3.906957	25787.235563
HLA A*0301	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.365059	0.458095	-3.906964	23177.086752
HLA A*0301	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.321229	0.414162	-3.907067	20952.179381
HLA B*3901	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.432982	0.525884	-3.907098	27100.821627
HLA A*2301	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.525078	0.617889	-3.907189	33502.527386
HLA A*0219	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.461482	0.554273	-3.907209	28938.879460
HLA A*2403	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.257791	0.350532	-3.907259	18104.676082
HLA A*3301	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.433206	0.525884	-3.907321	27114.753388
HLA A*0201	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.387078	0.479739	-3.907339	24382.499264
HLA B*1517	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.459764	0.552387	-3.907378	28824.662920
HLA A*2601	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.372359	0.464928	-3.907431	23569.951900
HLA A*2601	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.395189	0.487735	-3.907453	24842.119239
HLA B*0702	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.448205	0.540737	-3.907468	28067.567198
HLA B*3501	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.370691	0.463212	-3.907478	23479.592859
HLA A*2402	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.440353	0.532852	-3.907501	27564.669662
HLA B*5801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.350504	0.442960	-3.907544	22413.195885
HLA A*3201	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.414163	0.506563	-3.907600	25951.536911
HLA A*2601	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.398504	0.490880	-3.907624	25032.473515
HLA A*2601	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.326243	0.418508	-3.907735	21195.467722
HLA A*2602	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.553697	0.645932	-3.907765	35784.639604
HLA A*0216	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.462203	0.554273	-3.907930	28986.982126
HLA B*4403	1:122-130	9	ACQALNFSH	0.947431	-0.234529	-4.620899	0.712902	-3.907997	41773.317531
HLA B*1801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.500561	0.592477	-3.908084	31663.629479

HLA	B*1509	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.524502	0.616392	-3.908110	33458.151786
HLA	A*1101	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.492831	0.584529	-3.908302	31105.048956
HLA	B*5301	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.027501	0.119114	-3.908387	10653.720224
HLA	A*0211	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.419008	0.510481	-3.908527	26242.651976
HLA	A*6901	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.389869	0.481266	-3.908604	24539.708975
HLA	B*4002	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.639291	0.730675	-3.908616	43580.352207
HLA	B*0801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.377189	0.468482	-3.908707	23833.577561
HLA	B*4601	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.377239	0.468482	-3.908757	23836.285392
HLA	A*2301	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.503728	0.594934	-3.908793	31895.381467
HLA	A*0201	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.399747	0.490880	-3.908867	25104.214840
HLA	A*3002	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.525402	0.616515	-3.908886	33527.548529
HLA	B*4402	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.403031	0.494046	-3.908985	25294.798431
HLA	A*2402	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.571431	0.662443	-3.908988	37276.107926
HLA	B*4801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.419588	0.510481	-3.909107	26277.741965
HLA	A*6802	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.337760	0.428564	-3.909196	21765.075605
HLA	A*2902	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.451675	0.542449	-3.909226	28292.736863
HLA	A*1101	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.463636	0.554273	-3.909363	29082.798117
HLA	A*0202	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.138251	0.228841	-3.909411	13748.373171
HLA	A*0301	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.318184	0.408742	-3.909442	20805.792892
HLA	A*1101	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.442333	0.532852	-3.909482	27690.666433
HLA	A*0101	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.313380	0.403854	-3.909525	20576.882339
HLA	A*3101	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.382570	0.472905	-3.909664	24130.679867
HLA	A*2602	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.579499	0.669685	-3.909814	37975.079522
HLA	B*0803	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.526281	0.616392	-3.909888	33595.453442
HLA	A*0202	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.318922	0.409024	-3.909898	20841.165836
HLA	B*4402	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.409394	0.499448	-3.909945	25668.094430
HLA	B*5101	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.489906	0.579907	-3.909999	30896.250697
HLA	B*0702	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.431838	0.521798	-3.910040	27029.515342
HLA	B*5301	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.488874	0.578823	-3.910051	30822.960978
HLA	B*1503	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.420572	0.510481	-3.910091	26337.374428
HLA	B*5701	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.195912	0.285730	-3.910182	15700.459848
HLA	A*3301	1:495-503	9	KDIPDVAGQ	0.823135	-0.100173	-4.633269	0.722962	-3.910307	42980.256774
HLA	A*0212	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.319357	0.409024	-3.910332	20862.034731
HLA	A*6901	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.313382	0.403047	-3.910335	20576.993658
HLA	B*3501	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.454389	0.543984	-3.910404	28470.075287
HLA	A*0211	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.524410	0.613866	-3.910544	33451.093340
HLA	B*1501	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.259012	0.348457	-3.910555	18155.678818
HLA	A*3101	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.398328	0.487735	-3.910592	25022.318858
HLA	B*1502	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.485172	0.574537	-3.910634	30561.281987
HLA	A*0250	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.577210	0.666540	-3.910670	37775.506278
HLA	B*4501	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.601246	0.690572	-3.910674	39925.055190
HLA	A*0201	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.398617	0.487735	-3.910881	25038.974659
HLA	B*0801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.292681	0.381799	-3.910882	19619.169142
HLA	A*1101	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.451649	0.540737	-3.910912	28291.053247
HLA	A*2501	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.436913	0.525884	-3.911029	27347.217591
HLA	A*3001	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.273847	0.362756	-3.911091	18786.554623
HLA	A*2902	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.419548	0.508438	-3.911111	26275.325362
HLA	A*6801	1:185-193	9	PEQARGDSV	0.897460	-0.122979	-4.685630	0.774481	-3.911148	48487.481677
HLA	A*0101	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.369746	0.458556	-3.911190	23428.585503
HLA	B*3801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.554293	0.643088	-3.911205	35833.845500
HLA	B*2705	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.437103	0.525884	-3.911219	27359.203796
HLA	A*0211	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.343573	0.432298	-3.911275	22058.338958
HLA	B*4001	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.420796	0.509478	-3.911318	26350.913723
HLA	B*2705	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.472473	0.561125	-3.911348	29680.594916
HLA	B*5101	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.485923	0.574537	-3.911386	30614.234416
HLA	B*2705	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.272012	0.360485	-3.911527	18707.346561
HLA	A*0301	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.291619	0.379878	-3.911741	19571.253585
HLA	B*3501	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.030880	0.119119	-3.911761	10736.923210
HLA	B*0702	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.400108	0.488312	-3.911797	25125.138452
HLA	B*1509	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.515106	0.603309	-3.911798	32742.086878
HLA	A*2902	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.400120	0.488312	-3.911808	25125.818082
HLA	A*2601	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.344144	0.432298	-3.911846	22087.355987
HLA	A*0211	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.528275	0.616392	-3.911883	33750.112123
HLA	A*6802	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.420352	0.508438	-3.911914	26323.984499
HLA	A*6901	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.341010	0.429083	-3.911926	21928.529927

HLA A*6802	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.171186	0.259153	-3.912033	14831.544953
HLA B*1801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.330552	0.418508	-3.912044	21406.810281
HLA A*2301	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.525935	0.613866	-3.912069	33568.747154
HLA A*2301	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.511787	0.599665	-3.912122	32492.754872
HLA A*6801	1:276-284	9	VHNGEPPEA	0.939932	-0.184756	-4.667299	0.755176	-3.912122	46483.513428
HLA A*0202	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.517646	0.605498	-3.912148	32934.126539
HLA B*0802	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.470765	0.558588	-3.912176	29564.090706
HLA A*3301	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.504762	0.592477	-3.912285	31971.394110
HLA A*2601	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.393556	0.481266	-3.912290	24748.891399
HLA B*3501	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.366450	0.454147	-3.912303	23251.433941
HLA B*3501	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.246433	0.334125	-3.912308	17637.350623
HLA B*5101	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.490756	0.578365	-3.912391	30956.816579
HLA B*3801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.528811	0.616392	-3.912419	33791.767042
HLA B*0803	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.438316	0.525884	-3.912432	27435.683787
HLA A*6802	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.341529	0.429083	-3.912445	21954.763038
HLA A*3301	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.486649	0.574191	-3.912458	30665.453675
HLA B*4403	1:105-113	9	HTEGPMTPK	0.639282	0.111121	-4.662971	0.750403	-3.912568	46022.604777
HLA B*1517	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.498601	0.586005	-3.912596	31521.089811
HLA B*1501	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.375068	0.462438	-3.912630	23717.431364
HLA B*1501	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.070018	0.157255	-3.912763	11749.450832
HLA B*5301	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.567277	0.654485	-3.912792	36921.273378
HLA A*0101	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.379078	0.466242	-3.912836	23937.468695
HLA B*0702	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.408527	0.495678	-3.912849	25616.905629
HLA B*1501	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.400668	0.487735	-3.912932	25157.509249
HLA B*4601	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.401286	0.488312	-3.912974	25193.328851
HLA B*1801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.499010	0.586005	-3.913005	31550.775235
HLA A*2501	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.378505	0.465424	-3.913081	23905.891772
HLA A*3001	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.294910	0.381799	-3.913112	19720.152660
HLA A*2601	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.367298	0.454147	-3.913151	23296.887664
HLA B*5301	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.579785	0.666540	-3.913245	38000.151594
HLA A*3101	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.394528	0.481266	-3.913263	24804.383465
HLA A*2902	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.419875	0.506563	-3.913312	26295.091170
HLA B*3501	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.322096	0.408742	-3.913354	20994.046925
HLA B*1801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.529781	0.616392	-3.913389	33867.351862
HLA B*4402	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.417911	0.504447	-3.913463	26176.435742
HLA B*0802	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.464543	0.550986	-3.913558	29143.592771
HLA A*3002	1:62-70 9		NAAALNHPA	0.615967	-0.206247	-4.323313	0.409720	-3.913594	21052.961527
HLA A*3002	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.454074	0.540402	-3.913672	28449.444093
HLA A*0203	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.420312	0.506563	-3.913749	26321.563643
HLA A*6901	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.380025	0.466242	-3.913783	23989.713744
HLA A*0202	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.513638	0.599665	-3.913973	32631.566914
HLA A*6801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.086567	0.172544	-3.914024	12205.830665
HLA B*5301	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.603454	0.689311	-3.914143	40128.603017
HLA B*0803	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.494104	0.579907	-3.914197	31196.387779
HLA A*1101	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.472896	0.558588	-3.914307	29709.511364
HLA B*0801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.287686	0.373369	-3.914316	19394.813431
HLA B*1503	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.402679	0.488312	-3.914367	25274.280448
HLA A*3101	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.342934	0.428564	-3.914369	22025.904206
HLA A*8001	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.373012	0.458556	-3.914456	23605.426579
HLA A*3201	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.184268	0.269799	-3.914470	15285.101427
HLA A*0203	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.195997	0.281512	-3.914485	15703.517905
HLA B*5101	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.425029	0.510481	-3.914548	26609.054990
HLA A*2403	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.440510	0.525884	-3.914626	27574.662634
HLA B*4403	1:583-591	9	WTGMLDKGA	1.051440	-0.336505	-4.629695	0.714935	-3.914760	42628.047305
HLA B*1801	1:76-84 9		DTGEAETPA	0.744072	-0.471214	-4.187619	0.272858	-3.914760	15403.474378
HLA A*0211	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.507332	0.592477	-3.914855	32161.175255
HLA A*2601	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.288238	0.373369	-3.914868	19419.486202
HLA A*3301	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.590083	0.675193	-3.914890	38911.961352
HLA B*5101	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.507400	0.592477	-3.914923	32166.221315
HLA B*1517	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.343488	0.428564	-3.914924	22054.043382
HLA B*5801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.350976	0.436027	-3.914949	22437.580974
HLA B*3801	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.560898	0.645932	-3.914966	36382.942429
HLA A*2501	1:76-84 9		DTGEAETPA	0.744072	-0.471214	-4.187882	0.272858	-3.915023	15412.810288
HLA B*0803	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.489572	0.574537	-3.915035	30872.525180
HLA B*4001	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.388051	0.472905	-3.915146	24437.169804

HLA B*0802	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.419623	0.504447	-3.915176	26279.874447
HLA B*1501	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.323973	0.408742	-3.915231	21084.990133
HLA B*0803	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.499879	0.584529	-3.915351	31613.992376
HLA B*2705	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.437223	0.521798	-3.915425	27366.753361
HLA B*0802	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.459527	0.543984	-3.915543	28808.917461
HLA A*3101	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.341736	0.426183	-3.915552	21965.217536
HLA A*2902	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.441551	0.525884	-3.915667	27640.826795
HLA A*0301	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.365230	0.449508	-3.915722	23186.241699
HLA A*0201	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.388650	0.472905	-3.915745	24470.904674
HLA A*2602	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.411442	0.495678	-3.915765	25789.467757
HLA A*2301	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.459774	0.543984	-3.915789	28825.286680
HLA A*3101	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.411485	0.495678	-3.915807	25791.979206
HLA A*2902	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.456545	0.540737	-3.915809	28611.817276
HLA B*4001	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.379062	0.463212	-3.915849	23936.562219
HLA B*1503	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.134271	0.218420	-3.915852	13622.953809
HLA A*2602	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.613291	0.697387	-3.915904	41047.936968
HLA B*0702	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.466918	0.550986	-3.915933	29303.427377
HLA A*2301	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.529525	0.613540	-3.915985	33847.386919
HLA A*3002	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.477219	0.561125	-3.916094	30006.722459
HLA B*1517	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.437153	0.521039	-3.916114	27362.312188
HLA A*0201	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.342344	0.426123	-3.916221	21996.015920
HLA A*8001	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.381183	0.464928	-3.916256	24053.781517
HLA A*3201	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.585990	0.669685	-3.916306	38546.976497
HLA B*5701	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.415784	0.499448	-3.916336	26048.590447
HLA A*3101	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.073612	0.157255	-3.916358	11847.106164
HLA B*1502	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.573726	0.657361	-3.916365	37473.650959
HLA A*0212	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.424809	0.508438	-3.916371	26595.526938
HLA A*0201	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.381322	0.464928	-3.916394	24061.460312
HLA B*0803	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.490618	0.574191	-3.916427	30946.937252
HLA B*0803	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.487683	0.571232	-3.916451	30738.535171
HLA A*6901	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.385568	0.469073	-3.916494	24297.830657
HLA B*4403	1:500-508	9	VAGQTVDVA	1.034623	-0.312619	-4.638513	0.722004	-3.916509	43502.383862
HLA B*1509	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.542457	0.625924	-3.916533	34870.382514
HLA B*5801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.351726	0.435191	-3.916534	22476.336165
HLA A*0202	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.345131	0.428564	-3.916566	22137.598907
HLA A*3002	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.542525	0.625924	-3.916601	34875.853645
HLA B*4601	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.375296	0.458556	-3.916740	23729.880572
HLA B*0801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.345868	0.429083	-3.916785	22175.236119
HLA A*2403	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.398053	0.481266	-3.916787	25006.485816
HLA B*4801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.425246	0.508438	-3.916808	26622.301873
HLA A*2902	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.426369	0.509478	-3.916891	26691.234292
HLA B*0802	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.459539	0.542619	-3.916919	28809.696737
HLA B*7301	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.553668	0.636741	-3.916927	35782.316588
HLA A*3201	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.583559	0.666540	-3.917018	38331.746032
HLA B*0803	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.478226	0.561125	-3.917102	30076.444209
HLA B*1503	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.339252	0.421976	-3.917276	21839.973299
HLA A*0101	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.370016	0.452683	-3.917334	23443.165833
HLA A*0101	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.382774	0.465424	-3.917350	24142.039895
HLA B*3901	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.382797	0.465424	-3.917373	24143.345988
HLA B*4001	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.340114	0.422686	-3.917429	21883.378097
HLA B*4501	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.390440	0.472905	-3.917535	24571.990165
HLA A*3101	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.346667	0.429083	-3.917584	22216.061948
HLA A*8001	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.426049	0.508438	-3.917612	26671.603574
HLA B*0801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.411698	0.494046	-3.917653	25804.679721
HLA A*2603	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.608238	0.690572	-3.917666	40573.044054
HLA B*5301	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.458244	0.540402	-3.917842	28723.947250
HLA A*2402	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.560987	0.643088	-3.917899	36390.422649
HLA B*4001	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.376461	0.458556	-3.917905	23793.640585
HLA B*0802	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.457563	0.539629	-3.917934	28678.918504
HLA A*0219	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.460493	0.542449	-3.918043	28873.044330
HLA B*4402	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.346615	0.428564	-3.918051	22213.418004
HLA B*1517	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.476803	0.558588	-3.918214	29978.003263
HLA A*6801	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.648898	0.730675	-3.918223	44555.136649
HLA A*0219	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.332415	0.414162	-3.918253	21498.843670
HLA A*6901	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.298195	0.379878	-3.918317	19869.862083

HLA A*2601	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.332518	0.414162	-3.918356	21503.961759
HLA A*0201	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.386860	0.468482	-3.918378	24370.235034
HLA B*0802	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.442538	0.524138	-3.918399	27703.702399
HLA A*0301	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.369560	0.451064	-3.918497	23418.574704
HLA B*5101	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.477115	0.558588	-3.918527	29999.580655
HLA B*4002	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.613942	0.695361	-3.918581	41109.495027
HLA B*0803	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.332796	0.414162	-3.918633	21517.693560
HLA B*5801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.304010	0.385288	-3.918722	20137.698208
HLA A*2403	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.391747	0.472905	-3.918841	24646.011483
HLA A*2602	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.542262	0.623337	-3.918925	34854.728501
HLA A*0201	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.400249	0.481266	-3.918984	25133.295228
HLA B*5801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.347560	0.428564	-3.918996	22261.779769
HLA A*0301	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.354237	0.435191	-3.919046	22606.697259
HLA A*2301	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.524673	0.605498	-3.919175	33471.367752
HLA A*8001	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.458820	0.539629	-3.919191	28762.043867
HLA B*1502	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.323083	0.403854	-3.919229	21041.802855
HLA A*2403	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.385532	0.466242	-3.919290	24295.859008
HLA A*2402	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.565313	0.645932	-3.919381	36754.667776
HLA B*0702	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.392329	0.472905	-3.919424	24679.100057
HLA A*0219	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.387945	0.468482	-3.919463	24431.221421
HLA A*2501	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.461928	0.542449	-3.919479	28968.640418
HLA A*8001	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.473784	0.554273	-3.919511	29770.327637
HLA A*0216	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.399296	0.479739	-3.919557	25078.152662
HLA B*4601	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.410590	0.490880	-3.919710	25738.872360
HLA A*2603	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.536242	0.616515	-3.919727	34374.969666
HLA B*5801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.352043	0.432298	-3.919745	22492.757417
HLA B*5401	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.523073	0.603309	-3.919765	33348.281604
HLA A*3201	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.459424	0.539629	-3.919795	28802.060743
HLA A*6901	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.346000	0.426183	-3.919816	22181.955209
HLA A*3002	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.441673	0.521798	-3.919875	27648.603647
HLA B*5401	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.531884	0.612002	-3.919882	34031.730152
HLA A*0101	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.374144	0.454147	-3.919997	23667.059622
HLA A*2603	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.617396	0.697387	-3.920008	41437.723202
HLA A*3201	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.491257	0.571232	-3.920025	30992.508877
HLA B*5101	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.415721	0.495678	-3.920043	26044.785886
HLA B*4403	1:520-528	9	FSQASVDSP	0.682951	0.050091	-4.653089	0.733042	-3.920047	44987.230834
HLA A*3301	1:523-531	9	ASVDSPRPA	0.836749	-0.138901	-4.618028	0.697848	-3.920179	41498.069770
HLA B*1501	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.149073	0.228841	-3.920232	14095.258323
HLA B*3801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.472649	0.552387	-3.920262	29692.640014
HLA A*8001	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.461165	0.540737	-3.920428	28917.752099
HLA B*5801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.300817	0.380356	-3.920461	19990.187973
HLA A*6801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.532594	0.612002	-3.920592	34087.376179
HLA B*2705	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.373301	0.452683	-3.920618	23621.139243
HLA A*2902	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.324479	0.403854	-3.920624	21109.528904
HLA A*6901	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.378747	0.458095	-3.920652	23919.216291
HLA B*0802	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.461428	0.540737	-3.920691	28935.278893
HLA B*0802	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.441737	0.521039	-3.920698	27652.642491
HLA A*3301	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.505271	0.584529	-3.920743	32008.948838
HLA A*3001	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.277541	0.356622	-3.920918	18947.003267
HLA B*3801	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.544299	0.623337	-3.920962	35018.594205
HLA B*0803	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.473363	0.552387	-3.920976	29741.512895
HLA A*0212	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.373670	0.452683	-3.920987	23641.210442
HLA A*0212	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.328012	0.407006	-3.921007	21281.986670
HLA A*0101	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.383498	0.462438	-3.921060	24182.300001
HLA B*4801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.442117	0.521039	-3.921079	27676.887946
HLA A*2601	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.387363	0.466242	-3.921120	24398.465190
HLA B*5401	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.513605	0.592477	-3.921128	32629.095544
HLA A*1101	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.384346	0.463212	-3.921133	24229.573454
HLA B*4402	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.387391	0.466242	-3.921149	24400.049157
HLA B*1503	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.330916	0.409720	-3.921197	21424.768122
HLA B*0802	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.482507	0.561125	-3.921383	30374.368125
HLA A*2601	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.390558	0.469073	-3.921485	24578.637651
HLA A*3001	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.289142	0.367626	-3.921516	19459.975401
HLA A*0206	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.325376	0.403854	-3.921522	21153.198493
HLA A*0216	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.421127	0.499448	-3.921679	26371.021719

HLA B*1501	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.390809	0.469073	-3.921736	24592.869314
HLA B*4402	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.275128	0.353175	-3.921953	18842.026441
HLA A*0206	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.364918	0.442960	-3.921958	23169.564845
HLA A*2301	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.538387	0.616392	-3.921995	34545.175503
HLA B*4001	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.354373	0.432298	-3.922076	22613.791756
HLA A*0203	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.358168	0.436027	-3.922141	22812.233425
HLA B*5301	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.584588	0.662443	-3.922145	38422.682005
HLA B*5801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.348441	0.426183	-3.922258	22306.988271
HLA A*0216	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.462995	0.540737	-3.922258	29039.877443
HLA A*2602	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.565430	0.643088	-3.922342	36764.611055
HLA B*1503	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.302790	0.380356	-3.922434	20081.236241
HLA B*3801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.527939	0.605498	-3.922441	33724.012655
HLA B*5101	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.444260	0.521798	-3.922462	27813.778117
HLA B*0801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.348746	0.426183	-3.922563	22322.681972
HLA B*1502	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.548554	0.625924	-3.922629	35363.368373
HLA A*2601	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.139139	0.216497	-3.922642	13776.516509
HLA A*0250	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.329671	0.407006	-3.922665	21363.426126
HLA A*0212	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.427137	0.504447	-3.922690	26738.493775
HLA A*0202	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.473701	0.550986	-3.922716	29764.691275
HLA A*2902	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.285583	0.362756	-3.922826	19301.133613
HLA B*4402	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.080294	0.157340	-3.922954	12030.791924
HLA B*5701	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.395886	0.472905	-3.922981	24882.066077
HLA B*3501	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.417027	0.494046	-3.922981	26123.243892
HLA A*3101	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.389317	0.466242	-3.923075	24508.530878
HLA A*2902	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.417398	0.494046	-3.923353	26145.582607
HLA A*3101	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.148110	0.224721	-3.923388	14064.028918
HLA B*4001	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.376080	0.452683	-3.923398	23772.796925
HLA A*0212	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.386611	0.463212	-3.923398	24356.263972
HLA B*5301	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.427919	0.504447	-3.923472	26786.706401
HLA B*4601	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.404791	0.481266	-3.923525	25397.501065
HLA B*4601	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.386742	0.463212	-3.923530	24363.643912
HLA A*2301	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.540058	0.616515	-3.923542	34678.307019
HLA A*0206	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.165900	0.242192	-3.923708	14652.105976
HLA A*2601	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.387057	0.463212	-3.923845	24381.312134
HLA A*8001	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.449805	0.525884	-3.923921	28171.162603
HLA A*6802	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.382541	0.458556	-3.923985	24129.113386
HLA A*3301	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.614574	0.690572	-3.924002	41169.363590
HLA A*0201	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.387285	0.463212	-3.924073	24394.109810
HLA B*4601	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.389512	0.465424	-3.924088	24519.538189
HLA A*8001	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.420020	0.495678	-3.924342	26303.912368
HLA B*7301	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.586796	0.662443	-3.924354	38618.570361
HLA B*5401	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.561814	0.637402	-3.924412	36459.786262
HLA B*1517	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.467050	0.542619	-3.924431	29312.306307
HLA B*4402	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.434954	0.510481	-3.924473	27224.109047
HLA B*1502	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.502908	0.578365	-3.924543	31835.218164
HLA A*0216	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.374067	0.449508	-3.924559	23662.834805
HLA B*5301	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.516664	0.592081	-3.924583	32859.735633
HLA A*2601	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.387045	0.462438	-3.924607	24380.652642
HLA B*1509	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.560585	0.635971	-3.924614	36356.773762
HLA A*0301	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.367575	0.442960	-3.924615	23311.764374
HLA A*0202	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.579205	0.654485	-3.924720	37949.408082
HLA B*1517	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.504644	0.579907	-3.924737	31962.747194
HLA A*3301	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.634162	0.709300	-3.924862	43068.704658
HLA B*2705	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.347567	0.422686	-3.924881	22262.141073
HLA A*0101	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.382990	0.458095	-3.924896	24154.058615
HLA A*0201	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.393995	0.469073	-3.924922	24773.941266
HLA A*3201	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.082221	0.157255	-3.924966	12084.280382
HLA A*2601	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.393476	0.468482	-3.924994	24744.339600
HLA A*2902	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.446069	0.521039	-3.925031	27929.881251
HLA A*0219	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.469115	0.543984	-3.925131	29452.026841
HLA A*0202	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.467767	0.542619	-3.925147	29360.712011
HLA A*3002	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.390856	0.465424	-3.925432	24595.530352
HLA A*0211	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.379656	0.454147	-3.925509	23969.346669
HLA B*5401	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.166492	0.240938	-3.925554	14672.094698
HLA B*4002	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.651781	0.725976	-3.925804	44851.874478

HLA A*3301	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.637695	0.711889	-3.925806	43420.561518
HLA B*5301	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.583171	0.657361	-3.925810	38297.545167
HLA A*6901	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.354411	0.428564	-3.925847	22615.749250
HLA A*0101	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.369095	0.442960	-3.926135	23393.503139
HLA B*1503	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.389369	0.463212	-3.926157	24511.447997
HLA A*2402	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.542678	0.616392	-3.926285	34888.119644
HLA B*4402	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.435816	0.509478	-3.926338	27278.214285
HLA B*1509	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.354991	0.428564	-3.926427	22645.989578
HLA B*1502	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.469059	0.542619	-3.926440	29448.203117
HLA B*0801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.399399	0.472905	-3.926494	25084.122853
HLA B*4402	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.452417	0.525884	-3.926533	28341.145369
HLA B*5101	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.469200	0.542619	-3.926581	29457.763359
HLA B*5301	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.540469	0.613866	-3.926603	34711.153580
HLA B*1501	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.384719	0.458095	-3.926625	24250.424030
HLA B*1503	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.501202	0.574537	-3.926665	31710.428035
HLA A*2301	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.530026	0.603309	-3.926717	33886.411959
HLA B*5301	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.520167	0.593391	-3.926776	33125.858867
HLA A*2402	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.562789	0.635971	-3.926818	36541.734230
HLA A*2403	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.436380	0.509478	-3.926902	27313.654595
HLA A*3101	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.395464	0.468482	-3.926982	24857.848210
HLA B*4402	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.415340	0.488312	-3.927028	26021.970181
HLA B*7301	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.363062	0.436027	-3.927035	23070.753771
HLA A*0212	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.359467	0.432298	-3.927169	22880.582257
HLA B*0802	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.467593	0.540402	-3.927191	29348.960337
HLA A*8001	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.349270	0.421976	-3.927295	22349.628424
HLA A*3002	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.564718	0.637402	-3.927316	36704.396002
HLA B*0801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.392762	0.465424	-3.927338	24703.678348
HLA A*3001	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.235236	0.307875	-3.927361	17188.409944
HLA A*0301	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.275844	0.348457	-3.927387	18873.141753
HLA A*0206	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.345941	0.418508	-3.927434	22178.955364
HLA B*4601	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.400365	0.472905	-3.927459	25139.958560
HLA B*5101	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.501782	0.574191	-3.927591	31752.829183
HLA B*3801	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.539604	0.612002	-3.927603	34642.117997
HLA A*3101	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.381754	0.454147	-3.927607	24085.423486
HLA B*1801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.448679	0.521039	-3.927641	28098.256134
HLA B*0801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.418535	0.490880	-3.927656	26214.131548
HLA A*0201	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.393105	0.465424	-3.927681	24723.198103
HLA A*3301	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.590412	0.662443	-3.927969	38941.443831
HLA B*0803	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.506404	0.578365	-3.928039	32092.523218
HLA A*2501	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.449114	0.521039	-3.928075	28126.391774
HLA A*3001	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.299457	0.371335	-3.928121	19927.670156
HLA A*2602	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.594702	0.666540	-3.928162	39328.031533
HLA A*0203	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.391420	0.463212	-3.928208	24627.485275
HLA A*3301	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.598046	0.669685	-3.928361	39631.957780
HLA B*4601	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.347031	0.418508	-3.928524	22234.698658
HLA A*6901	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.257765	0.329236	-3.928529	18103.598727
HLA B*1517	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.382701	0.454147	-3.928554	24137.991456
HLA B*2705	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.468218	0.539629	-3.928589	29391.224789
HLA A*3301	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.545126	0.616515	-3.928610	35085.342982
HLA A*3002	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.542485	0.613866	-3.928619	34872.646326
HLA A*0250	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.571774	0.643088	-3.928686	37305.561859
HLA B*3501	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.277172	0.348457	-3.928714	18930.917413
HLA A*0201	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.391159	0.462438	-3.928721	24612.700966
HLA B*5301	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.552134	0.623337	-3.928797	35656.132928
HLA B*1801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.469226	0.540402	-3.928824	29459.516407
HLA A*3201	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.540941	0.612002	-3.928940	34748.918591
HLA A*3101	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.428446	0.499448	-3.928997	26819.186614
HLA A*0219	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.361401	0.432298	-3.929103	22982.681482
HLA B*3801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.555123	0.625924	-3.929199	35902.342451
HLA B*5801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.343392	0.414162	-3.929229	22049.152218
HLA A*0250	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.566635	0.637402	-3.929233	36866.784606
HLA A*2603	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.624658	0.695361	-3.929297	42136.469379
HLA A*1101	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.471956	0.542619	-3.929337	29645.290809
HLA A*0201	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.382036	0.452683	-3.929353	24101.064499
HLA B*0801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.382067	0.452683	-3.929384	24102.759551

HLA A*0212	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.402331	0.472905	-3.929426	25254.052351
HLA B*4001	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.394404	0.464928	-3.929476	24797.272469
HLA B*1801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.423554	0.494046	-3.929508	26518.806502
HLA A*0219	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.455436	0.525884	-3.929552	28538.851124
HLA A*0201	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.395879	0.466242	-3.929637	24881.662252
HLA A*0201	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.387762	0.458095	-3.929667	24420.914320
HLA B*4801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.388312	0.458556	-3.929756	24451.848675
HLA A*0216	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.473760	0.543984	-3.929776	29768.717139
HLA A*6802	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.429320	0.499448	-3.929871	26873.214004
HLA B*5301	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.565855	0.635971	-3.929884	36800.628223
HLA A*2603	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.522011	0.592081	-3.929930	33266.835674
HLA A*2402	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.543817	0.613866	-3.929951	34979.779156
HLA B*4001	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.424026	0.494046	-3.929980	26547.658411
HLA A*0101	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.356107	0.426123	-3.929984	22704.257751
HLA B*4402	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.388171	0.458095	-3.930076	24443.913055
HLA B*5801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.332822	0.402654	-3.930167	21518.974089
HLA B*7301	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.567570	0.637402	-3.930168	36946.249321
HLA A*2501	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.463032	0.532852	-3.930181	29042.391192
HLA A*0202	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.337279	0.407006	-3.930273	21740.950923
HLA A*2301	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.488940	0.558588	-3.930352	30827.630298
HLA B*4002	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.639803	0.709300	-3.930503	43631.779269
HLA B*2705	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.474589	0.543984	-3.930605	29825.620503
HLA B*2705	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.426446	0.495678	-3.930768	26695.999805
HLA B*3801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.567657	0.636741	-3.930916	36953.645441
HLA B*1503	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.456816	0.525884	-3.930931	28629.623292
HLA B*7301	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.471340	0.540402	-3.930938	29603.301607
HLA B*1517	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.333996	0.403047	-3.930949	21577.260517
HLA B*4002	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.419316	0.488312	-3.931004	26261.256617
HLA B*5301	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.312806	0.381799	-3.931008	20549.738507
HLA A*2501	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.145892	0.214737	-3.931155	13992.387921
HLA A*2902	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.206386	0.275124	-3.931263	16083.715290
HLA A*0211	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.505469	0.574191	-3.931278	32023.497992
HLA A*3301	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.345481	0.414162	-3.931318	22155.450632
HLA B*1501	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.360405	0.429083	-3.931321	22930.024384
HLA A*3101	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.281866	0.350532	-3.931334	19136.650793
HLA B*1509	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.545213	0.613866	-3.931346	35092.366574
HLA A*6901	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.201189	0.269799	-3.931391	15892.393724
HLA A*3001	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.146141	0.214737	-3.931404	14000.414132
HLA A*0301	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.206551	0.275124	-3.931427	16089.807221
HLA A*3001	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.227344	0.295880	-3.931464	16878.886116
HLA A*3301	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.628892	0.697387	-3.931505	42549.250572
HLA A*8001	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.452594	0.521039	-3.931555	28352.646887
HLA A*6802	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.438135	0.506563	-3.931572	27424.257519
HLA A*0211	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.516124	0.584529	-3.931595	32818.874528
HLA A*0206	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.509973	0.578365	-3.931608	32357.333997
HLA B*4801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.427308	0.495678	-3.931631	26749.055478
HLA B*3801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.524269	0.592477	-3.931793	33440.237099
HLA B*1509	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.524314	0.592477	-3.931837	33443.674527
HLA B*1503	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.360708	0.428564	-3.932143	22946.032275
HLA B*0802	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.474679	0.542449	-3.932229	29831.752559
HLA B*1517	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.510595	0.578365	-3.932231	32403.755406
HLA A*0101	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.383347	0.451064	-3.932284	24173.928742
HLA B*5301	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.569690	0.637402	-3.932287	37126.977265
HLA B*0801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.431737	0.499448	-3.932289	27023.228326
HLA B*1503	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.436775	0.504447	-3.932327	27338.490205
HLA B*3801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.548927	0.616515	-3.932412	35393.800052
HLA A*0301	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.361046	0.428564	-3.932482	22963.914751
HLA A*0202	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.267356	0.334871	-3.932484	18507.830461
HLA B*1517	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.441969	0.509478	-3.932491	27667.456633
HLA A*3201	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.621858	0.689311	-3.932546	41865.622882
HLA A*2603	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.510927	0.578365	-3.932562	32428.482238
HLA B*1509	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.385391	0.452683	-3.932709	24287.974014
HLA A*0301	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.368757	0.436027	-3.932730	23375.286135
HLA B*5401	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.527693	0.594934	-3.932758	33704.861562
HLA A*0201	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.351406	0.418508	-3.932898	22459.805397

HLA A*2603	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.205766	0.272858	-3.932908	16060.760751
HLA B*4601	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.420652	0.487735	-3.932917	26342.219271
HLA A*0216	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.385631	0.452683	-3.932948	24301.380027
HLA B*2705	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.384038	0.451064	-3.932974	24212.408148
HLA A*2902	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.432482	0.499448	-3.933034	27069.611162
HLA B*5801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.355727	0.422686	-3.933041	22684.368410
HLA B*0801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.438060	0.505009	-3.933051	27419.510339
HLA A*2601	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.361633	0.428564	-3.933069	22994.993821
HLA B*4601	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.342795	0.409720	-3.933076	22018.875023
HLA B*4001	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.398523	0.465424	-3.933098	25033.556922
HLA A*8001	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.401654	0.468482	-3.933172	25214.735960
HLA A*2402	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.599777	0.666540	-3.933237	39790.289326
HLA B*1501	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.398227	0.464928	-3.933299	25016.498712
HLA B*7301	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.474066	0.540737	-3.933329	29789.660413
HLA B*5101	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.477317	0.543984	-3.933333	30013.541221
HLA A*2603	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.599927	0.666540	-3.933387	39804.068419
HLA A*6801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.546940	0.613540	-3.933400	35232.181032
HLA A*2402	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.590898	0.657361	-3.933537	38985.076719
HLA A*0201	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.365907	0.432298	-3.933609	23222.395136
HLA B*0803	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.457767	0.524138	-3.933629	28692.419711
HLA B*0801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.421437	0.487735	-3.933702	26389.860133
HLA A*0206	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.487993	0.554273	-3.933721	30760.493563
HLA A*0216	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.473382	0.539629	-3.933753	29742.800109
HLA A*2601	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.208891	0.275124	-3.933767	16176.737108
HLA B*4002	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.624369	0.690572	-3.933797	42108.440410
HLA B*4801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.427844	0.494046	-3.933798	26782.069583
HLA A*2501	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.492413	0.558588	-3.933824	31075.110447
HLA B*5401	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.550245	0.616392	-3.933853	35501.381558
HLA A*2602	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.319143	0.385288	-3.933855	20851.766881
HLA A*0202	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.545906	0.612002	-3.933904	35148.415802
HLA A*6802	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.398906	0.464928	-3.933978	25055.641547
HLA A*0301	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.363081	0.429083	-3.933997	23071.752275
HLA A*3002	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.591408	0.657361	-3.934047	39030.869966
HLA B*7301	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.588260	0.654207	-3.934053	38748.948469
HLA B*4601	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.400376	0.466242	-3.934134	25140.638591
HLA B*5801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.219887	0.285730	-3.934156	16591.533090
HLA A*3001	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.268314	0.334125	-3.934189	18548.726705
HLA A*6802	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.425088	0.490880	-3.934209	26612.654034
HLA B*3501	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.473993	0.539629	-3.934364	29784.664910
HLA B*0803	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.477047	0.542619	-3.934428	29994.874486
HLA A*0212	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.443936	0.509478	-3.934458	27793.021081
HLA B*3501	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.403005	0.468482	-3.934523	25293.293213
HLA B*5701	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.425429	0.490880	-3.934549	26633.538093
HLA B*1501	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.366854	0.432298	-3.934556	23273.079491
HLA B*0801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.388758	0.454147	-3.934611	24476.995137
HLA B*1502	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.571379	0.636741	-3.934638	37271.671678
HLA B*4501	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.660631	0.725976	-3.934655	45775.290390
HLA B*5701	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.387496	0.452683	-3.934814	24405.989951
HLA B*5101	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.459052	0.524138	-3.934914	28777.452341
HLA B*7301	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.604603	0.669685	-3.934918	40234.901200
HLA B*4001	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.403431	0.468482	-3.934949	25318.072281
HLA B*3501	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.434500	0.499448	-3.935052	27195.698955
HLA A*2601	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.361279	0.426183	-3.935095	22976.217036
HLA A*2601	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.338169	0.403047	-3.935122	21785.573168
HLA B*3901	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.387823	0.452683	-3.935140	24424.349537
HLA A*8001	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.444641	0.509478	-3.935163	27838.164853
HLA A*0203	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.439678	0.504447	-3.935231	27521.904911
HLA B*4001	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.384846	0.449508	-3.935338	24257.509438
HLA A*0101	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.349548	0.414162	-3.935385	22363.900243
HLA A*3002	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.578491	0.643088	-3.935403	37887.047540
HLA B*3901	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.361615	0.426183	-3.935431	22993.998640
HLA B*4601	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.404565	0.469073	-3.935492	25384.314314
HLA A*0301	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.367805	0.432298	-3.935508	23324.126829
HLA B*4403	1:604-612	9	VYQNPPAGT	0.889540	-0.158865	-4.666244	0.730675	-3.935569	46370.740125
HLA A*0219	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.475351	0.539629	-3.935722	29877.944816

HLA A*0211	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.506968	0.571232	-3.935736	32134.218358
HLA A*0216	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.461634	0.525884	-3.935750	28949.057398
HLA B*0803	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.444192	0.508438	-3.935754	27809.414845
HLA B*5701	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.423505	0.487735	-3.935769	26515.793934
HLA B*4002	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.633170	0.697387	-3.935783	42970.492109
HLA B*4001	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.402117	0.466242	-3.935875	25241.622843
HLA B*4402	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.444385	0.508438	-3.935947	27821.754141
HLA B*5801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.344938	0.408742	-3.936196	22127.780604
HLA A*2602	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.522347	0.586005	-3.936343	33292.581326
HLA B*3801	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.528552	0.592081	-3.936471	33771.663956
HLA A*6801	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.645876	0.709300	-3.936576	44246.237102
HLA A*0101	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.343599	0.407006	-3.936593	22059.651662
HLA B*5301	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.479063	0.542449	-3.936614	30134.424866
HLA B*0801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.165463	0.228841	-3.936622	14637.369865
HLA A*0219	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.446133	0.509478	-3.936655	27933.961183
HLA B*1517	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.409565	0.472905	-3.936660	25678.233324
HLA A*2603	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.548742	0.612002	-3.936740	35378.676638
HLA A*2602	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.550292	0.613540	-3.936752	35505.222936
HLA A*0301	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.362949	0.426183	-3.936766	23064.763659
HLA B*0802	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.447333	0.510481	-3.936852	28011.290152
HLA B*4801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.427771	0.490880	-3.936892	26777.578431
HLA B*7301	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.436345	0.499448	-3.936896	27311.438227
HLA A*0201	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.386425	0.449508	-3.936917	24345.856786
HLA A*2402	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.574398	0.637402	-3.936996	37531.676130
HLA B*1502	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.442089	0.505009	-3.937080	27675.091258
HLA B*1801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.447648	0.510481	-3.937167	28031.603603
HLA B*3901	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.461451	0.524138	-3.937313	28936.844302
HLA B*1517	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.478288	0.540737	-3.937551	30080.674973
HLA B*0801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.283619	0.346054	-3.937564	19214.038108
HLA A*6901	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.351763	0.414162	-3.937601	22478.281761
HLA B*4601	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.369899	0.432298	-3.937601	23436.825444
HLA B*7301	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.580800	0.643088	-3.937712	38089.064546
HLA A*0211	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.152513	0.214737	-3.937775	14207.337115
HLA A*3002	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.551465	0.613540	-3.937925	35601.200005
HLA A*0101	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.370357	0.432298	-3.938059	23461.562663
HLA A*8001	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.437869	0.499448	-3.938421	27407.497714
HLA A*2501	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.391223	0.452683	-3.938540	24616.296332
HLA A*3201	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.618697	0.680074	-3.938623	41562.101608
HLA B*4601	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.367709	0.429083	-3.938626	23318.953984
HLA B*3801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.524648	0.586005	-3.938643	33469.375971
HLA B*3501	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.155586	0.216943	-3.938643	14308.226683
HLA A*1101	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.426998	0.488312	-3.938686	26729.960652
HLA A*3002	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.574671	0.635971	-3.938699	37555.236418
HLA B*5801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.345713	0.407006	-3.938708	22167.319805
HLA A*3101	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.348486	0.409720	-3.938766	22309.281277
HLA B*0702	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.445331	0.506563	-3.938768	27882.476891
HLA A*3301	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.443233	0.504447	-3.938786	27748.100630
HLA B*4501	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.648097	0.709300	-3.938796	44473.018340
HLA B*4801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.396899	0.458095	-3.938804	24940.150340
HLA B*0801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.367505	0.428564	-3.938940	23307.981260
HLA A*3101	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.397073	0.458095	-3.938978	24950.136674
HLA B*0803	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.478614	0.539629	-3.938986	30103.303383
HLA B*0702	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.402237	0.463212	-3.939025	25248.588077
HLA A*0202	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.523602	0.584529	-3.939073	33388.898683
HLA B*0802	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.448710	0.509478	-3.939232	28100.232313
HLA A*0202	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.542541	0.603309	-3.939233	34877.174391
HLA B*5401	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.497849	0.558588	-3.939261	31466.568824
HLA B*4501	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.601720	0.662443	-3.939277	39968.709043
HLA B*0801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.335091	0.395731	-3.939360	21631.725595
HLA A*0201	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.393518	0.454147	-3.939371	24746.749272
HLA A*6801	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.557261	0.617889	-3.939372	36079.525429
HLA A*6802	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.365604	0.426123	-3.939480	23206.194444
HLA A*0301	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.362202	0.422686	-3.939516	23025.118425
HLA A*6801	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.556053	0.616515	-3.939538	35979.339063
HLA B*4501	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.635052	0.695361	-3.939691	43157.101080

HLA B*5401	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.556248	0.616515	-3.939733	35995.498163
HLA A*0203	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.412803	0.472905	-3.939897	25870.375421
HLA A*2902	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.095218	0.155271	-3.939947	12451.398834
HLA B*5801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.369081	0.429083	-3.939998	23392.743814
HLA B*3901	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.501195	0.561125	-3.940070	31709.913389
HLA B*1801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.466004	0.525884	-3.940120	29241.824714
HLA A*2602	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.398687	0.458556	-3.940131	25043.038731
HLA A*3001	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.172507	0.232368	-3.940139	14876.706775
HLA A*2501	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.480590	0.540402	-3.940188	30240.576928
HLA A*0101	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.343018	0.402654	-3.940364	22030.194301
HLA B*1502	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.532453	0.592081	-3.940371	34076.313439
HLA B*1517	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.482824	0.542449	-3.940375	30396.559693
HLA A*0250	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.594888	0.654485	-3.940403	39344.843189
HLA B*5101	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.481330	0.540737	-3.940593	30292.154286
HLA B*1501	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.383749	0.442960	-3.940789	24196.302174
HLA B*3801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.554686	0.613866	-3.940819	35866.234270
HLA A*6901	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.349865	0.409024	-3.940840	22380.239348
HLA A*3101	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.409967	0.469073	-3.940894	25701.999019
HLA B*5801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.359422	0.418508	-3.940915	22878.230531
HLA B*1503	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.155656	0.214737	-3.940919	14310.549050
HLA A*2603	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.621026	0.680074	-3.940952	41785.522720
HLA B*1503	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.406410	0.465424	-3.940986	25492.344708
HLA A*1101	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.289476	0.348457	-3.941018	19474.930381
HLA A*2602	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.621148	0.680074	-3.941074	41797.279236
HLA B*5401	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.440637	0.499448	-3.941189	27582.719307
HLA B*0802	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.462988	0.521798	-3.941190	29039.406139
HLA B*5401	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.554843	0.613540	-3.941303	35879.236794
HLA A*1101	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.450796	0.509478	-3.941318	28235.550082
HLA A*2301	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.495646	0.554273	-3.941373	31307.296928
HLA A*0202	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.451865	0.510481	-3.941384	28305.137486
HLA A*3301	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.492387	0.550986	-3.941401	31073.261260
HLA A*0216	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.395651	0.454147	-3.941505	24868.608795
HLA B*1517	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.495873	0.554273	-3.941601	31323.730033
HLA A*0212	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.209281	0.267585	-3.941696	16191.271016
HLA B*3801	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.555299	0.613540	-3.941759	35916.912484
HLA B*2705	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.484281	0.542449	-3.941832	30498.684919
HLA A*2403	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.348840	0.407006	-3.941835	22327.513024
HLA A*2601	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.377864	0.436027	-3.941837	23870.611226
HLA B*4402	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.437536	0.495678	-3.941858	27386.451243
HLA A*3101	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.404305	0.462438	-3.941867	25369.075668
HLA A*2601	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.384879	0.442960	-3.941919	24259.346734
HLA B*1801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.451400	0.509478	-3.941922	28274.834443
HLA A*0216	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.322282	0.380356	-3.941926	21003.021305
HLA A*2603	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.587879	0.645932	-3.941948	38715.003689
HLA A*2501	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.452446	0.510481	-3.941965	28342.985298
HLA B*4601	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.345859	0.403854	-3.942004	22174.756262
HLA B*5701	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.404563	0.462438	-3.942125	25384.176988
HLA B*3801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.537100	0.594934	-3.942165	34442.913869
HLA A*2601	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.351930	0.409720	-3.942210	22486.917375
HLA A*3001	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.271486	0.329236	-3.942250	18684.690445
HLA B*1517	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.404812	0.462438	-3.942374	25398.737674
HLA A*1101	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.484836	0.542449	-3.942386	30537.648490
HLA B*5701	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.423655	0.481266	-3.942389	26524.976163
HLA A*2602	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.157160	0.214737	-3.942423	14360.182754
HLA A*0203	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.407453	0.464928	-3.942525	25553.650683
HLA A*2403	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.277491	0.334871	-3.942620	18944.850865
HLA A*2601	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.401208	0.458556	-3.942652	25188.831580
HLA B*5401	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.503808	0.561125	-3.942683	31901.248723
HLA A*3002	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.184912	0.242192	-3.942720	15307.775481
HLA A*0212	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.408256	0.465424	-3.942832	25600.973354
HLA B*4001	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.378895	0.436027	-3.942868	23927.369900
HLA B*4501	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.633739	0.690866	-3.942873	43026.785626
HLA A*0202	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.537887	0.594934	-3.942953	34505.391802
HLA A*2403	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.405449	0.462438	-3.943011	25436.001564
HLA B*5701	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.422765	0.479739	-3.943026	26470.646448

HLA A*0216	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.365021	0.421976	-3.943046	23175.080672
HLA B*1502	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.504202	0.561125	-3.943078	31930.255715
HLA B*4601	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.405555	0.462438	-3.943117	25442.194585
HLA A*3201	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.579174	0.635971	-3.943203	37946.739249
HLA A*0203	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.405693	0.462438	-3.943255	25450.316609
HLA A*0206	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.392851	0.449508	-3.943343	24708.757348
HLA A*0216	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.485862	0.542449	-3.943413	30609.928609
HLA B*5801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.352449	0.409024	-3.943425	22513.818486
HLA B*3801	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.543096	0.599665	-3.943431	34921.731698
HLA B*3801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.579421	0.635971	-3.943450	37968.300575
HLA A*2301	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.536865	0.593391	-3.943474	34424.285673
HLA B*1503	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.379536	0.436027	-3.943509	23962.734335
HLA A*2301	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.522390	0.578823	-3.943567	33295.823449
HLA B*4801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.396279	0.452683	-3.943596	24904.555974
HLA B*4402	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.393133	0.449508	-3.943625	24724.803153
HLA B*1501	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.186397	0.242669	-3.943728	15360.203105
HLA A*0201	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.386747	0.442960	-3.943787	24363.907523
HLA B*1801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.502403	0.558588	-3.943814	31798.211315
HLA B*3801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.547146	0.603309	-3.943838	35248.958018
HLA A*3201	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.076023	0.132130	-3.943893	11913.046910
HLA B*1801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.409394	0.465424	-3.943970	25668.094430
HLA A*2403	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.448459	0.504447	-3.944011	28083.970972
HLA A*0201	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.395088	0.451064	-3.944024	24836.341007
HLA B*5801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.352778	0.408739	-3.944039	22530.876562
HLA A*2603	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.587165	0.643088	-3.944077	38651.385078
HLA B*1517	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.488111	0.543984	-3.944127	30768.815232
HLA A*2902	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.376428	0.432298	-3.944130	23791.838560
HLA A*8001	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.347292	0.403047	-3.944245	22248.054553
HLA B*4501	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.523431	0.578823	-3.944608	33375.715279
HLA A*6802	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.417718	0.472905	-3.944813	26164.826165
HLA A*2403	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.413315	0.468482	-3.944833	25900.903797
HLA B*4501	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.642275	0.697387	-3.944887	43880.804553
HLA A*1101	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.440567	0.495678	-3.944889	27578.243087
HLA B*1502	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.588004	0.643088	-3.944916	38726.105806
HLA A*3301	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.562935	0.617889	-3.945046	36553.992863
HLA A*0211	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.548359	0.603309	-3.945050	35347.493050
HLA A*0211	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.550553	0.605498	-3.945055	35526.550143
HLA B*0801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.426399	0.481266	-3.945133	26693.111514
HLA B*0803	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.489135	0.543984	-3.945151	30841.475654
HLA A*2601	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.403269	0.458095	-3.945174	25308.623255
HLA A*0301	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.307931	0.362756	-3.945175	20320.346935
HLA B*4402	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.396382	0.451064	-3.945319	24910.484838
HLA A*2601	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.394998	0.449508	-3.945490	24831.235782
HLA B*2705	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.469801	0.524138	-3.945663	29498.588611
HLA B*1517	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.471599	0.525884	-3.945714	29620.923413
HLA B*0802	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.500037	0.554273	-3.945764	31625.453342
HLA A*2603	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.636659	0.690866	-3.945793	43317.093904
HLA A*3001	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.299036	0.353175	-3.945861	19908.382135
HLA A*0101	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.381959	0.436027	-3.945932	24096.762208
HLA A*2301	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.538559	0.592477	-3.946082	34558.820844
HLA A*0101	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.375253	0.429083	-3.946170	23727.569916
HLA B*1503	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.292291	0.346054	-3.946236	19601.558221
HLA A*8001	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.425995	0.479739	-3.946256	26668.285101
HLA A*2902	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.456759	0.510481	-3.946278	28625.906339
HLA A*3101	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.426080	0.479739	-3.946341	26673.479415
HLA A*0212	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.404460	0.458095	-3.946365	25378.135382
HLA B*3801	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.583772	0.637402	-3.946370	38350.621393
HLA A*0212	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.440428	0.494046	-3.946382	27569.441972
HLA B*4403	1:496-504	9	DIPDVAGQT	1.077044	-0.351068	-4.672360	0.725976	-3.946384	47028.349513
HLA A*0206	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.445834	0.499448	-3.946386	27914.775581
HLA A*3101	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.372561	0.426123	-3.946437	23580.920382
HLA A*2601	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.397508	0.451064	-3.946444	24975.120007
HLA A*8001	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.408924	0.462438	-3.946486	25640.337140
HLA A*0301	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.355534	0.409024	-3.946510	22674.307608
HLA A*2402	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.486931	0.540402	-3.946529	30685.367743

HLA B*1502	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.583984	0.637402	-3.946582	38369.298475
HLA A*6901	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.397665	0.451064	-3.946601	24984.174194
HLA B*3501	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.456130	0.509478	-3.946652	28584.433133
HLA A*0216	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.188784	0.242067	-3.946717	15444.862102
HLA A*0212	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.368905	0.421976	-3.946929	23383.254328
HLA B*1501	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.353976	0.407006	-3.946971	22593.126064
HLA B*4002	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.636305	0.689311	-3.946993	43281.722911
HLA A*0202	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.565019	0.617889	-3.947130	36729.821343
HLA A*2403	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.327493	0.380356	-3.947137	21256.557439
HLA A*0219	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.410369	0.463212	-3.947156	25725.786709
HLA B*5401	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.539283	0.592081	-3.947201	34616.452336
HLA B*0702	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.398292	0.451064	-3.947229	25020.288420
HLA A*0203	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.416118	0.468482	-3.947636	26068.608774
HLA A*0202	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.443353	0.495678	-3.947675	27755.757508
HLA A*1101	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.468850	0.521039	-3.947811	29434.027805
HLA A*3101	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.380194	0.432298	-3.947896	23999.059846
HLA A*2403	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.413364	0.465424	-3.947940	25903.846506
HLA B*3901	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.164965	0.216943	-3.948022	14620.591940
HLA A*2603	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.657330	0.709300	-3.948030	45428.676207
HLA B*5701	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.412958	0.464928	-3.948030	25879.614157
HLA B*3901	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.469080	0.521039	-3.948041	29449.636955
HLA A*2902	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.376632	0.428564	-3.948068	23803.039071
HLA B*0702	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.447566	0.499448	-3.948117	28026.296430
HLA A*0201	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.384146	0.436027	-3.948119	24218.434274
HLA A*2602	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.374419	0.426123	-3.948296	23682.044595
HLA B*5301	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.585135	0.636741	-3.948394	38471.144493
HLA B*5401	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.456931	0.508438	-3.948493	28637.213569
HLA A*3201	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.571856	0.623337	-3.948519	37312.626192
HLA A*3002	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.566433	0.617889	-3.948545	36849.636307
HLA A*0211	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.543495	0.594934	-3.948561	34953.863330
HLA B*5301	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.591678	0.643088	-3.948590	39055.160079
HLA A*3101	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.357376	0.408742	-3.948634	22770.681586
HLA A*3101	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.398194	0.449508	-3.948686	25014.604073
HLA B*0803	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.489093	0.540402	-3.948691	30838.472519
HLA A*3101	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.223862	0.275124	-3.948738	16744.101431
HLA A*2601	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.377840	0.429083	-3.948757	23869.319887
HLA B*4402	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.351413	0.402654	-3.948759	22460.169915
HLA B*1517	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-3.987123	0.038251	-3.948872	9707.849578
HLA A*6802	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.428629	0.479739	-3.948890	26830.505931
HLA A*2501	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.230419	0.281512	-3.948907	16998.838930
HLA A*0212	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.400057	0.451064	-3.948993	25122.148297
HLA A*3301	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.523567	0.574537	-3.949030	33386.189339
HLA A*0203	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.436915	0.487735	-3.949180	27347.365537
HLA A*0219	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.418512	0.469073	-3.949439	26212.713431
HLA A*1101	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.489095	0.539629	-3.949467	30838.639352
HLA B*5801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.353478	0.403854	-3.949624	22567.228941
HLA A*3301	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.629717	0.680074	-3.949642	42630.122872
HLA A*0101	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.378230	0.428564	-3.949666	23890.765157
HLA A*0203	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.378230	0.428564	-3.949666	23890.765157
HLA A*2501	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.458134	0.508438	-3.949696	28716.644690
HLA B*5701	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.407803	0.458095	-3.949708	25574.257108
HLA A*0219	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.375883	0.426123	-3.949759	23761.996291
HLA A*2403	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.443832	0.494046	-3.949787	27786.406153
HLA B*0801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.407928	0.458095	-3.949833	25581.590915
HLA B*4002	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.640707	0.690866	-3.949841	43722.750563
HLA A*3002	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.555391	0.605498	-3.949892	35924.491237
HLA B*2705	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.413113	0.463212	-3.949900	25888.856192
HLA B*4801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.437667	0.487735	-3.949932	27394.749329
HLA A*0301	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.356941	0.407006	-3.949936	22747.903417
HLA A*0250	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.535977	0.586005	-3.949972	34353.962068
HLA B*5101	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.458507	0.508438	-3.950070	28741.356581
HLA A*0203	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.440954	0.490880	-3.950075	27602.871291
HLA A*2402	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.568010	0.617889	-3.950121	36983.644880
HLA A*6901	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.385351	0.435191	-3.950160	24285.740397
HLA A*0219	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.415096	0.464928	-3.950168	26007.333598

HLA A*2902	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.430046	0.479739	-3.950307	26918.174335
HLA A*0301	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.360029	0.409720	-3.950309	22910.185149
HLA A*6802	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.419391	0.469073	-3.950318	26265.803266
HLA B*5301	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.576310	0.625924	-3.950386	37697.316931
HLA B*0801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.430161	0.479739	-3.950422	26925.310874
HLA A*2301	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.535157	0.584529	-3.950628	34289.161218
HLA B*4601	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.408759	0.458095	-3.950665	25630.629181
HLA A*6802	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.413254	0.462438	-3.950816	25897.260907
HLA A*0201	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.359577	0.408742	-3.950835	22886.400723
HLA A*3101	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.013489	0.062590	-3.950898	10315.468544
HLA B*4801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.377048	0.426123	-3.950925	23825.842596
HLA B*0802	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.459407	0.508438	-3.950970	28800.970052
HLA A*0211	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.330855	0.379878	-3.950977	21421.754788
HLA A*8001	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.441866	0.490880	-3.950986	27660.871590
HLA B*0702	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.377131	0.426123	-3.951007	23830.354354
HLA A*0250	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.360738	0.409720	-3.951019	22947.646094
HLA B*0802	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.445181	0.494046	-3.951135	27872.824731
HLA B*4002	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.617701	0.666540	-3.951161	41466.876006
HLA B*1501	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.347010	0.395731	-3.951279	22233.616099
HLA A*0101	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.377485	0.426183	-3.951302	23849.829163
HLA B*5701	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.417551	0.466242	-3.951309	26154.778129
HLA A*0250	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.377483	0.426123	-3.951359	23849.700138
HLA B*4403	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.648762	0.697387	-3.951374	44541.158618
HLA B*4601	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.416466	0.464928	-3.951538	26089.489318
HLA B*2705	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.472628	0.521039	-3.951589	29691.194345
HLA A*0219	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.424571	0.472905	-3.951666	26580.999143
HLA A*0201	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.052533	0.100651	-3.951881	11285.809125
HLA A*0212	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.442782	0.490880	-3.951902	27719.293677
HLA A*0212	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.433187	0.481266	-3.951921	27113.579911
HLA B*1509	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.456383	0.504447	-3.951936	28601.138983
HLA B*4001	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.360992	0.409024	-3.951968	22961.057587
HLA B*0702	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.420542	0.468482	-3.952060	26335.522223
HLA A*0203	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.433342	0.481266	-3.952076	27123.262616
HLA A*0211	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.360858	0.408742	-3.952116	22953.978322
HLA A*0201	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.380681	0.428564	-3.952116	24025.950176
HLA A*0219	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.460558	0.508438	-3.952121	28877.418260
HLA B*3801	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.478048	0.525884	-3.952164	30064.080774
HLA A*1101	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.462673	0.510481	-3.952192	29018.362372
HLA A*2403	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.410329	0.458095	-3.952234	25723.420866
HLA B*4601	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.374269	0.421976	-3.952293	23673.846511
HLA A*0216	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.461787	0.509478	-3.952309	28959.238916
HLA A*6801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.457391	0.505009	-3.952382	28667.594807
HLA B*5701	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.406678	0.454147	-3.952531	25508.071383
HLA B*5701	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.421017	0.468482	-3.952535	26364.317350
HLA A*3101	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.356406	0.403854	-3.952551	22719.862206
HLA B*4801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.381155	0.428564	-3.952591	24052.220028
HLA A*0216	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.461035	0.508438	-3.952598	28909.149078
HLA B*4402	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.433892	0.481266	-3.952626	27157.620078
HLA A*2301	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.505060	0.552387	-3.952673	31993.367793
HLA B*1517	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.355501	0.402654	-3.952847	22672.590356
HLA A*2902	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.362606	0.409720	-3.952886	23046.553290
HLA A*6901	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.333284	0.380356	-3.952928	21541.920122
HLA B*0801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.287091	0.334125	-3.952966	19368.285870
HLA B*4002	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.615451	0.662443	-3.953008	41252.522656
HLA A*8001	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.418526	0.465424	-3.953102	26213.564292
HLA B*1509	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.367373	0.414162	-3.953211	23300.921088
HLA B*1801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.497234	0.543984	-3.953250	31421.999987
HLA B*3501	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.433065	0.479739	-3.953326	27105.953548
HLA A*2402	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.569878	0.616515	-3.953362	37143.048969
HLA B*0801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.375446	0.421976	-3.953470	23738.098060
HLA B*4601	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.402982	0.449508	-3.953474	25291.924911
HLA B*1503	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.421996	0.468482	-3.953514	26423.860377
HLA B*4403	1:217-225	9	TGDSPVSVA	1.190269	-0.478380	-4.665443	0.711889	-3.953554	46285.275528
HLA B*1501	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.356220	0.402654	-3.953566	22710.154237
HLA B*1503	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.403106	0.449508	-3.953598	25299.177755

HLA A*0206	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.524859	0.571232	-3.953627	33485.675844
HLA A*0203	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.411745	0.458095	-3.953651	25807.471881
HLA B*3501	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.441455	0.487735	-3.953719	27634.696589
HLA B*0702	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.447808	0.494046	-3.953762	28041.917555
HLA B*2705	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.419231	0.465424	-3.953807	26256.142577
HLA B*1801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.475614	0.521798	-3.953816	29896.053575
HLA A*2402	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.579774	0.625924	-3.953849	37999.123724
HLA A*0250	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.494255	0.540402	-3.953853	31207.190865
HLA A*0206	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.553598	0.599665	-3.953933	35776.509708
HLA A*2403	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.333945	0.379878	-3.954067	21574.692597
HLA B*3501	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.376219	0.421976	-3.954243	23780.386019
HLA A*0219	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.458728	0.504447	-3.954281	28755.976128
HLA B*4801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.427207	0.472905	-3.954302	26742.833696
HLA B*1517	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.407000	0.452683	-3.954317	25526.983821
HLA B*3801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.533233	0.578823	-3.954410	34137.572329
HLA B*5401	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.498406	0.543984	-3.954422	31506.939363
HLA B*1517	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.383521	0.429083	-3.954438	24183.608272
HLA B*1502	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.568007	0.613540	-3.954467	36983.444803
HLA A*6802	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.397484	0.442960	-3.954524	24973.768917
HLA B*5701	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.339818	0.385288	-3.954530	21868.466462
HLA A*6802	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.408715	0.454147	-3.954568	25627.994798
HLA B*4001	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.417013	0.462438	-3.954575	26122.395963
HLA A*0101	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.303084	0.348457	-3.954627	20094.820491
HLA B*4402	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.383716	0.429083	-3.954633	24194.469653
HLA B*5801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.334548	0.379878	-3.954671	21604.709649
HLA B*0803	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.513347	0.558588	-3.954758	32609.684143
HLA A*2501	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.509085	0.554273	-3.954812	32291.232862
HLA B*0801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.363884	0.409024	-3.954860	23114.478731
HLA A*3101	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.397874	0.442960	-3.954914	24996.206474
HLA A*3001	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.197120	0.242192	-3.954928	15744.178606
HLA B*5701	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.373447	0.418508	-3.954939	23629.063413
HLA A*0301	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.358861	0.403854	-3.955007	22848.668929
HLA B*4403	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.112374	0.157340	-3.955034	12953.110901
HLA B*4002	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.635184	0.680074	-3.955110	43170.177668
HLA B*3901	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.509468	0.554273	-3.955195	32319.720214
HLA A*0206	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.550151	0.594934	-3.955217	35493.700047
HLA A*3301	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.591333	0.635971	-3.955362	39024.113665
HLA B*1801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.516521	0.561125	-3.955396	32848.893603
HLA A*0219	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.449445	0.494046	-3.955399	28147.854612
HLA B*0702	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.359277	0.403854	-3.955422	22870.558159
HLA A*0219	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.454880	0.499448	-3.955431	28502.283662
HLA A*2902	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.414121	0.458556	-3.955565	25949.009925
HLA A*2301	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.547682	0.592081	-3.955601	35292.462837
HLA B*5401	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.540218	0.584529	-3.955689	34691.066560
HLA B*0801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.304158	0.348457	-3.955700	20144.562769
HLA A*6802	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.422053	0.466242	-3.955810	26427.291403
HLA B*1502	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.610376	0.654485	-3.955891	40773.277584
HLA A*2501	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.499976	0.543984	-3.955991	31621.005310
HLA B*5801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.351817	0.395731	-3.956086	22481.078850
HLA A*2402	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.592992	0.636741	-3.956251	39173.446650
HLA A*0212	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.443997	0.487735	-3.956262	27796.930642
HLA B*5401	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-3.847207	-0.109105	-3.956312	7034.067111
HLA A*0250	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.477352	0.521039	-3.956314	30015.976869
HLA A*6802	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.437616	0.481266	-3.956350	27391.489067
HLA A*2403	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.365376	0.409024	-3.956352	23194.019973
HLA B*7301	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.572847	0.616392	-3.956455	37397.907228
HLA A*3101	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.391662	0.435191	-3.956471	24641.211991
HLA A*2601	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.391679	0.435191	-3.956487	24642.145152
HLA A*3201	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.613987	0.657361	-3.956625	41113.720802
HLA A*0201	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.365663	0.409024	-3.956638	23209.333230
HLA B*0801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.421627	0.464928	-3.956700	26401.426731
HLA B*5401	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.535192	0.578365	-3.956827	34291.943840
HLA B*4402	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.415394	0.458556	-3.956838	26025.208230
HLA A*0219	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.409582	0.452683	-3.956899	25679.205757
HLA A*3002	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.359975	0.403047	-3.956928	22907.334670

HLA B*5701	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.426108	0.469073	-3.957035	26675.211078
HLA A*2501	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.336931	0.379878	-3.957053	21723.550702
HLA B*5101	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.462210	0.505009	-3.957201	28987.452579
HLA A*0201	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.392400	0.435191	-3.957208	24683.105718
HLA A*0201	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.364239	0.407006	-3.957233	23133.368507
HLA A*2301	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.528585	0.571232	-3.957354	33774.221866
HLA B*0702	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.437129	0.479739	-3.957390	27360.831957
HLA A*3001	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.282883	0.325463	-3.957420	19181.530597
HLA B*3501	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.416083	0.458556	-3.957527	26066.493435
HLA B*4402	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.393558	0.436027	-3.957531	24749.025288
HLA B*3901	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.501536	0.543984	-3.957552	31734.797480
HLA A*1101	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.448433	0.490880	-3.957553	28082.299779
HLA B*4002	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.640515	0.682948	-3.957567	43703.358975
HLA A*3301	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.410291	0.452683	-3.957608	25721.194389
HLA B*3801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.537586	0.579907	-3.957679	34481.506269
HLA A*6802	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.226287	0.268569	-3.957718	16837.845286
HLA A*3001	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.282117	0.324299	-3.957818	19147.731406
HLA B*2705	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.462920	0.505009	-3.957911	29034.850597
HLA A*6801	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.550407	0.592477	-3.957931	35514.636070
HLA A*0301	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.366713	0.408739	-3.957974	23265.526430
HLA B*0802	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.462985	0.505009	-3.957977	29039.249039
HLA A*6802	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-3.910234	-0.047884	-3.958117	8132.682021
HLA B*4801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.424423	0.466242	-3.958181	26571.941271
HLA A*2402	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.553224	0.594934	-3.958290	35745.748975
HLA A*0250	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.576181	0.617889	-3.958293	37686.101993
HLA A*2301	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.536682	0.578365	-3.958317	34409.762675
HLA B*4601	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.384513	0.426183	-3.958329	24238.881872
HLA A*0201	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.387482	0.429083	-3.958399	24405.197761
HLA A*1101	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.426904	0.468482	-3.958422	26724.177033
HLA B*5801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.361481	0.403047	-3.958434	22986.909219
HLA A*3201	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.306911	0.348457	-3.958454	20272.692923
HLA B*7301	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.501099	0.542619	-3.958480	31702.880738
HLA B*2705	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.439848	0.481266	-3.958582	27532.627111
HLA B*4402	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.449492	0.490880	-3.958613	28150.900312
HLA B*0803	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.499435	0.540737	-3.958699	31581.684567
HLA B*4501	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.604690	0.645932	-3.958758	40242.955662
HLA B*1501	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.338686	0.379878	-3.958808	21811.517261
HLA A*0201	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.385048	0.426183	-3.958865	24268.797882
HLA A*2602	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.338773	0.379878	-3.958895	21815.883620
HLA B*4801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.440191	0.481266	-3.958925	27554.382177
HLA B*4001	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.417130	0.458095	-3.959036	26129.462882
HLA A*0211	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.501717	0.542619	-3.959097	31748.019727
HLA B*4403	1:156-164	9	DFGIARAIA	1.039980	-0.350669	-4.648437	0.689311	-3.959126	44507.918170
HLA B*2705	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.467581	0.508438	-3.959143	29348.166474
HLA A*0212	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.395175	0.436027	-3.959148	24841.312893
HLA B*4501	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.595193	0.635971	-3.959222	39372.523582
HLA A*3002	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.424170	0.464928	-3.959242	26556.420670
HLA A*6901	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.368031	0.408742	-3.959289	23336.243346
HLA B*1502	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.577196	0.617889	-3.959308	37774.280130
HLA A*2402	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.511732	0.552387	-3.959346	32488.712133
HLA B*0803	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.510339	0.550986	-3.959354	32384.653260
HLA B*0702	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.417539	0.458095	-3.959445	26154.070666
HLA B*2705	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.369229	0.409720	-3.959510	23400.717958
HLA B*1501	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.312731	0.353175	-3.959556	20546.181317
HLA A*1101	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.503648	0.543984	-3.959664	31889.515290
HLA A*0212	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.428746	0.469073	-3.959673	26837.764416
HLA B*1509	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.534245	0.574537	-3.959708	34217.262486
HLA A*0212	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.422147	0.462438	-3.959709	26433.010771
HLA A*0219	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.439467	0.479739	-3.959728	27508.508031
HLA B*4601	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.395783	0.436027	-3.959756	24876.143976
HLA B*2705	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.464285	0.504447	-3.959837	29126.254933
HLA A*1101	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.447683	0.487735	-3.959948	28033.878413
HLA B*1502	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.605935	0.645932	-3.960003	40358.507502
HLA A*2602	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.572046	0.612002	-3.960045	37328.980205
HLA B*3901	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.499743	0.539629	-3.960114	31604.074297

HLA A*0202	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.538526	0.578365	-3.960161	34556.203511
HLA A*6801	1:104-112	9	VHTEGPMTP	0.635174	0.062213	-4.657619	0.697387	-3.960232	45458.915251
HLA B*4501	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.643238	0.682948	-3.960290	43978.242593
HLA A*1101	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.419062	0.458556	-3.960506	26245.917486
HLA A*0101	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.395738	0.435191	-3.960547	24873.587141
HLA A*2402	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.546554	0.586005	-3.960549	35200.936135
HLA B*3901	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.467167	0.506563	-3.960604	29320.236196
HLA B*4601	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.403600	0.442960	-3.960640	25327.935895
HLA A*2403	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.363341	0.402654	-3.960687	23085.610969
HLA A*0216	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.454765	0.494046	-3.960719	28494.729148
HLA A*6802	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.323494	0.362756	-3.960738	21061.733207
HLA B*0702	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.410263	0.449508	-3.960755	25719.524657
HLA A*6801	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.651635	0.690866	-3.960769	44836.833093
HLA B*4002	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.584127	0.623337	-3.960790	38381.962557
HLA A*3201	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.501275	0.540402	-3.960873	31715.746528
HLA A*0211	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.501618	0.540737	-3.960881	31740.806910
HLA B*1503	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.442272	0.481266	-3.961007	27686.771818
HLA B*5801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.334398	0.373369	-3.961029	21597.230683
HLA B*4601	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.389700	0.428564	-3.961136	24530.152324
HLA B*5801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.296090	0.334871	-3.961218	19773.780735
HLA A*2902	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.414006	0.452683	-3.961323	25942.132155
HLA A*2501	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.457011	0.495678	-3.961333	28642.481475
HLA A*2301	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.541282	0.579907	-3.961375	34776.187515
HLA A*1101	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.415533	0.454147	-3.961386	26033.516372
HLA A*2902	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.384078	0.422686	-3.961392	24214.635020
HLA B*0801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.404359	0.442960	-3.961399	25372.232474
HLA A*3001	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.227649	0.266144	-3.961505	16890.760968
HLA B*1509	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.371287	0.409720	-3.961568	23511.878623
HLA A*2902	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.411078	0.449508	-3.961570	25767.851506
HLA A*0101	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.370324	0.408742	-3.961582	23459.785788
HLA B*5101	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.468152	0.506563	-3.961589	29386.773034
HLA B*5101	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.515884	0.554273	-3.961611	32800.769784
HLA A*0250	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.578021	0.616392	-3.961629	37846.076763
HLA A*2501	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.501313	0.539629	-3.961684	31718.491905
HLA B*1503	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.466881	0.505009	-3.961872	29300.891034
HLA B*3501	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.368935	0.407006	-3.961930	23384.898896
HLA B*4001	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.371661	0.409720	-3.961941	23532.111592
HLA A*3101	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.342351	0.380356	-3.961995	21996.372911
HLA B*1517	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.501681	0.539629	-3.962053	31745.443533
HLA B*3501	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.452967	0.490880	-3.962088	28377.045542
HLA A*0101	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.380638	0.418508	-3.962131	24023.610691
HLA B*4001	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.431213	0.469073	-3.962140	26990.647017
HLA B*1801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.470595	0.508438	-3.962158	29552.577380
HLA B*1509	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.501792	0.539629	-3.962163	31753.516308
HLA A*0203	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.416311	0.454147	-3.962164	26080.175658
HLA A*6802	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.420401	0.458095	-3.962306	26326.975275
HLA B*4801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.430826	0.468482	-3.962344	26966.565060
HLA A*2501	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.467379	0.505009	-3.962370	29334.515402
HLA B*4501	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.536992	0.574537	-3.962455	34434.343647
HLA A*8001	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.431582	0.469073	-3.962509	27013.581332
HLA B*4403	1:355-363	9	GITRDVQVP	0.716363	-0.007063	-4.671899	0.709300	-3.962599	46978.509983
HLA A*2902	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.435518	0.472905	-3.962612	27259.479063
HLA A*0216	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.342736	0.379878	-3.962859	22015.897233
HLA A*0216	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.398978	0.436027	-3.962951	25059.843895
HLA A*2602	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.620387	0.657361	-3.963025	41724.080964
HLA B*1801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.503772	0.540737	-3.963036	31898.660095
HLA A*8001	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.381604	0.418508	-3.963096	24077.085763
HLA A*0219	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.406299	0.442960	-3.963339	25485.863726
HLA A*2603	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.467811	0.504447	-3.963364	29363.730092
HLA A*0203	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.413226	0.449508	-3.963718	25895.579746
HLA A*0206	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.416423	0.452683	-3.963741	26086.948899
HLA A*0212	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.417922	0.454147	-3.963775	26177.143810
HLA B*5801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.326586	0.362756	-3.963830	21212.215444
HLA A*0212	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.430111	0.466242	-3.963869	26922.252126
HLA A*0212	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.392444	0.428564	-3.963880	24685.642973

HLA B*3901	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.310020	0.346054	-3.963965	20418.310823
HLA B*4001	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.418115	0.454147	-3.963968	26188.758852
HLA B*1502	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.239110	0.275124	-3.963986	17342.432141
HLA A*0206	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.429103	0.464928	-3.964176	26859.842270
HLA B*4801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.429148	0.464928	-3.964220	26862.603278
HLA A*3002	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.392827	0.428564	-3.964263	24707.420668
HLA B*0803	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.518565	0.554273	-3.964292	33003.864730
HLA A*3201	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.618827	0.654485	-3.964342	41574.469998
HLA B*1502	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.559368	0.594934	-3.964434	36255.032976
HLA A*1101	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.463890	0.499448	-3.964441	29099.795231
HLA A*6901	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.346249	0.381799	-3.964450	22194.679060
HLA B*0801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.426928	0.462438	-3.964490	26725.622821
HLA B*0801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.368388	0.403854	-3.964534	23355.440704
HLA B*4001	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.338171	0.373369	-3.964802	21785.691025
HLA B*5701	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.393445	0.428564	-3.964881	24742.599427
HLA B*5801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.360054	0.395099	-3.964956	22911.548546
HLA B*0702	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.393542	0.428564	-3.964977	24748.088080
HLA A*3002	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.428192	0.463212	-3.964979	26803.521598
HLA A*0101	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.360806	0.395731	-3.965075	22951.246558
HLA B*4402	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.430523	0.465424	-3.965098	26947.752315
HLA B*2705	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.393718	0.428564	-3.965154	24758.131448
HLA B*4601	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.416219	0.451064	-3.965155	26074.673695
HLA B*7301	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.578728	0.613540	-3.965188	37907.754634
HLA B*4801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.434279	0.469073	-3.965206	27181.872653
HLA A*0216	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.428478	0.463212	-3.965266	26821.217935
HLA B*1503	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.486325	0.521039	-3.965287	30642.568474
HLA B*4402	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.374158	0.408739	-3.965419	23667.827851
HLA A*6901	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.388234	0.422686	-3.965548	24447.483765
HLA B*1502	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.568881	0.603309	-3.965573	37057.948143
HLA A*2601	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.391749	0.426123	-3.965626	24646.144815
HLA A*0101	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.374725	0.409024	-3.965700	23698.705694
HLA B*4402	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.419893	0.454147	-3.965746	26296.229223
HLA A*2501	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.339121	0.373369	-3.965751	21833.357799
HLA A*3001	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.238823	0.272858	-3.965965	17330.989800
HLA A*8001	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.460011	0.494046	-3.965965	28841.041086
HLA A*0250	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.579846	0.613866	-3.965980	38005.496961
HLA A*2601	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.374828	0.408742	-3.966086	23704.347490
HLA A*1101	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.375883	0.409720	-3.966163	23761.996291
HLA A*0202	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.510194	0.543984	-3.966209	32373.792843
HLA A*2301	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.517197	0.550986	-3.966212	32900.113650
HLA B*5701	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.375949	0.409720	-3.966229	23765.595957
HLA B*3501	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.439171	0.472905	-3.966266	27489.763355
HLA A*0212	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.431232	0.464928	-3.966304	26991.815174
HLA B*4601	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.401598	0.435191	-3.966407	25211.462358
HLA B*5701	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.369185	0.402654	-3.966530	23398.312772
HLA B*1801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.462210	0.495678	-3.966532	28987.452579
HLA A*0219	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.431982	0.465424	-3.966558	27038.436641
HLA A*6901	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.373738	0.407006	-3.966732	23644.919726
HLA B*4402	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.392919	0.426183	-3.966736	24712.634130
HLA B*5101	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.499593	0.532852	-3.966741	31593.133820
HLA A*2602	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.592754	0.625924	-3.966830	39152.048172
HLA A*0211	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.419546	0.452683	-3.966863	26275.183216
HLA B*0702	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.435948	0.469073	-3.966874	27286.479575
HLA A*0202	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.583295	0.616392	-3.966903	38308.527572
HLA B*5401	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.566588	0.599665	-3.966923	36862.795917
HLA B*1502	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.580845	0.613866	-3.966979	38092.979841
HLA B*1509	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.499865	0.532852	-3.967014	31612.966223
HLA B*1502	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.433278	0.466242	-3.967036	27119.301092
HLA A*2902	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.410030	0.442960	-3.967070	25705.753507
HLA B*4001	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.393288	0.426123	-3.967164	24733.632786
HLA B*3501	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.455577	0.488312	-3.967266	28548.116148
HLA A*2602	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.604077	0.636741	-3.967336	40186.173467
HLA B*0801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.235990	0.268569	-3.967421	17218.284829
HLA A*3301	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.633974	0.666540	-3.967433	43050.068937
HLA A*0202	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.472625	0.505009	-3.967617	29691.033719

HLA A*8001	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.316126	0.348457	-3.967669	20707.426198
HLA A*0211	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.526372	0.558588	-3.967784	33602.542349
HLA B*0803	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.477301	0.509478	-3.967823	30012.404653
HLA B*1501	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.353180	0.385288	-3.967892	22551.729318
HLA A*2601	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.348300	0.380356	-3.967944	22299.748746
HLA A*3101	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.363045	0.395099	-3.967946	23069.880116
HLA A*0203	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.394136	0.426183	-3.967953	24781.984027
HLA B*3901	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.508518	0.540402	-3.968116	32249.159525
HLA B*7301	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.584700	0.616515	-3.968185	38432.660698
HLA B*1501	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.404241	0.436027	-3.968214	25365.370353
HLA B*0702	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.371384	0.403047	-3.968337	23517.094264
HLA A*1101	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.394496	0.426123	-3.968372	24802.504890
HLA A*8001	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.456111	0.487735	-3.968375	28583.196050
HLA A*0212	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.303281	0.334871	-3.968410	20103.954270
HLA B*4501	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.580457	0.612002	-3.968456	38058.992011
HLA A*0250	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.548387	0.579907	-3.968480	35349.787836
HLA B*4501	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.623058	0.654485	-3.968573	41981.518564
HLA B*4403	1:163-171	9	IADSGNSVT	0.978961	-0.283600	-4.663958	0.695361	-3.968597	46127.294087
HLA B*5701	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.418113	0.449508	-3.968605	26188.617174
HLA B*5701	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.394792	0.426183	-3.968608	24819.417183
HLA B*4002	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.623115	0.654485	-3.968630	41986.969686
HLA B*1503	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.292998	0.324299	-3.968698	19633.502942
HLA B*3801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.547090	0.578365	-3.968725	35244.381685
HLA B*0802	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.468199	0.499448	-3.968750	29389.952790
HLA A*8001	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.404056	0.435191	-3.968864	25354.531986
HLA B*1501	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.419997	0.451064	-3.968933	26302.489394
HLA A*0212	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.241976	0.272858	-3.969118	17457.271874
HLA B*0801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.376160	0.407006	-3.969155	23777.170006
HLA A*0101	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.372276	0.403047	-3.969230	23565.489443
HLA A*2403	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.378958	0.409720	-3.969239	23930.865154
HLA B*3501	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.294772	0.325463	-3.969308	19713.859318
HLA A*2601	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.378063	0.408739	-3.969324	23881.590426
HLA A*2501	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.468796	0.499448	-3.969347	29430.365632
HLA B*1517	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-3.935152	-0.034337	-3.969490	8612.959997
HLA A*0212	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.419048	0.449508	-3.969540	26245.065574
HLA B*1501	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.378399	0.408739	-3.969660	23900.072710
HLA B*5301	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.530839	0.561125	-3.969714	33949.900680
HLA A*3201	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.615657	0.645932	-3.969725	41272.166430
HLA A*2301	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.544320	0.574537	-3.969783	35020.299267
HLA A*2601	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.378855	0.409024	-3.969831	23925.169446
HLA B*4801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.435341	0.465424	-3.969917	27248.420999
HLA A*0301	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.365134	0.395099	-3.970035	23181.099435
HLA A*2501	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.479639	0.509478	-3.970161	30174.392202
HLA A*2403	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.422894	0.452683	-3.970211	26478.523800
HLA B*3501	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.250839	0.280603	-3.970235	17817.166274
HLA A*2301	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.510668	0.540402	-3.970266	32409.190184
HLA B*4801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.402620	0.432298	-3.970322	25270.862403
HLA A*0202	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.238924	0.268569	-3.970356	17335.021895
HLA A*2403	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.439498	0.469073	-3.970424	27510.442733
HLA B*4501	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.650524	0.680074	-3.970449	44722.247794
HLA A*0219	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.392466	0.421976	-3.970490	24686.844922
HLA A*8001	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.406523	0.436027	-3.970496	25498.965284
HLA A*0202	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.563012	0.592477	-3.970536	36560.519296
HLA A*0219	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.432975	0.462438	-3.970538	27100.381793
HLA A*8001	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.402987	0.432298	-3.970689	25292.198565
HLA B*4402	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.434049	0.463212	-3.970837	27167.465483
HLA B*4403	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.625332	0.654485	-3.970848	42201.942886
HLA B*5401	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.477432	0.506563	-3.970869	30021.498402
HLA B*3501	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.439963	0.469073	-3.970890	27539.926553
HLA A*2402	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.525165	0.554273	-3.970892	33509.234121
HLA A*0219	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.425058	0.454147	-3.970911	26610.782470
HLA A*2402	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.564366	0.593391	-3.970975	36674.623077
HLA B*4801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.433556	0.462438	-3.971118	27136.618683
HLA A*0301	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.356436	0.385288	-3.971148	22721.460117
HLA A*1101	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.450890	0.479739	-3.971151	28241.660791

HLA A*0250	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.563325	0.592081	-3.971243	36586.834614
HLA A*0203	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.437552	0.466242	-3.971310	27387.488366
HLA B*3901	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.493115	0.521798	-3.971317	31125.416881
HLA A*3301	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.566288	0.594934	-3.971353	36837.278528
HLA B*0802	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.403666	0.432298	-3.971368	25331.772783
HLA B*1509	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.481854	0.510481	-3.971373	30328.720953
HLA B*1502	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.594784	0.623337	-3.971448	39335.478849
HLA A*0250	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.583486	0.612002	-3.971484	38325.318086
HLA B*4403	1:409-417	9	SVSAGDEIT	0.912292	-0.221720	-4.662100	0.690572	-3.971528	45930.326875
HLA B*4402	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.459280	0.487735	-3.971545	28792.557538
HLA A*0216	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.437017	0.465424	-3.971592	27353.727964
HLA B*4801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.434810	0.463212	-3.971598	27215.126485
HLA A*0301	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.367371	0.395731	-3.971640	23300.795033
HLA B*7301	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.607671	0.635971	-3.971700	40520.180066
HLA A*0201	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.394564	0.422686	-3.971878	24806.396381
HLA A*0250	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.436845	0.464928	-3.971917	27342.927511
HLA B*4601	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.367032	0.395099	-3.971933	23282.650222
HLA A*3101	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.318076	0.346054	-3.972022	20800.615913
HLA A*3002	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.480520	0.508438	-3.972082	30235.669381
HLA B*0802	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.467809	0.495678	-3.972131	29363.571238
HLA A*2902	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.307017	0.334871	-3.972146	20277.628810
HLA A*2402	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.577685	0.605498	-3.972186	37816.809825
HLA A*0203	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.144891	0.172544	-3.972347	13960.178015
HLA B*4402	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.437313	0.464928	-3.972385	27372.379881
HLA A*3301	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.512794	0.540402	-3.972392	32568.253012
HLA B*7301	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.575761	0.603309	-3.972452	37649.625560
HLA A*2902	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.323041	0.350532	-3.972509	21039.753946
HLA A*0203	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.368245	0.395731	-3.972514	23347.734604
HLA A*2402	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.565059	0.592477	-3.972582	36733.199471
HLA B*5701	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.423913	0.451064	-3.972850	26540.765551
HLA B*4601	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.358187	0.385288	-3.972898	22813.220740
HLA A*6802	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.441436	0.468482	-3.972954	27633.500610
HLA A*0206	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.512639	0.539629	-3.973011	32556.626506
HLA A*2301	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.547210	0.574191	-3.973019	35254.107104
HLA A*2402	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.572875	0.599665	-3.973211	37400.335129
HLA A*2602	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.609213	0.635971	-3.973241	40664.237087
HLA B*1509	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.515781	0.542449	-3.973331	32792.962978
HLA A*2301	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.516034	0.542619	-3.973415	32812.128456
HLA A*2402	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.552470	0.578823	-3.973647	35683.727689
HLA B*4001	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.395628	0.421976	-3.973652	24867.263467
HLA B*5801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.355468	0.381799	-3.973670	22670.873235
HLA A*2403	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.423270	0.449508	-3.973762	26501.453062
HLA A*0101	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.382621	0.408739	-3.973882	24133.552013
HLA B*1517	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.473337	0.499448	-3.973889	29739.743066
HLA B*4002	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.628117	0.654207	-3.973909	42473.356717
HLA A*0206	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.380951	0.407006	-3.973945	24040.902266
HLA A*2403	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.395938	0.421976	-3.973962	24885.027656
HLA B*3801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.532565	0.558588	-3.973977	34085.163343
HLA A*2403	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.425076	0.451064	-3.974013	26611.934186
HLA A*2501	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.480642	0.506563	-3.974079	30244.176302
HLA B*0702	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.440325	0.466242	-3.974082	27562.880258
HLA B*7301	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.566175	0.592081	-3.974093	36827.714061
HLA B*5801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.320306	0.346054	-3.974251	20907.680558
HLA B*4001	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.388481	0.414162	-3.974318	24461.374819
HLA A*3301	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.631718	0.657361	-3.974357	42827.068258
HLA A*0201	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.354376	0.379878	-3.974498	22613.914094
HLA A*2602	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.591465	0.616515	-3.974949	39035.937959
HLA B*1502	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.384670	0.409720	-3.974950	24247.669152
HLA A*0203	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.337711	0.362756	-3.974954	21762.603066
HLA B*5301	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.559498	0.584529	-3.974969	36265.822045
HLA B*3501	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.437437	0.462438	-3.974999	27380.229328
HLA A*0211	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.529283	0.554273	-3.975010	33828.531780
HLA B*5101	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.514683	0.539629	-3.975055	32710.218805
HLA A*8001	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.456390	0.481266	-3.975125	28601.603174
HLA A*2402	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.578448	0.603309	-3.975140	37883.358354

HLA A*3201	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.618394	0.643088	-3.975306	41533.106546
HLA B*4403	1:74-82	9	VYDTGEAET	0.865291	-0.174425	-4.666317	0.690866	-3.975451	46378.517455
HLA B*1801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.529746	0.554273	-3.975473	33864.603694
HLA B*1517	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.385194	0.409720	-3.975474	24276.939320
HLA B*3501	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.355837	0.380356	-3.975481	22690.136979
HLA B*4801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.410801	0.435191	-3.975610	25751.407411
HLA A*2601	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.338392	0.362756	-3.975636	21796.772511
HLA A*2403	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.401864	0.426123	-3.975740	25226.879278
HLA B*4601	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.384809	0.409024	-3.975784	24255.409842
HLA B*1517	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.135982	0.160089	-3.975893	13676.712232
HLA A*6901	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.371703	0.395731	-3.975972	23534.403214
HLA A*0301	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.356363	0.380356	-3.976007	22717.649898
HLA B*4403	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.601974	0.625924	-3.976050	39992.068305
HLA B*0802	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.482625	0.506563	-3.976062	30382.585335
HLA A*6901	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.384968	0.408739	-3.976229	24264.334381
HLA A*2902	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.439570	0.463212	-3.976358	27515.056802
HLA B*3501	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-3.787694	-0.188668	-3.976362	6133.297803
HLA B*1501	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.310492	0.334125	-3.976367	20440.525519
HLA B*5301	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.593013	0.616515	-3.976497	39175.354012
HLA A*1101	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.480947	0.504447	-3.976500	30265.454077
HLA B*5301	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.527566	0.550986	-3.976580	33695.016664
HLA B*1503	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.520649	0.543984	-3.976665	33162.616727
HLA B*0702	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.464513	0.487735	-3.976777	29141.543216
HLA B*4402	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.445371	0.468482	-3.976889	27885.041308
HLA B*4001	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.385678	0.408742	-3.976936	24304.009525
HLA A*2902	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.446022	0.469073	-3.976949	27926.859463
HLA B*3901	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.481976	0.505009	-3.976968	30337.254054
HLA B*0803	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.465290	0.488312	-3.976978	29193.772949
HLA A*0212	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.419973	0.442960	-3.977013	26301.066497
HLA B*3901	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.486518	0.509478	-3.977040	30656.164867
HLA A*8001	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.426571	0.449508	-3.977063	26703.655290
HLA A*2603	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.602989	0.625924	-3.977065	40085.641954
HLA A*2301	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.538258	0.561125	-3.977134	34534.898325
HLA B*4801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.413186	0.436027	-3.977159	25893.198288
HLA A*2501	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.465544	0.488312	-3.977232	29210.834921
HLA A*0212	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.403417	0.426183	-3.977233	25317.250486
HLA A*0203	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.357205	0.379878	-3.977327	22761.690721
HLA B*4403	1:428-436	9	EIPDVSTLT	0.971789	-0.288841	-4.660300	0.682948	-3.977352	45740.386571
HLA B*5401	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.552038	0.574537	-3.977501	35648.225080
HLA B*4801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.428580	0.451064	-3.977516	26827.457953
HLA A*2902	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.458808	0.481266	-3.977542	28761.265881
HLA B*4002	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.583288	0.605498	-3.977790	38307.905842
HLA A*8001	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.444119	0.466242	-3.977877	27804.751415
HLA A*0206	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.552151	0.574191	-3.977960	35657.483224
HLA B*4801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.427595	0.449508	-3.978087	26766.715855
HLA A*3201	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.615046	0.636741	-3.978305	41214.154998
HLA B*7301	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.592238	0.613866	-3.978371	39105.478078
HLA B*4002	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.648148	0.669685	-3.978464	44478.311725
HLA B*0803	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.499633	0.521039	-3.978594	31596.039515
HLA A*2902	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.469559	0.490880	-3.978680	29482.156028
HLA B*1502	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.595078	0.616392	-3.978686	39362.087917
HLA B*3501	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.404876	0.426183	-3.978692	25402.447863
HLA B*7301	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.411052	0.432298	-3.978755	25766.318138
HLA A*8001	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.451694	0.472905	-3.978788	28293.961374
HLA B*3801	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.553347	0.574537	-3.978809	35755.806177
HLA B*5101	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.504769	0.525884	-3.978884	31971.912999
HLA A*0219	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.445179	0.466242	-3.978936	27872.673942
HLA B*4403	1:469-477	9	GTNPPANQT	1.093453	-0.431010	-4.641382	0.662443	-3.978939	43790.688903
HLA A*0203	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.101402	0.122446	-3.978956	12629.960400
HLA A*2403	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.444025	0.464928	-3.979097	27798.735241
HLA B*2705	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.458937	0.479739	-3.979198	28769.824893
HLA B*7301	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.571689	0.592477	-3.979212	37298.297085
HLA A*0206	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.521668	0.542449	-3.979219	33240.570444
HLA B*0702	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.388072	0.408739	-3.979333	24438.359654
HLA A*2501	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.415615	0.436027	-3.979588	26038.446184

HLA A*0219	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.386601	0.407006	-3.979596	24355.736919
HLA B*5701	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.422567	0.442960	-3.979607	26458.620107
HLA A*6802	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.314481	0.334871	-3.979610	20629.157075
HLA A*2603	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.637247	0.657361	-3.979885	43375.718708
HLA B*0803	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.398454	0.418508	-3.979947	25029.629796
HLA B*1801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.260566	0.280603	-3.979962	18220.718597
HLA B*0702	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.461266	0.481266	-3.980000	28924.479880
HLA A*8001	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.432724	0.452683	-3.980041	27084.699056
HLA B*4402	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.087404	0.107303	-3.980101	12229.360777
HLA A*0202	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.520867	0.540737	-3.980131	33179.305691
HLA B*0702	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.471098	0.490880	-3.980218	29586.810692
HLA A*1101	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.388981	0.408742	-3.980239	24489.578064
HLA B*3801	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.564798	0.584529	-3.980269	36711.147891
HLA A*0250	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.384132	0.403854	-3.980278	24217.648172
HLA A*0219	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.438450	0.458095	-3.980355	27444.145260
HLA A*6901	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.121749	0.141319	-3.980429	13235.749192
HLA B*1501	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.415629	0.435191	-3.980438	26039.291388
HLA B*1801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.375538	0.395099	-3.980439	23743.106987
HLA B*3501	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.255603	0.275124	-3.980480	18013.719197
HLA A*2601	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.387623	0.407006	-3.980618	24413.120812
HLA B*3901	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.443908	0.463212	-3.980695	27791.216854
HLA A*2902	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.389461	0.408742	-3.980719	24516.620107
HLA B*4402	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.413092	0.432298	-3.980794	25887.595721
HLA A*3001	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.222955	0.242067	-3.980888	16709.172592
HLA B*3501	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.409457	0.428564	-3.980893	25671.843965
HLA A*1101	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.462161	0.481266	-3.980895	28984.159569
HLA B*0702	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.100082	0.119119	-3.980962	12591.619118
HLA B*7301	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.552233	0.571232	-3.981001	35664.235469
HLA A*3002	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.565616	0.584529	-3.981087	36780.326918
HLA A*0250	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.532091	0.550986	-3.981105	34047.935503
HLA A*0206	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.525230	0.543984	-3.981246	33514.310380
HLA B*4002	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.576188	0.594934	-3.981254	37686.713631
HLA A*2602	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.599145	0.617889	-3.981256	39732.426215
HLA B*2705	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.403243	0.421976	-3.981267	25307.117214
HLA B*4402	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.391061	0.409720	-3.981341	24607.109218
HLA B*0802	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.461139	0.479739	-3.981400	28916.031290
HLA B*1502	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.507400	0.525884	-3.981516	32166.221315
HLA A*0219	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.417678	0.436027	-3.981651	26162.419946
HLA A*0202	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.440252	0.458556	-3.981696	27558.258170
HLA B*1509	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.450782	0.469073	-3.981709	28234.633590
HLA A*0219	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.463018	0.481266	-3.981753	29041.448510
HLA B*5701	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.417798	0.436027	-3.981771	26169.639267
HLA A*2601	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.384466	0.402654	-3.981811	24236.259421
HLA B*4002	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.491311	0.509478	-3.981833	30996.365435
HLA A*2403	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.363698	0.381799	-3.981900	23104.602147
HLA B*5101	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.391624	0.409720	-3.981905	24639.079184
HLA A*0219	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.390666	0.408742	-3.981924	24584.754927
HLA B*0801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.390694	0.408742	-3.981952	24586.350988
HLA B*1509	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.481417	0.499448	-3.981969	30298.218349
HLA B*5701	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.390758	0.408742	-3.982015	24589.942505
HLA A*0202	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.553368	0.571232	-3.982136	35757.547134
HLA B*3501	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.463425	0.481266	-3.982159	29068.641439
HLA B*1509	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.533183	0.550986	-3.982198	34133.694259
HLA B*4801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.408529	0.426183	-3.982346	25617.044214
HLA B*1501	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.405115	0.422686	-3.982429	25416.469023
HLA A*2602	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.263110	0.280603	-3.982507	18327.785487
HLA B*5301	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.574988	0.592477	-3.982511	37582.674341
HLA A*1101	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.476587	0.494046	-3.982541	29963.086629
HLA B*4402	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.378296	0.395731	-3.982565	23894.384330
HLA B*3501	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.020852	0.038251	-3.982601	10491.854158
HLA B*1502	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.568611	0.586005	-3.982606	37034.900183
HLA B*4001	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.389665	0.407006	-3.982659	24528.161824
HLA B*3801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.523471	0.540737	-3.982734	33378.784921
HLA A*0219	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.433814	0.451064	-3.982751	27152.772160
HLA B*4801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.405524	0.422686	-3.982838	25440.405336

HLA B*5301	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.568874	0.586005	-3.982869	37057.346710
HLA B*4002	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.620349	0.637402	-3.982947	41720.469558
HLA A*3001	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.300422	0.317460	-3.982962	19972.027917
HLA A*8001	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.411539	0.428564	-3.982974	25795.188636
HLA A*3001	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.307536	0.324517	-3.983020	20301.886947
HLA A*2403	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.409206	0.426183	-3.983022	25656.987909
HLA B*5701	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.412175	0.429083	-3.983092	25833.034180
HLA B*3501	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.441194	0.458095	-3.983099	27618.106999
HLA A*0212	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.363471	0.380356	-3.983115	23092.480974
HLA B*1517	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.471441	0.488312	-3.983129	29610.188883
HLA B*3901	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.478840	0.495678	-3.983162	30118.941575
HLA B*7301	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.561586	0.578365	-3.983221	36440.658671
HLA A*3201	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.561617	0.578365	-3.983252	36443.221580
HLA B*0801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.200297	0.216943	-3.983354	15859.756370
HLA B*1509	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.448285	0.464928	-3.983357	28072.730315
HLA A*8001	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.387377	0.403854	-3.983522	24399.257161
HLA A*2301	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.516389	0.532852	-3.983538	32838.943413
HLA B*0803	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.505342	0.521798	-3.983544	32014.144205
HLA A*8001	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.393276	0.409720	-3.983557	24732.963764
HLA A*0101	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.406337	0.422686	-3.983651	25488.069833
HLA B*4001	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.387750	0.403854	-3.983896	24420.253757
HLA A*8001	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.410070	0.426123	-3.983947	25708.117726
HLA B*2705	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.410134	0.426183	-3.983950	25711.873108
HLA B*1801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.523604	0.539629	-3.983976	33389.079313
HLA A*0201	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.392783	0.408739	-3.984044	24704.881175
HLA A*0219	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.363931	0.379878	-3.984053	23116.979802
HLA A*0301	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.365858	0.381799	-3.984059	23219.757043
HLA A*0212	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.363962	0.379878	-3.984084	23118.605643
HLA B*1517	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.442272	0.458095	-3.984178	27686.771818
HLA B*5301	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.602162	0.617889	-3.984273	40009.380264
HLA B*0801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.407101	0.422686	-3.984415	25532.922732
HLA A*6901	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.379536	0.395099	-3.984437	23962.734335
HLA B*4403	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.621209	0.636741	-3.984468	41803.158735
HLA A*6802	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.435536	0.451064	-3.984473	27260.658854
HLA B*3501	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.449457	0.464928	-3.984529	28148.616006
HLA A*3201	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.602430	0.617889	-3.984541	40034.062754
HLA A*2501	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.453026	0.468482	-3.984544	28380.883718
HLA A*3201	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.525430	0.540737	-3.984693	33529.725164
HLA A*2603	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.196138	0.211378	-3.984760	15708.615990
HLA A*3101	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.358130	0.373369	-3.984761	22810.258924
HLA A*8001	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.442975	0.458095	-3.984880	27731.592986
HLA A*0250	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.559129	0.574191	-3.984938	36235.032652
HLA B*5301	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.601337	0.616392	-3.984945	39933.479694
HLA B*5101	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.494464	0.509478	-3.984986	31222.220125
HLA A*2603	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.509188	0.524138	-3.985050	32298.920224
HLA B*3901	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.475955	0.490880	-3.985075	29919.514254
HLA B*5801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.356490	0.371335	-3.985155	22724.287466
HLA A*8001	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.448395	0.463212	-3.985183	28079.869130
HLA B*2705	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.393958	0.408742	-3.985215	24771.796970
HLA B*1517	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.117393	0.132177	-3.985216	13103.659030
HLA B*0803	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.480907	0.495678	-3.985229	30262.670748
HLA B*1509	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.479277	0.494046	-3.985231	30149.263693
HLA B*4002	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.621214	0.635971	-3.985242	41803.611038
HLA B*5801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.345983	0.360485	-3.985498	22181.115211
HLA B*1502	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.570040	0.584529	-3.985511	37156.916402
HLA A*0212	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.394296	0.408739	-3.985557	24791.102314
HLA B*5101	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.411767	0.426123	-3.985643	25808.728452
HLA A*2602	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.591194	0.605498	-3.985696	39011.659801
HLA B*5101	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.474021	0.488312	-3.985709	29786.598554
HLA B*1502	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.621681	0.635971	-3.985710	41848.639699
HLA A*1101	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.394801	0.409024	-3.985777	24819.954270
HLA B*4403	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.631725	0.645932	-3.985794	42827.763333
HLA A*6801	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.652384	0.666540	-3.985844	44914.277271
HLA B*1517	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.452105	0.466242	-3.985863	28320.760817
HLA B*5701	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.421071	0.435191	-3.985879	26367.597998

HLA B*1503	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.452133	0.466242	-3.985891	28322.599423
HLA A*0203	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.118032	0.132130	-3.985902	13122.955125
HLA B*7301	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.310215	0.324299	-3.985916	20427.481128
HLA A*3201	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.611938	0.625924	-3.986014	40920.226732
HLA A*0206	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.494633	0.508438	-3.986195	31234.383924
HLA A*6901	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.160031	0.173777	-3.986254	14455.430754
HLA B*1509	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.466002	0.479739	-3.986263	29241.666519
HLA B*3801	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.490761	0.504447	-3.986314	30957.151527
HLA A*2601	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.409018	0.422686	-3.986332	25645.886195
HLA B*4001	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.437414	0.451064	-3.986350	27378.748128
HLA B*1517	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.467684	0.481266	-3.986419	29355.153200
HLA A*3301	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.599986	0.613540	-3.986446	39809.452173
HLA A*0206	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.512393	0.525884	-3.986509	32538.138345
HLA B*4601	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.400738	0.414162	-3.986576	25161.592561
HLA B*0702	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.349371	0.362756	-3.986615	22354.828117
HLA A*2501	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.466423	0.479739	-3.986684	29269.996991
HLA A*0206	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.455761	0.469073	-3.986688	28560.165178
HLA B*4001	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.229383	0.242669	-3.986714	16958.332100
HLA B*5101	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.452178	0.465424	-3.986754	28325.510793
HLA A*0219	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.477656	0.490880	-3.986776	30036.931601
HLA A*2501	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.415371	0.428564	-3.986806	26023.800333
HLA B*0802	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.475196	0.488312	-3.986884	29867.278720
HLA A*0216	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.491346	0.504447	-3.986899	30998.880841
HLA A*0201	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.367317	0.380356	-3.986961	23297.895955
HLA B*4501	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.656670	0.669685	-3.986985	45359.668959
HLA B*4801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.441156	0.454147	-3.987009	27615.716528
HLA A*3001	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.109508	0.122446	-3.987062	12867.901035
HLA A*6901	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.390927	0.403854	-3.987072	24599.522449
HLA B*0803	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.460044	0.472905	-3.987139	28843.225544
HLA B*4501	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.592884	0.605498	-3.987385	39163.699359
HLA B*1503	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.529882	0.542449	-3.987433	33875.231179
HLA B*0702	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.383220	0.395731	-3.987489	24166.867747
HLA A*0203	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.216348	0.228841	-3.987508	16456.906175
HLA B*3901	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.446229	0.458556	-3.987673	27940.157775
HLA B*5701	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.413804	0.426123	-3.987680	25930.065373
HLA A*2902	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.475557	0.487735	-3.987822	29892.172203
HLA B*5401	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.562098	0.574191	-3.987907	36483.660527
HLA B*5701	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.391079	0.403047	-3.988033	24608.174215
HLA A*0250	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.591378	0.603309	-3.988069	39028.125077
HLA B*1509	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.414281	0.426183	-3.988097	25958.557608
HLA B*1502	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.593607	0.605498	-3.988109	39229.010107
HLA B*1509	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.549266	0.561125	-3.988141	35421.383416
HLA B*1503	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.423411	0.435191	-3.988219	26510.056654
HLA B*4601	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.395325	0.407006	-3.988319	24849.915263
HLA B*2705	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.402484	0.414162	-3.988321	25262.934318
HLA A*2403	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.424503	0.436027	-3.988476	26576.829263
HLA A*0201	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.391143	0.402654	-3.988489	24611.768920
HLA A*0101	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.368903	0.380356	-3.988547	23383.127828
HLA A*2601	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.258435	0.269799	-3.988636	18131.532718
HLA A*2902	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.442789	0.454147	-3.988642	27719.743555
HLA B*3901	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.360083	0.371335	-3.988747	22913.035982
HLA A*0216	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.476518	0.487735	-3.988783	29958.386185
HLA B*4501	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.631902	0.643088	-3.988814	42845.143867
HLA A*0203	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.391864	0.403047	-3.988817	24652.678994
HLA A*3001	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.301146	0.312328	-3.988817	20005.333966
HLA A*1101	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.451278	0.462438	-3.988840	28266.881448
HLA B*1509	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.529598	0.540737	-3.988861	33853.063824
HLA A*3301	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.632216	0.643088	-3.989128	42876.214650
HLA B*5801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.356887	0.367626	-3.989261	22745.073130
HLA A*3002	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.575331	0.586005	-3.989326	37612.370510
HLA A*0101	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.362733	0.373369	-3.989364	23053.286956
HLA B*5701	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.421672	0.432298	-3.989374	26404.140617
HLA B*5401	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.543693	0.554273	-3.989420	34969.751048
HLA B*4601	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.398168	0.408742	-3.989426	25013.115528
HLA A*6901	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.324396	0.334871	-3.989525	21105.532275

HLA B*4402	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.411539	0.421976	-3.989563	25795.188636
HLA B*3801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.550748	0.561125	-3.989623	35542.505885
HLA A*2501	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.270234	0.280603	-3.989630	18630.891285
HLA A*8001	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.363019	0.373369	-3.989650	23068.507297
HLA B*1501	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.371454	0.381799	-3.989656	23520.911320
HLA A*0212	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.307144	0.317460	-3.989684	20283.553460
HLA B*0803	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.494701	0.505009	-3.989692	31239.284570
HLA A*2403	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.418822	0.429083	-3.989739	26231.438755
HLA A*6802	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.398494	0.408742	-3.989752	25031.931830
HLA A*2403	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.315254	0.325463	-3.989791	20665.906648
HLA A*2402	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.540859	0.550986	-3.989873	34742.339641
HLA B*4501	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.627313	0.637402	-3.989911	42394.845925
HLA B*0803	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.500420	0.510481	-3.989939	31653.353343
HLA B*0702	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.454889	0.464928	-3.989961	28502.900445
HLA B*1509	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.441083	0.451064	-3.990020	27611.085579
HLA A*2402	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.561274	0.571232	-3.990042	36414.448492
HLA A*0206	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.398816	0.408742	-3.990074	25050.491243
HLA B*1502	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.408759	0.418508	-3.990252	25630.629181
HLA A*0216	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.459386	0.469073	-3.990313	28799.567796
HLA A*0219	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.478062	0.487735	-3.990327	30065.056649
HLA A*0203	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.425535	0.435191	-3.990343	26640.022684
HLA A*0301	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.232419	0.242067	-3.990352	17077.278873
HLA A*0202	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.293738	0.303321	-3.990417	19666.989215
HLA B*1503	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.408966	0.418508	-3.990459	25642.834066
HLA B*4403	1:426-434	9	QREIPDVST	1.013642	-0.347102	-4.657065	0.666540	-3.990524	45400.913350
HLA B*5301	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.604086	0.613540	-3.990546	40187.043088
HLA B*4002	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.433532	0.442960	-3.990572	27135.150662
HLA B*0802	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.443261	0.452683	-3.990579	27749.902058
HLA A*2501	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.478370	0.487735	-3.990635	30086.371171
HLA A*0201	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.393683	0.403047	-3.990636	24756.122448
HLA A*3002	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.544926	0.554273	-3.990653	35069.213026
HLA A*2402	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.582753	0.592081	-3.990671	38260.683903
HLA A*2501	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.412695	0.421976	-3.990719	25863.938252
HLA A*0211	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.500258	0.509478	-3.990780	31641.539910
HLA A*2601	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.272355	0.281512	-3.990843	18722.128280
HLA B*0803	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.533338	0.542449	-3.990889	34145.883963
HLA B*2705	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.485005	0.494046	-3.990959	30549.545588
HLA A*1101	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.205714	0.214737	-3.990977	16058.849352
HLA A*2603	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.585925	0.594934	-3.990990	38541.137963
HLA A*3301	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.645540	0.654485	-3.991055	44212.020824
HLA B*4601	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.386822	0.395731	-3.991091	24368.125681
HLA A*3101	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.353882	0.362756	-3.991126	22588.237541
HLA B*1509	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.499567	0.508438	-3.991129	31591.253808
HLA B*1509	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.464160	0.472905	-3.991255	29117.904930
HLA A*0216	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.482268	0.490880	-3.991388	30357.611908
HLA B*4601	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.414158	0.422686	-3.991473	25951.256123
HLA A*2601	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.395358	0.403854	-3.991503	24851.797428
HLA A*3002	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.586528	0.594934	-3.991594	38594.760575
HLA A*0219	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.395454	0.403854	-3.991600	24857.310303
HLA A*3201	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.605482	0.613866	-3.991615	40316.390828
HLA A*6801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.394293	0.402654	-3.991639	24790.968197
HLA A*0219	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.387527	0.395731	-3.991796	24407.706449
HLA A*0212	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.420930	0.429083	-3.991846	26359.040640
HLA A*3001	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.305730	0.313851	-3.991879	20217.602383
HLA B*3501	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.394965	0.403047	-3.991919	24829.355174
HLA B*0803	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.400952	0.409024	-3.991928	25173.982660
HLA B*4403	1:353-361	9	FGGITRDVQ	0.950557	-0.270483	-4.672038	0.680074	-3.991964	46993.507139
HLA B*4002	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.585525	0.593391	-3.992134	38505.708699
HLA B*7301	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.401246	0.409024	-3.992221	25191.011974
HLA B*1501	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.387424	0.395099	-3.992325	24401.897249
HLA B*4001	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.410843	0.418508	-3.992336	25753.915154
HLA B*1502	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.500774	0.508438	-3.992337	31679.221319
HLA A*0203	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.443407	0.451064	-3.992344	27759.211301
HLA A*3002	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.572312	0.579907	-3.992405	37351.807040
HLA B*4001	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.401145	0.408739	-3.992405	25185.152591

HLA B*1509	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.501947	0.509478	-3.992469	31764.856010
HLA B*1509	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.536454	0.543984	-3.992470	34391.710571
HLA A*2403	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.421038	0.428564	-3.992473	26365.601033
HLA A*0203	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.401295	0.408739	-3.992556	25193.874029
HLA A*3002	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.567133	0.574537	-3.992596	36909.091248
HLA B*5701	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.415286	0.422686	-3.992600	26018.732535
HLA B*0801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.372483	0.379878	-3.992605	23576.710943
HLA B*5801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.152738	0.160089	-3.992650	14214.717603
HLA A*0101	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.387762	0.395099	-3.992663	24420.914320
HLA A*0203	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.395398	0.402654	-3.992744	24854.083106
HLA B*0702	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.455204	0.462438	-3.992766	28523.570406
HLA A*0206	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.480583	0.487735	-3.992848	30240.086138
HLA B*5701	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.407068	0.414162	-3.992905	25530.988981
HLA B*5401	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.472691	0.479739	-3.992952	29695.531565
HLA B*5801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.346188	0.353175	-3.993013	22191.557440
HLA A*0250	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.598631	0.605498	-3.993132	39685.380473
HLA A*2402	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.577706	0.584529	-3.993177	37818.651132
HLA B*4801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.436279	0.442960	-3.993319	27307.301488
HLA A*2403	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.402249	0.408739	-3.993510	25249.271047
HLA B*5301	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.605526	0.612002	-3.993525	40320.535078
HLA A*0211	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.537567	0.543984	-3.993583	34480.013972
HLA B*3901	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.502062	0.508438	-3.993624	31773.277500
HLA A*3101	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.257008	0.263371	-3.993637	18072.089994
HLA B*4002	1:248-256	9	DAVVLKALA	0.937221	-0.291289	-4.639580	0.645932	-3.993648	43609.360937
HLA B*7301	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.517890	0.524138	-3.993752	32952.661430
HLA B*0801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.429963	0.436027	-3.993936	26913.077966
HLA B*5701	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.373881	0.379878	-3.994003	23652.723914
HLA B*1509	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.499043	0.505009	-3.994034	31553.164932
HLA B*4801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.403851	0.409720	-3.994132	25342.601421
HLA A*2902	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.374013	0.379878	-3.994135	23659.890682
HLA B*0803	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.457387	0.463212	-3.994174	28667.284632
HLA B*0702	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.459644	0.465424	-3.994220	28816.711168
HLA A*0201	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.390041	0.395731	-3.994310	24549.402157
HLA B*5401	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.535072	0.540737	-3.994336	34282.483848
HLA A*2403	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.426794	0.432298	-3.994496	26717.382880
HLA B*5801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.351190	0.356622	-3.994568	22448.629713
HLA A*2602	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.267428	0.272858	-3.994570	18510.934605
HLA B*5301	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.600075	0.605498	-3.994577	39817.636873
HLA B*7301	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.594324	0.599665	-3.994659	39293.792040
HLA B*5301	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.597973	0.603309	-3.994664	39625.311797
HLA B*5701	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.209436	0.214737	-3.994699	16197.053185
HLA B*5701	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.403456	0.408739	-3.994717	25319.578973
HLA A*0301	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.329673	0.334871	-3.994802	21363.541700
HLA B*5101	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.376602	0.381799	-3.994803	23801.365096
HLA A*2501	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.459741	0.464928	-3.994813	28823.103580
HLA A*8001	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.448980	0.454147	-3.994833	28117.719953
HLA A*2501	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.449025	0.454147	-3.994878	28120.610263
HLA A*6801	1:564-572	9	PDLSGMFWV	0.858413	-0.183220	-4.670186	0.675193	-3.994994	46793.600567
HLA B*5101	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.494527	0.499448	-3.995079	31226.780994
HLA A*0219	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.404215	0.409024	-3.995191	25363.860936
HLA B*0801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.397902	0.402654	-3.995248	24997.829247
HLA B*4601	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.375129	0.379878	-3.995251	23720.767624
HLA B*3901	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.463758	0.468482	-3.995276	29090.980673
HLA B*0801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.362944	0.367626	-3.995318	23064.514104
HLA A*2902	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.431359	0.436027	-3.995332	26999.701553
HLA B*2705	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.486278	0.490880	-3.995399	30639.253195
HLA A*2501	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.464503	0.469073	-3.995430	29140.912612
HLA A*2501	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.427750	0.432298	-3.995452	26776.274689
HLA A*2602	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.573874	0.578365	-3.995509	37486.425019
HLA A*2601	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.390722	0.395099	-3.995623	24587.947153
HLA A*0101	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.380944	0.385288	-3.995656	24040.512093
HLA B*0802	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.454259	0.458556	-3.995703	28461.605450
HLA B*3501	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.409958	0.414162	-3.995795	25701.442845
HLA A*6801	1:587-595	9	LDKGADVDA	1.005632	-0.348271	-4.653216	0.657361	-3.995855	45000.375054
HLA A*3201	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.570061	0.574191	-3.995870	37158.725579

HLA A*0250	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.428192	0.432298	-3.995894	26803.521598
HLA B*0702	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.414466	0.418508	-3.995959	25969.654179
HLA A*3201	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.506465	0.510481	-3.995984	32097.037577
HLA B*1501	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.255324	0.259153	-3.996170	18002.126114
HLA B*7301	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.529027	0.532852	-3.996175	33808.589722
HLA B*1503	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.330315	0.334125	-3.996190	21395.116820
HLA A*0206	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.505913	0.509478	-3.996435	32056.257772
HLA A*2601	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.376395	0.379878	-3.996517	23790.036671
HLA B*4801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.425643	0.429083	-3.996559	26646.653009
HLA B*1509	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.487446	0.490880	-3.996566	30721.744260
HLA B*5101	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.465659	0.469073	-3.996586	29218.579289
HLA B*0802	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.459085	0.462438	-3.996647	28779.631983
HLA B*1503	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.450813	0.454147	-3.996666	28236.619361
HLA A*6901	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.368026	0.371335	-3.996691	23335.990854
HLA A*3001	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.265974	0.269282	-3.996692	18449.050317
HLA A*0211	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.425781	0.429083	-3.996698	26655.159537
HLA A*0250	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.589188	0.592477	-3.996711	38831.839872
HLA B*1503	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.551011	0.554273	-3.996738	35564.047885
HLA B*2705	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.459252	0.462438	-3.996814	28790.688424
HLA A*6801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.006666	0.009850	-3.996816	10154.675614
HLA B*0801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.377194	0.380356	-3.996838	23833.835436
HLA B*4001	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.423025	0.426183	-3.996842	26486.546784
HLA B*5401	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.529788	0.532852	-3.996937	33867.901522
HLA A*0101	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.378813	0.381799	-3.997014	23922.839774
HLA A*0301	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.368365	0.371335	-3.997029	23354.177235
HLA B*4501	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.154383	0.157340	-3.997043	14268.649689
HLA A*2403	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.392172	0.395099	-3.997073	24670.156428
HLA B*1503	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.459562	0.462438	-3.997124	28811.255352
HLA A*3001	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.264741	0.267585	-3.997155	18396.725817
HLA A*6801	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.633130	0.635971	-3.997159	42966.540376
HLA A*3002	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.157277	0.160089	-3.997189	14364.067629
HLA A*1101	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.462241	0.464928	-3.997313	28989.491297
HLA A*2403	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.401232	0.403854	-3.997377	25190.194304
HLA B*5101	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.491445	0.494046	-3.997399	31005.925063
HLA B*1801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.446910	0.449508	-3.997402	27984.026593
HLA A*6801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.493136	0.495678	-3.997458	31126.932383
HLA A*2403	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.416050	0.418508	-3.997542	26064.519274
HLA A*3101	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.448642	0.451064	-3.997578	28095.824104
HLA B*0802	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.416186	0.418508	-3.997678	26072.698915
HLA A*0250	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.301007	0.303321	-3.997686	19998.949614
HLA A*0202	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.491774	0.494046	-3.997728	31029.417364
HLA A*0211	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.400395	0.402654	-3.997741	25141.726679
HLA A*2501	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.423930	0.426123	-3.997806	26541.770648
HLA A*1101	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.273227	0.275124	-3.998103	18759.742616
HLA A*0216	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.460568	0.462438	-3.998130	28878.043162
HLA B*4002	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.641229	0.643088	-3.998141	43775.292930
HLA A*2603	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.530998	0.532852	-3.998147	33962.392211
HLA B*4501	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.652422	0.654207	-3.998215	44918.165140
HLA B*3801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.531142	0.532852	-3.998290	33973.601760
HLA B*5401	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.522444	0.524138	-3.998305	33299.966621
HLA A*2603	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.507788	0.509478	-3.998310	32194.946722
HLA B*1517	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.489253	0.490880	-3.998373	30849.819230
HLA B*1801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.471288	0.472905	-3.998383	29599.778504
HLA B*3501	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.416975	0.418508	-3.998468	26120.134952
HLA A*6901	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.323020	0.324517	-3.998503	21038.729567
HLA B*4601	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.407288	0.408739	-3.998549	25543.975546
HLA A*6801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.213350	0.214737	-3.998613	16343.695046
HLA B*4403	1:468-476	9	IGTNPPANQ	0.818175	-0.148490	-4.668361	0.669685	-3.998676	46597.317248
HLA A*0219	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.424907	0.426183	-3.998724	26601.570536
HLA B*0803	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.451417	0.452683	-3.998734	28275.905209
HLA B*1509	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.553015	0.554273	-3.998743	35728.542249
HLA B*4001	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.441720	0.442960	-3.998760	27651.595327
HLA A*0216	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.361537	0.362756	-3.998781	22989.893972
HLA A*2301	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.539600	0.540737	-3.998863	34641.743179
HLA B*5101	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.462130	0.463212	-3.998918	28982.121227

HLA A*0219	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.427539	0.428564	-3.998974	26763.240761
HLA B*1517	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.478814	0.479739	-3.999075	30117.149286
HLA A*0202	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.498566	0.499448	-3.999118	31518.532030
HLA A*6802	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.379085	0.379878	-3.999207	23937.857195
HLA A*2403	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.442171	0.442960	-3.999211	27680.331925
HLA B*1801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.505965	0.506563	-3.999401	32060.073257
HLA A*0301	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.345516	0.346054	-3.999461	22157.248583
HLA B*5801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.350024	0.350532	-3.999493	22388.473937
HLA A*0211	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.384863	0.385288	-3.999574	24258.428069
HLA A*2902	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.457730	0.458095	-3.999635	28689.936254
HLA A*3001	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.269531	0.269799	-3.999733	18600.779120
HLA B*5301	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.599418	0.599665	-3.999753	39757.368011
HLA B*1501	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.135789	0.135996	-3.999793	13670.646439
HLA B*4501	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.462241	0.462438	-3.999803	28989.491297
HLA A*3301	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-3.988942	-0.010996	-3.999937	9748.584035
HLA A*2403	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.385300	0.385288	-4.000011	24282.850140
HLA A*0202	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.558654	0.558588	-4.000066	36195.456723
HLA B*3901	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.488510	0.488312	-4.000198	30797.125747
HLA B*5701	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.409269	0.409024	-4.000245	25660.735823
HLA A*2603	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.654767	0.654485	-4.000282	45161.337290
HLA B*2705	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.403024	0.402654	-4.000370	25294.387908
HLA B*5301	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.324920	0.324517	-4.000404	21131.009466
HLA A*0250	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.595339	0.594934	-4.000404	39385.731858
HLA B*3801	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.522277	0.521798	-4.000479	33287.178489
HLA B*0702	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.443452	0.442960	-4.000492	27762.064758
HLA B*4601	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.403151	0.402654	-4.000497	25301.778338
HLA A*3101	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.385795	0.385288	-4.000507	24310.584514
HLA A*0212	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.263890	0.263371	-4.000519	18360.733295
HLA A*3201	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.324836	0.324299	-4.000536	21126.894475
HLA A*0206	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.436645	0.436027	-4.000618	27330.357014
HLA A*2301	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.526513	0.525884	-4.000629	33613.451281
HLA B*0702	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.422671	0.421976	-4.000695	26464.918938
HLA A*0301	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.368459	0.367626	-4.000832	23359.231522
HLA B*4001	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.436053	0.435191	-4.000862	27293.123141
HLA B*5101	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.450406	0.449508	-4.000898	28210.204766
HLA B*4402	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.396018	0.395099	-4.000919	24889.605335
HLA B*1801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.489231	0.488312	-4.000920	30848.317220
HLA A*2603	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.419466	0.418508	-4.000958	26270.350702
HLA B*4402	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.427139	0.426123	-4.001016	26738.638428
HLA B*0802	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.465972	0.464928	-4.001044	29239.610067
HLA A*6801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.541489	0.540402	-4.001087	34792.747365
HLA A*0211	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.540739	0.539629	-4.001111	34732.755400
HLA B*4801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.404984	0.403854	-4.001129	25408.770173
HLA A*0250	1:414-422	9	DEITVNVST	1.070685	-0.486156	-4.585685	0.584529	-4.001156	38519.876495
HLA B*1502	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.453886	0.452683	-4.001203	28437.134090
HLA A*0211	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.543653	0.542449	-4.001203	34966.535093
HLA A*2603	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.606739	0.605498	-4.001240	40433.247210
HLA A*3101	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.437350	0.436027	-4.001323	27374.749288
HLA A*0101	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.381223	0.379878	-4.001345	24055.993800
HLA B*1801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.464607	0.463212	-4.001394	29147.849999
HLA A*0219	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.436591	0.435191	-4.001400	27326.956579
HLA A*0202	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.430513	0.429083	-4.001430	26947.169183
HLA A*6901	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.212819	0.211378	-4.001441	16323.724883
HLA B*0803	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.460016	0.458556	-4.001460	28841.353141
HLA A*0216	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.444436	0.442960	-4.001476	27825.065616
HLA A*2301	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.544003	0.542449	-4.001553	34994.732053
HLA B*4402	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.420084	0.418508	-4.001576	26307.754782
HLA B*2705	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.470060	0.468482	-4.001578	29516.148085
HLA A*1101	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.467844	0.466242	-4.001602	29365.954139
HLA A*0212	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.424395	0.422686	-4.001709	26570.216312
HLA A*3101	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.383641	0.381799	-4.001842	24190.281555
HLA B*0801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.437056	0.435191	-4.001865	27356.243751
HLA B*2705	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.466836	0.464928	-4.001908	29297.879412
HLA A*2501	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.492843	0.490880	-4.001963	31105.890342
HLA B*0803	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.501432	0.499448	-4.001984	31727.244383

HLA B*5801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.336127	0.334125	-4.002002	21683.395336
HLA B*1503	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.410745	0.408742	-4.002003	25748.064134
HLA B*1503	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.431086	0.429083	-4.002003	26982.763283
HLA A*2301	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.526231	0.524138	-4.002093	33591.636958
HLA B*4002	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.618620	0.616515	-4.002104	41554.682340
HLA B*3801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.541801	0.539629	-4.002173	34817.790286
HLA A*3002	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-3.954775	-0.047418	-4.002194	9011.048535
HLA A*8001	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.397930	0.395731	-4.002199	24999.452125
HLA B*0702	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.350713	0.348457	-4.002255	22423.989992
HLA A*0219	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.431350	0.429083	-4.002266	26999.117298
HLA A*3301	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.628208	0.625924	-4.002284	42482.318932
HLA A*2403	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.362810	0.360485	-4.002325	23057.402942
HLA B*5101	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.490127	0.487735	-4.002391	30911.966350
HLA B*4801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.405049	0.402654	-4.002395	25412.619306
HLA B*0803	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.508962	0.506563	-4.002399	32282.150156
HLA A*2501	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.405475	0.403047	-4.002428	25437.515274
HLA B*4601	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.405498	0.403047	-4.002451	25438.891453
HLA B*4402	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.455270	0.452683	-4.002587	28527.891395
HLA A*6802	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-3.994397	-0.008210	-4.002607	9871.815817
HLA A*0216	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.475520	0.472905	-4.002615	29889.584902
HLA B*3901	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.496771	0.494046	-4.002725	31388.529887
HLA B*5301	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.498404	0.495678	-4.002726	31506.768914
HLA A*3301	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.639559	0.636741	-4.002817	43607.237692
HLA A*6802	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.438039	0.435191	-4.002847	27418.175343
HLA A*2501	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.412624	0.409720	-4.002905	25859.740961
HLA A*3001	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-3.937093	-0.065831	-4.002924	8651.533719
HLA A*2902	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.454013	0.451064	-4.002949	28445.442757
HLA A*0201	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.398161	0.395099	-4.003062	25012.709577
HLA A*0211	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.412114	0.409024	-4.003090	25829.400836
HLA A*0212	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.398844	0.395731	-4.003113	25052.117541
HLA A*8001	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.365888	0.362756	-4.003132	23221.390113
HLA B*3801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.547170	0.543984	-4.003186	35250.865000
HLA B*3501	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.244126	0.240938	-4.003189	17543.900449
HLA A*0216	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.461334	0.458095	-4.003239	28929.018105
HLA A*3001	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.306564	0.303321	-4.003243	20256.467812
HLA B*1502	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.561835	0.558588	-4.003247	36461.561496
HLA A*3201	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.619656	0.616392	-4.003264	41653.940241
HLA B*3801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.524328	0.521039	-4.003289	33444.760105
HLA B*4002	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.615364	0.612002	-4.003362	41244.266134
HLA B*7301	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.545847	0.542449	-4.003398	35143.662397
HLA A*0101	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.366375	0.362756	-4.003618	23247.409084
HLA A*3001	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.177445	0.173777	-4.003669	15046.844072
HLA A*0206	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.494574	0.490880	-4.003695	31230.159845
HLA B*2705	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.436009	0.432298	-4.003711	27290.317882
HLA A*2501	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.469970	0.466242	-4.003728	29510.080904
HLA A*0202	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.578028	0.574191	-4.003837	37846.690997
HLA B*5101	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.446861	0.442960	-4.003901	27980.847574
HLA A*3001	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.294483	0.290447	-4.004036	19700.745757
HLA A*0301	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.364535	0.360485	-4.004050	23149.142652
HLA A*2602	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.620450	0.616392	-4.004058	41730.175921
HLA A*0216	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.470342	0.466242	-4.004099	29535.315797
HLA A*3101	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.218843	0.214737	-4.004106	16551.728205
HLA A*8001	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.411132	0.407006	-4.004127	25771.057933
HLA A*3001	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.297502	0.293372	-4.004130	19838.176716
HLA B*5401	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.399251	0.395099	-4.004152	25075.575064
HLA B*4001	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.399279	0.395099	-4.004180	25077.202990
HLA A*0203	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.277075	0.272858	-4.004217	18926.718898
HLA B*5301	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.578770	0.574537	-4.004233	37911.446195
HLA A*2402	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.582609	0.578365	-4.004245	38248.059837
HLA A*2402	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.578784	0.574537	-4.004247	37912.676795
HLA A*0201	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.389606	0.385288	-4.004318	24524.844683
HLA B*0702	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.406997	0.402654	-4.004343	25526.845723
HLA B*4403	1:165-173	9	DSGNSVTQT	1.067931	-0.430529	-4.641814	0.637402	-4.004412	43834.300716
HLA A*0206	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.277416	0.272858	-4.004558	18941.571483
HLA A*0202	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.367361	0.362756	-4.004605	23300.290819

HLA B*5101	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.495500	0.490880	-4.004620	31296.797810
HLA B*1502	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.514105	0.509478	-4.004628	32666.715930
HLA B*0802	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.492415	0.487735	-4.004680	31075.278560
HLA B*0802	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.473838	0.469073	-4.004765	29774.032114
HLA B*0802	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.468058	0.463212	-4.004845	29380.414555
HLA A*3101	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.413623	0.408739	-4.004884	25919.266156
HLA A*2603	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.641631	0.636741	-4.004890	43815.807799
HLA B*3801	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.529051	0.524138	-4.004912	33810.418779
HLA B*5401	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.457633	0.452683	-4.004951	28683.573375
HLA B*5701	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.408820	0.403854	-4.004966	25634.234565
HLA A*2402	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.493291	0.488312	-4.004979	31138.048322
HLA B*4403	1:102-110	9	DIVHTEGPM	0.512619	0.141588	-4.659245	0.654207	-4.005038	45629.416162
HLA A*1101	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.513492	0.508438	-4.005055	32620.623694
HLA A*0216	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.400811	0.395731	-4.005080	25165.812679
HLA A*1101	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.474263	0.469073	-4.005190	29803.200825
HLA A*0216	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.486511	0.481266	-4.005245	30655.667332
HLA B*1509	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.545685	0.540402	-4.005283	35130.546337
HLA A*0202	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.485068	0.479739	-4.005329	30554.008195
HLA B*1501	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.220084	0.214737	-4.005347	16599.074506
HLA B*4002	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.591401	0.586005	-4.005396	39030.236513
HLA A*1101	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.431636	0.426183	-4.005453	27016.942772
HLA A*0203	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.412530	0.407006	-4.005525	25854.145634
HLA A*0212	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.440846	0.435191	-4.005655	27596.003036
HLA B*3501	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.456733	0.451064	-4.005670	28624.202897
HLA B*0803	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.510161	0.504447	-4.005713	32371.340995
HLA A*3101	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.291508	0.285730	-4.005778	19566.277937
HLA B*5401	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.474904	0.469073	-4.005831	29847.249684
HLA B*0702	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.441044	0.435191	-4.005852	27608.546357
HLA B*4002	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.623754	0.617889	-4.005865	42048.798565
HLA B*5301	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.600837	0.594934	-4.005902	39887.490592
HLA B*4002	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.619799	0.613866	-4.005933	41667.688445
HLA B*4402	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.149515	0.143550	-4.005965	14109.601327
HLA B*5101	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.319871	0.313851	-4.006020	20886.766002
HLA B*3501	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.441241	0.435191	-4.006050	27621.095379
HLA B*0802	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.479063	0.472905	-4.006158	30134.424866
HLA A*2403	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.415150	0.408742	-4.006408	26010.569826
HLA A*2403	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.409481	0.403047	-4.006434	25673.232821
HLA B*1801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.474987	0.468482	-4.006505	29852.901680
HLA A*0101	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.374137	0.367626	-4.006511	23666.675516
HLA A*1101	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.464705	0.458095	-4.006611	29154.473590
HLA B*0802	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.487937	0.481266	-4.006671	30756.499962
HLA A*3201	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.585523	0.578823	-4.006700	38505.500388
HLA B*3501	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.378049	0.371335	-4.006714	23880.815258
HLA A*6901	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.374396	0.367626	-4.006769	23680.763457
HLA A*0202	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.433032	0.426123	-4.006908	27103.900663
HLA B*4001	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.436002	0.429083	-4.006918	27289.874973
HLA B*5301	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.586848	0.579907	-4.006941	38623.166923
HLA B*7301	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.528755	0.521798	-4.006956	33787.379894
HLA B*4403	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.150516	0.143550	-4.006966	14142.155993
HLA A*0211	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.279867	0.272858	-4.007008	19048.751671
HLA B*1509	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.502692	0.495678	-4.007014	31819.377406
HLA B*4801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.428998	0.421976	-4.007022	26853.304171
HLA B*4801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.378442	0.371335	-4.007106	23902.400165
HLA B*4403	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.578416	0.571232	-4.007184	37880.489236
HLA A*3201	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.282435	0.275124	-4.007311	19161.720773
HLA A*3002	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.549771	0.542449	-4.007321	35462.606923
HLA A*2603	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.529142	0.521798	-4.007344	33817.553046
HLA A*0203	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.392654	0.385288	-4.007365	24697.531482
HLA B*4002	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.324986	0.317460	-4.007526	21134.210568
HLA B*1509	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.529340	0.521798	-4.007541	33832.924272
HLA B*0801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.458658	0.451064	-4.007594	28751.309508
HLA A*3301	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.529429	0.521798	-4.007631	33839.880217
HLA B*4001	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.403407	0.395731	-4.007676	25316.702638
HLA A*0202	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.249824	0.242067	-4.007756	17775.574892
HLA A*1101	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.422257	0.414162	-4.008095	26439.732609

HLA A*6901	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.370893	0.362756	-4.008136	23490.519293
HLA A*2301	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.529955	0.521798	-4.008157	33880.912754
HLA B*0801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.332702	0.324517	-4.008185	21513.037730
HLA A*6901	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.342313	0.334125	-4.008189	21994.469026
HLA B*3801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.550828	0.542619	-4.008209	35549.044041
HLA B*1801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.151784	0.143550	-4.008234	14183.530446
HLA A*6901	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.218660	0.210423	-4.008237	16544.745324
HLA A*3201	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.613778	0.605498	-4.008279	41093.930127
HLA A*3301	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.613787	0.605498	-4.008289	41094.819391
HLA A*6801	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.651487	0.643088	-4.008399	44821.554272
HLA A*0206	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.471615	0.463212	-4.008403	29622.045156
HLA A*3101	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.415427	0.407006	-4.008422	26027.179414
HLA B*7301	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.548056	0.539629	-4.008427	35322.833499
HLA B*5301	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.304325	0.295880	-4.008444	20152.301824
HLA B*1517	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.476953	0.468482	-4.008471	29988.384431
HLA B*0802	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.499351	0.490880	-4.008471	31575.534443
HLA A*2301	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.496785	0.488312	-4.008473	31389.548754
HLA B*3901	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.496386	0.487735	-4.008650	31360.693649
HLA B*2705	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.462797	0.454147	-4.008650	29026.683829
HLA A*3101	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.302036	0.293372	-4.008664	20046.393942
HLA B*1509	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.467226	0.458556	-4.008670	29324.201944
HLA B*3901	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.437256	0.428564	-4.008692	27368.826155
HLA B*4403	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.632104	0.623337	-4.008767	42865.082228
HLA A*2501	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.471249	0.462438	-4.008811	29597.056393
HLA A*6901	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.362115	0.353175	-4.008940	23020.510043
HLA A*8001	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.417711	0.408739	-4.008972	26164.401522
HLA A*8001	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.460044	0.451064	-4.008980	28843.225544
HLA A*3201	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.608689	0.599665	-4.009024	40615.209117
HLA B*4403	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.471467	0.462438	-4.009029	29611.951002
HLA A*0301	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.343187	0.334125	-4.009063	22038.776998
HLA B*5401	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.504759	0.495678	-4.009081	31971.221149
HLA B*2705	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.478189	0.469073	-4.009116	30073.840958
HLA B*1801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.435405	0.426183	-4.009221	27252.401385
HLA A*2402	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.589261	0.579907	-4.009354	38838.352773
HLA A*0212	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.394700	0.385288	-4.009412	24814.181194
HLA A*0211	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.452413	0.442960	-4.009453	28340.838726
HLA B*2705	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.382833	0.373369	-4.009463	24145.305260
HLA B*7301	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.584104	0.574537	-4.009566	38379.886191
HLA B*2705	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.497351	0.487735	-4.009616	31430.500614
HLA A*2902	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.438722	0.429083	-4.009639	27461.373160
HLA B*1502	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.505370	0.495678	-4.009692	32016.222588
HLA A*2902	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.416837	0.407006	-4.009831	26111.799168
HLA A*6802	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.418871	0.409024	-4.009847	26234.419017
HLA A*0212	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.165172	0.155271	-4.009901	14627.554026
HLA A*6801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.464151	0.454147	-4.010004	29117.274839
HLA B*5101	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.468584	0.458556	-4.010028	29416.039768
HLA B*5401	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.452988	0.442960	-4.010028	28378.427226
HLA B*5101	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.334581	0.324517	-4.010065	21606.346019
HLA A*0211	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.536010	0.525884	-4.010126	34356.564083
HLA A*0202	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.516732	0.506563	-4.010169	32864.891296
HLA A*0201	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.345116	0.334871	-4.010245	22136.880347
HLA A*2602	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.590264	0.579907	-4.010357	38928.173952
HLA A*2402	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.584710	0.574191	-4.010519	38433.492373
HLA B*7301	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.520085	0.509478	-4.010607	33119.587208
HLA A*2601	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.406360	0.395731	-4.010629	25489.448746
HLA A*6801	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.571769	0.561125	-4.010644	37305.158224
HLA B*1801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.510468	0.499448	-4.011020	32394.290549
HLA B*5701	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.406219	0.395099	-4.011121	25481.176383
HLA B*4001	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.413792	0.402654	-4.011138	25929.363989
HLA A*6801	1:227-235	9	QHVREDPIP	0.590751	0.063734	-4.665636	0.654485	-4.011151	46305.812737
HLA A*1101	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.439794	0.428564	-4.011229	27529.201510
HLA B*1517	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.346113	0.334871	-4.011241	22187.716049
HLA B*4402	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.396542	0.385288	-4.011254	24919.650406
HLA A*6901	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.325183	0.313851	-4.011333	21143.816784
HLA B*4001	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.414403	0.403047	-4.011356	25965.861147

HLA B*3901	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.492629	0.481266	-4.011363	31090.580684
HLA B*3501	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.454450	0.442960	-4.011490	28474.080088
HLA B*1501	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.371995	0.360485	-4.011510	23550.196006
HLA A*0212	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.357602	0.346054	-4.011547	22782.510597
HLA A*6802	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.418590	0.407006	-4.011584	26217.393508
HLA B*2705	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.279230	0.267585	-4.011645	19020.845140
HLA A*0219	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.346528	0.334871	-4.011657	22208.972080
HLA A*0301	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.368440	0.356622	-4.011818	23358.220577
HLA A*0301	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.365002	0.353175	-4.011828	23174.077696
HLA A*6901	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.372314	0.360485	-4.011829	23567.529319
HLA B*3901	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.438043	0.426123	-4.011920	27418.472004
HLA A*3201	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.615295	0.603309	-4.011987	41237.795961
HLA A*2602	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.385375	0.373369	-4.012006	24287.054264
HLA A*0250	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.590419	0.578365	-4.012054	38942.075843
HLA A*2603	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.648043	0.635971	-4.012071	44467.485020
HLA B*1801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.517148	0.505009	-4.012139	32896.376157
HLA B*0802	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.477616	0.465424	-4.012192	30034.169288
HLA A*3201	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.592099	0.579907	-4.012192	39092.998248
HLA B*5101	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.492063	0.479739	-4.012324	31050.071718
HLA A*0250	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.466479	0.454147	-4.012332	29273.797577
HLA A*0250	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.480865	0.468482	-4.012383	30259.723973
HLA A*0301	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.362933	0.350532	-4.012401	23063.890230
HLA A*2602	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.604890	0.592477	-4.012413	40261.465261
HLA A*3101	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.408158	0.395731	-4.012427	25595.157081
HLA A*2601	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.394244	0.381799	-4.012446	24788.151913
HLA B*2705	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.478696	0.466242	-4.012454	30109.003866
HLA B*3501	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.435250	0.422686	-4.012564	27242.672579
HLA A*2501	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.462088	0.449508	-4.012580	28979.299143
HLA B*4801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.392980	0.380356	-4.012624	24716.110382
HLA A*0211	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.478081	0.465424	-4.012657	30066.357867
HLA A*2603	1:432-440	9	VSTLTYAEA	0.886349	-0.263012	-4.635997	0.623337	-4.012660	43251.060216
HLA A*2501	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.361192	0.348457	-4.012734	22971.618441
HLA B*1502	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.438971	0.426123	-4.012848	27477.125353
HLA A*2402	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.571532	0.558588	-4.012943	37284.780298
HLA A*6802	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.421717	0.408739	-4.012978	26406.854783
HLA B*4601	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.393387	0.380356	-4.013031	24739.253286
HLA A*8001	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.421851	0.408742	-4.013109	26414.998953
HLA B*3501	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.398563	0.385288	-4.013274	25035.859317
HLA B*5701	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.420464	0.407006	-4.013459	26330.821058
HLA A*0211	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.507616	0.494046	-4.013570	32182.234743
HLA A*3201	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.482117	0.468482	-4.013635	30347.102923
HLA B*4001	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.398964	0.385288	-4.013676	25059.030482
HLA A*3002	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.518149	0.504447	-4.013702	32972.276993
HLA A*3002	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.572349	0.558588	-4.013761	37355.040286
HLA B*4002	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.605982	0.592081	-4.013901	40362.874440
HLA B*4501	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.608884	0.594934	-4.013949	40633.450286
HLA A*3001	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.295610	0.281512	-4.014099	19751.970085
HLA B*5101	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.466853	0.452683	-4.014170	29298.988921
HLA A*3002	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.416935	0.402654	-4.014281	26117.732843
HLA B*0803	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.508337	0.494046	-4.014292	32235.728566
HLA B*5101	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.443391	0.429083	-4.014307	27758.160101
HLA B*5101	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.495589	0.481266	-4.014323	31303.232336
HLA B*4801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.171609	0.157255	-4.014355	14845.994650
HLA B*1503	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.505253	0.490880	-4.014373	32007.563549
HLA B*4801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.428655	0.414162	-4.014492	26832.102629
HLA A*3301	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.480021	0.465424	-4.014597	30201.012076
HLA A*0203	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.317989	0.303321	-4.014668	20796.452756
HLA A*2403	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.363146	0.348457	-4.014689	23075.247377
HLA A*2603	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.555475	0.540737	-4.014738	35931.488429
HLA A*2601	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.363259	0.348457	-4.014802	23081.240212
HLA B*3901	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.469136	0.454147	-4.014989	29453.460866
HLA B*5301	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.424712	0.409720	-4.014993	26589.628559
HLA A*0216	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.418063	0.403047	-4.015016	26185.642116
HLA A*2402	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.536895	0.521798	-4.015097	34426.706769
HLA A*0216	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.278478	0.263371	-4.015107	18987.945413

HLA A*0216	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.283682	0.268569	-4.015113	19216.844850
HLA A*3002	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.593530	0.578365	-4.015165	39222.007321
HLA B*1801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.481438	0.466242	-4.015196	30299.693575
HLA B*5101	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.451494	0.436027	-4.015467	28280.953654
HLA A*2501	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.496759	0.481266	-4.015493	31387.680856
HLA A*8001	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.458456	0.442960	-4.015495	28737.936059
HLA A*3002	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.567946	0.552387	-4.015560	36978.243184
HLA A*2403	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.450874	0.435191	-4.015682	28240.591322
HLA B*0702	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.444770	0.429083	-4.015686	27846.449162
HLA B*3801	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.556117	0.540402	-4.015715	35984.594842
HLA B*1517	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.484854	0.469073	-4.015781	30538.970161
HLA A*3001	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.280928	0.264968	-4.015961	19095.388006
HLA B*5701	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.396511	0.380356	-4.016155	24917.897904
HLA A*3101	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.387518	0.371335	-4.016182	24407.178283
HLA B*7301	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.504496	0.488312	-4.016184	31951.855411
HLA A*0211	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.524669	0.508438	-4.016231	33471.005602
HLA A*2902	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.098352	0.082090	-4.016263	12541.583020
HLA A*2602	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.537422	0.521039	-4.016383	34468.450862
HLA A*0216	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.425408	0.409024	-4.016383	26632.241364
HLA A*3301	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.587644	0.571232	-4.016413	38694.064965
HLA A*0219	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.289300	0.272858	-4.016441	19467.030192
HLA A*3001	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.276723	0.260101	-4.016622	18911.366411
HLA B*0802	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.482878	0.466242	-4.016636	30400.342095
HLA A*3201	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.611590	0.594934	-4.016656	40887.476509
HLA A*1101	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.396681	0.379878	-4.016803	24927.605615
HLA A*0203	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.158847	0.141914	-4.016933	14416.070490
HLA B*0802	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.485510	0.468482	-4.017028	30585.099236
HLA B*3801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.527547	0.510481	-4.017066	33693.558405
HLA B*1517	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.203948	0.186843	-4.017105	15993.650864
HLA A*0201	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.398936	0.381799	-4.017138	25057.403736
HLA A*1101	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.435651	0.418508	-4.017144	27267.886192
HLA B*4501	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.505492	0.488312	-4.017180	32025.230474
HLA B*5301	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.595579	0.578365	-4.017214	39407.471245
HLA B*0801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.425955	0.408739	-4.017216	26665.832582
HLA B*4002	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.426385	0.409024	-4.017361	26692.245087
HLA B*4501	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.568494	0.550986	-4.017508	37024.883803
HLA A*0202	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.538578	0.521039	-4.017539	34560.316551
HLA A*0201	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.380547	0.362756	-4.017790	24018.542588
HLA A*2602	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.596652	0.578823	-4.017829	39505.019634
HLA B*1801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.475947	0.458095	-4.017853	29919.028675
HLA B*5401	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.439883	0.421976	-4.017907	27534.861429
HLA B*5801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.342297	0.324299	-4.017998	21993.636129
HLA B*1501	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.335476	0.317460	-4.018016	21650.926250
HLA A*2301	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.524735	0.506563	-4.018172	33476.076070
HLA B*0803	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.497934	0.479739	-4.018195	31472.697724
HLA B*0803	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.483130	0.464928	-4.018202	30417.944674
HLA A*2602	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.632068	0.613866	-4.018202	42861.603939
HLA A*6802	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.441018	0.422686	-4.018332	27606.903455
HLA A*0201	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.293653	0.275124	-4.018530	19663.159323
HLA B*5101	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.491459	0.472905	-4.018553	31006.931511
HLA B*3801	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.569680	0.550986	-4.018695	37126.173863
HLA B*4402	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.427489	0.408742	-4.018747	26760.200424
HLA B*4402	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.343051	0.324299	-4.018752	22031.862897
HLA B*2705	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.422689	0.403854	-4.018835	26466.064341
HLA B*1517	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.468377	0.449508	-4.018869	29402.039000
HLA B*0801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.300387	0.281512	-4.018875	19970.407286
HLA A*0101	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.364934	0.346054	-4.018880	23170.442275
HLA B*2705	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.343281	0.324299	-4.018982	22043.546607
HLA B*1801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.481426	0.462438	-4.018989	30298.873996
HLA B*2705	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.468540	0.449508	-4.019032	29413.016311
HLA B*4801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.427868	0.408742	-4.019126	26783.518502
HLA B*1517	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.282547	0.263371	-4.019176	19166.697232
HLA B*5301	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.593389	0.574191	-4.019198	39209.278184
HLA B*0702	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.441946	0.422686	-4.019260	27665.959895
HLA A*6802	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.242543	0.223276	-4.019266	17480.047217

HLA B*1502	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.599239	0.579907	-4.019332	39741.025067
HLA B*0702	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.365444	0.346054	-4.019390	23197.659094
HLA B*4801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.365486	0.346054	-4.019432	23199.918146
HLA B*1801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.488517	0.469073	-4.019444	30797.625579
HLA A*0202	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.082085	0.062590	-4.019494	12080.489249
HLA B*1801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.484455	0.464928	-4.019527	30510.896957
HLA B*3901	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.287115	0.267585	-4.019529	19369.333702
HLA A*6901	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.234404	0.214737	-4.019667	17155.523907
HLA B*4501	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.448249	0.428564	-4.019685	28070.452352
HLA B*0803	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.486017	0.466242	-4.019775	30620.859917
HLA A*0211	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.175082	0.155271	-4.019811	14965.176337
HLA A*8001	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.101933	0.082090	-4.019843	12645.411675
HLA B*4403	1:107-115	9	EGPMTPKRA	1.081302	-0.438214	-4.663046	0.643088	-4.019958	46030.572737
HLA A*6801	1:572-580	9	VDAEPRLRA	0.981004	-0.355080	-4.645952	0.625924	-4.020027	44253.897517
HLA A*0250	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.591310	0.571232	-4.020078	39022.002561
HLA B*4403	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.429113	0.409024	-4.020089	26860.423511
HLA A*2603	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.442068	0.421976	-4.020092	27673.743818
HLA A*3301	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.293160	0.272858	-4.020302	19640.833150
HLA B*7301	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.526870	0.506563	-4.020307	33641.103096
HLA A*3301	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.634401	0.613866	-4.020535	43092.476901
HLA B*4402	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.434742	0.414162	-4.020580	27210.857126
HLA B*4403	1:51-59	9	SFYLRFRRE	1.176203	-0.564201	-4.632583	0.612002	-4.020581	42912.414992
HLA B*4403	1:203-211	9	GCVLYEVLT	0.957742	-0.321771	-4.656569	0.635971	-4.020597	45349.118383
HLA A*0212	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.391946	0.371335	-4.020611	24657.347325
HLA A*0203	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.058919	0.038251	-4.020667	11452.982604
HLA B*4801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.429416	0.408739	-4.020677	26879.175291
HLA A*3101	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.354817	0.334125	-4.020692	22636.925483
HLA B*1801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.508441	0.487735	-4.020706	32243.402715
HLA A*3101	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.152837	0.132130	-4.020707	14217.947772
HLA B*4501	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.637270	0.616515	-4.020755	43378.065350
HLA B*0801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.383519	0.362756	-4.020762	24183.477442
HLA B*2705	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.400658	0.379878	-4.020780	25156.964858
HLA B*4801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.439307	0.418508	-4.020800	27498.390270
HLA A*0202	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.456860	0.436027	-4.020833	28632.566222
HLA B*3801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.575225	0.554273	-4.020952	37603.215080
HLA B*3801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.563503	0.542449	-4.021054	36601.880441
HLA B*0802	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.479321	0.458095	-4.021227	30152.362831
HLA A*0206	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.381853	0.360485	-4.021368	24090.896685
HLA B*5801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.350631	0.329236	-4.021395	22419.744498
HLA B*1517	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.195259	0.173777	-4.021482	15676.864902
HLA B*7301	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.517190	0.495678	-4.021512	32899.579696
HLA B*1509	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.440069	0.418508	-4.021561	27546.631827
HLA B*3901	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.346054	0.324299	-4.021755	22184.715425
HLA A*1101	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.474484	0.452683	-4.021801	29818.360488
HLA A*3001	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.291205	0.269402	-4.021803	19552.627871
HLA A*8001	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.401683	0.379878	-4.021805	25216.372920
HLA A*6802	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.393147	0.371335	-4.021811	24725.605716
HLA A*0212	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.382353	0.360485	-4.021868	24118.672780
HLA A*0216	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.450963	0.429083	-4.021880	28246.397501
HLA A*0203	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.281095	0.259153	-4.021942	19102.723994
HLA A*2501	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.451179	0.429083	-4.022096	28260.459509
HLA B*5701	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.418108	0.395731	-4.022377	26188.333821
HLA A*0212	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.425528	0.403047	-4.022481	26639.590329
HLA B*0702	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.417586	0.395099	-4.022487	26156.900632
HLA A*3301	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.625920	0.603309	-4.022611	42259.058459
HLA B*7301	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.583747	0.561125	-4.022622	38348.339262
HLA B*0702	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.431371	0.408742	-4.022629	27000.431890
HLA A*3001	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.285862	0.263202	-4.022660	19313.563236
HLA B*1509	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.431411	0.408739	-4.022672	27002.915183
HLA B*7301	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.573677	0.550986	-4.022691	37469.393907
HLA B*1503	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.448931	0.426183	-4.022747	28114.525746
HLA A*0211	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.486053	0.463212	-4.022840	30623.344850
HLA A*2603	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.575237	0.552387	-4.022850	37604.232240
HLA A*1101	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.465838	0.442960	-4.022878	29230.595023
HLA A*2602	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.617943	0.594934	-4.023009	41489.988559

HLA B*4801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.430034	0.407006	-4.023028	26917.446223
HLA A*2603	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.636678	0.613540	-4.023138	43318.968670
HLA B*3901	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.485578	0.462438	-4.023140	30589.898011
HLA A*0219	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.408473	0.385288	-4.023184	25613.718381
HLA A*2602	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.574403	0.550986	-4.023417	37532.082217
HLA B*3901	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.492521	0.469073	-4.023448	31082.844603
HLA A*2402	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.519136	0.495678	-4.023458	33047.280243
HLA A*2301	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.488884	0.465424	-4.023460	30823.627981
HLA A*0201	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.296334	0.272858	-4.023476	19784.909158
HLA A*2902	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.426178	0.402654	-4.023524	26679.540728
HLA A*2603	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.637402	0.613866	-4.023535	43391.208890
HLA A*0202	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.145986	0.122446	-4.023540	13995.416139
HLA A*2902	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.449957	0.426183	-4.023774	28181.070532
HLA B*1801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.403722	0.379878	-4.023844	25335.062006
HLA A*0203	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.446555	0.422686	-4.023870	27961.175965
HLA A*0201	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.391617	0.367626	-4.023991	24638.679303
HLA A*2301	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.545036	0.521039	-4.023998	35078.131026
HLA A*2402	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.585156	0.561125	-4.024032	38473.017660
HLA A*1101	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.370216	0.346054	-4.024162	23453.948431
HLA A*6901	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.203797	0.179592	-4.024205	15988.114295
HLA A*0206	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.478363	0.454147	-4.024216	30085.882883
HLA B*5101	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.492702	0.468482	-4.024220	31095.795215
HLA A*0202	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.478445	0.454147	-4.024298	30091.580068
HLA B*5401	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.564025	0.539629	-4.024396	36645.865539
HLA B*4801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.419501	0.395099	-4.024402	26272.482584
HLA B*1502	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.565172	0.540737	-4.024435	36742.739391
HLA B*7301	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.576879	0.552387	-4.024492	37746.702321
HLA B*0803	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.505845	0.481266	-4.024579	32051.228964
HLA A*6901	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.375143	0.350532	-4.024611	23721.537597
HLA B*3901	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.489558	0.464928	-4.024630	30871.523095
HLA A*2402	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.518689	0.494046	-4.024644	33013.329091
HLA A*8001	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.453855	0.429083	-4.024772	28435.134217
HLA B*4001	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.404742	0.379878	-4.024864	25394.615878
HLA B*4001	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.387628	0.362756	-4.024872	24413.384958
HLA A*0101	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.378134	0.353175	-4.024959	23885.466643
HLA B*1517	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.457297	0.432298	-4.025000	28661.391938
HLA B*0702	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.432010	0.407006	-4.025004	27040.191997
HLA A*8001	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.427846	0.402654	-4.025192	26782.214471
HLA B*0702	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.479352	0.454147	-4.025205	30154.483478
HLA B*4002	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.641647	0.616392	-4.025255	43817.467101
HLA A*0101	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.385840	0.360485	-4.025355	24313.083476
HLA A*0101	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.381994	0.356622	-4.025372	24098.717699
HLA B*5801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.350889	0.325463	-4.025426	22433.090185
HLA B*3901	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.448113	0.422686	-4.025427	28061.645968
HLA B*5701	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.388486	0.362756	-4.025729	24461.639487
HLA B*0802	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.435487	0.409720	-4.025767	27257.562010
HLA B*4402	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.397125	0.371335	-4.025789	24953.106355
HLA A*2501	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.468763	0.442960	-4.025803	29428.136706
HLA B*3501	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.428516	0.402654	-4.025862	26823.539632
HLA B*4001	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.407690	0.381799	-4.025892	25567.616983
HLA A*2402	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.568830	0.542619	-4.026210	37053.537859
HLA A*6901	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.293907	0.267585	-4.026322	19674.651235
HLA A*2602	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.568968	0.542619	-4.026349	37065.366623
HLA B*5401	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.491776	0.465424	-4.026352	31029.585230
HLA A*0211	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.360550	0.334125	-4.026425	22937.716705
HLA A*6801	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.631949	0.605498	-4.026450	42849.779868
HLA A*0206	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.520581	0.494046	-4.026535	33157.414359
HLA A*0206	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.372676	0.346054	-4.026621	23587.172149
HLA A*3301	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.618782	0.592081	-4.026701	41570.196865
HLA B*1509	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.507985	0.481266	-4.026719	32209.580419
HLA A*2403	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.422457	0.395731	-4.026726	26451.893467
HLA B*1509	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.422527	0.395731	-4.026796	26456.186870
HLA B*4001	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.407190	0.380356	-4.026834	25538.172222
HLA B*5801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.351422	0.324517	-4.026906	22460.655948
HLA A*3201	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.612944	0.586005	-4.026939	41015.084533

HLA B*3801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.536428	0.509478	-4.026950	34389.664023
HLA B*1501	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.377598	0.350532	-4.027066	23856.023164
HLA B*5401	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.552957	0.525884	-4.027072	35723.710390
HLA A*3201	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.436100	0.409024	-4.027076	27296.076356
HLA A*0201	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.387569	0.360485	-4.027084	24410.083339
HLA A*3002	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.553090	0.525884	-4.027206	35734.727983
HLA B*0802	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.463239	0.436027	-4.027212	29056.220702
HLA B*1502	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.567653	0.540402	-4.027251	36953.245612
HLA A*0201	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.398675	0.371335	-4.027340	25042.361340
HLA B*4801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.430403	0.403047	-4.027356	26940.318338
HLA B*1503	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.515106	0.487735	-4.027371	32742.086878
HLA A*8001	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.450073	0.422686	-4.027387	28188.541889
HLA B*1801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.456057	0.428564	-4.027492	28579.639737
HLA B*4601	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.409293	0.381799	-4.027494	25662.124078
HLA A*3101	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.351805	0.324299	-4.027506	22480.470758
HLA B*1801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.453653	0.426123	-4.027530	28421.907835
HLA B*1501	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.250789	0.223225	-4.027564	17815.142223
HLA B*5101	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.493813	0.466242	-4.027571	31175.467440
HLA A*1101	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.477085	0.449508	-4.027577	29997.470902
HLA B*4002	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.630894	0.603309	-4.027585	42745.822339
HLA A*6901	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.384280	0.356622	-4.027658	24225.903511
HLA A*6801	1:301-309	9	AGNLSGPRT	0.970495	-0.333754	-4.664505	0.636741	-4.027764	46185.474394
HLA A*0203	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.361962	0.334125	-4.027837	23012.416469
HLA B*1801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.481986	0.454147	-4.027839	30337.910546
HLA B*0702	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.436930	0.409024	-4.027905	27348.253229
HLA B*0802	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.477468	0.449508	-4.027960	30023.934696
HLA B*1501	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.399364	0.371335	-4.028028	25082.087401
HLA B*3901	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.423129	0.395099	-4.028030	26492.852263
HLA B*3501	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.436819	0.408739	-4.028080	27341.300415
HLA B*1509	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.486191	0.458095	-4.028097	30633.120875
HLA A*0202	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.431176	0.403047	-4.028129	26988.310856
HLA A*0203	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.423234	0.395099	-4.028136	26499.302601
HLA B*1801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.509432	0.481266	-4.028167	32317.097629
HLA B*0802	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.482432	0.454147	-4.028285	30369.110277
HLA A*0219	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.423406	0.395099	-4.028307	26509.769823
HLA B*1801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.298134	0.269799	-4.028335	19867.067442
HLA A*0219	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.431129	0.402654	-4.028475	26985.390938
HLA A*3101	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.396173	0.367626	-4.028547	24898.493822
HLA A*2501	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.491943	0.463212	-4.028730	31041.506049
HLA A*2301	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.537182	0.508438	-4.028745	34449.436118
HLA B*1517	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.442911	0.414162	-4.028749	27727.542611
HLA A*0250	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.583063	0.554273	-4.028790	38288.015821
HLA B*1509	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.354395	0.325463	-4.028931	22614.892826
HLA A*0202	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.538444	0.509478	-4.028966	34549.661048
HLA B*1517	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.516702	0.487735	-4.028966	32862.580037
HLA A*0101	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.363847	0.334871	-4.028975	23112.478069
HLA A*0202	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.481692	0.452683	-4.029009	30317.401890
HLA B*0702	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.465053	0.436027	-4.029026	29177.825863
HLA A*1101	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.464303	0.435191	-4.029112	29127.515519
HLA B*4402	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.451856	0.422686	-4.029170	28304.524982
HLA A*3301	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.645613	0.616392	-4.029221	44219.436092
HLA A*0219	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.437989	0.408739	-4.029250	27415.060605
HLA A*2902	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.424421	0.395099	-4.029322	26571.797520
HLA A*0203	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.377793	0.348457	-4.029336	23866.737420
HLA B*5101	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.483489	0.454147	-4.029342	30443.132426
HLA A*0212	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.080257	0.050897	-4.029360	12029.750605
HLA B*5101	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.491882	0.462438	-4.029444	31037.140148
HLA A*3201	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.518010	0.488312	-4.029698	32961.754467
HLA A*2601	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.401105	0.371335	-4.029769	25182.836466
HLA A*2501	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.392562	0.362756	-4.029806	24692.321206
HLA A*0212	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.424947	0.395099	-4.029848	26604.017145
HLA B*4001	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.390349	0.360485	-4.029864	24566.806374
HLA B*4601	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.392644	0.362756	-4.029888	24696.997044
HLA B*7301	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.499066	0.469073	-4.029993	31554.871970
HLA B*3901	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.448508	0.418508	-4.030000	28087.161707

HLA B*7301	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.458705	0.428564	-4.030140	28754.420504
HLA A*0250	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.552104	0.521798	-4.030305	35653.625372
HLA B*4501	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.648263	0.617889	-4.030375	44490.103802
HLA B*0802	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.444540	0.414162	-4.030377	27831.689747
HLA B*0702	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.390922	0.360485	-4.030437	24599.256289
HLA B*3901	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.481556	0.451064	-4.030492	30307.890582
HLA A*0202	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.570141	0.539629	-4.030512	37165.561044
HLA A*0216	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.415963	0.385288	-4.030675	26059.302568
HLA A*2501	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.503728	0.472905	-4.030822	31895.381467
HLA B*5101	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.495782	0.464928	-4.030854	31317.121872
HLA B*2705	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.457067	0.426123	-4.030944	28646.200580
HLA B*4403	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.648863	0.617889	-4.030974	44551.521220
HLA B*1517	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.453674	0.422686	-4.030989	28423.291703
HLA B*4403	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.617060	0.586005	-4.031055	41405.678790
HLA B*5701	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.412866	0.381799	-4.031068	25874.154505
HLA A*0201	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.245808	0.214737	-4.031071	17611.988190
HLA B*1517	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.273311	0.242192	-4.031119	18763.396544
HLA A*6802	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.201899	0.170651	-4.031248	15918.379725
HLA A*0206	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.497586	0.466242	-4.031344	31447.508766
HLA A*8001	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.445611	0.414162	-4.031449	27900.432762
HLA A*0203	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.360757	0.329236	-4.031521	22948.639269
HLA B*3501	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.299172	0.267585	-4.031587	19914.629839
HLA A*0211	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.531099	0.499448	-4.031651	33970.293639
HLA A*2601	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.392141	0.360485	-4.031656	24668.421473
HLA A*0202	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.540145	0.508438	-4.031707	34685.249129
HLA B*4601	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.377821	0.346054	-4.031767	23868.286867
HLA B*5401	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.536776	0.505009	-4.031767	34417.209601
HLA B*0702	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.388406	0.356622	-4.031784	24457.140519
HLA A*2301	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.454485	0.422686	-4.031799	28476.390806
HLA A*3201	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.590447	0.558588	-4.031859	38944.603993
HLA B*0803	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.522796	0.490880	-4.031917	33326.999957
HLA A*3101	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.392433	0.360485	-4.031948	24684.975249
HLA A*0212	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.394768	0.362756	-4.032012	24818.074516
HLA A*2301	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.450557	0.418508	-4.032049	28219.973758
HLA B*0801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.295488	0.263371	-4.032117	19746.414356
HLA B*3901	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.498474	0.466242	-4.032232	31511.882773
HLA B*1517	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.441013	0.408739	-4.032274	27606.604756
HLA A*2602	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.542976	0.510481	-4.032495	34912.097970
HLA B*4601	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.380965	0.348457	-4.032507	24041.682630
HLA A*8001	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.458719	0.426183	-4.032535	28755.353868
HLA A*0301	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.361774	0.329236	-4.032538	23002.459055
HLA A*0101	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.403901	0.371335	-4.032565	25345.480698
HLA B*5101	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.458827	0.426183	-4.032643	28762.510670
HLA A*0250	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.573397	0.540737	-4.032660	37445.279743
HLA B*1501	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.335989	0.303321	-4.032668	21676.475459
HLA B*4002	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.565590	0.532852	-4.032738	36778.138231
HLA A*0101	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.383361	0.350532	-4.032829	24174.713425
HLA B*3501	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.261672	0.228841	-4.032831	18267.205241
HLA A*2301	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.542318	0.509478	-4.032840	34859.254240
HLA A*0219	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.206650	0.173777	-4.032873	16093.463488
HLA A*2902	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.301489	0.268569	-4.032920	20021.141297
HLA A*2602	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.554735	0.521798	-4.032937	35870.309181
HLA B*3801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.532403	0.499448	-4.032955	34072.442328
HLA B*0801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.393459	0.360485	-4.032974	24743.402569
HLA A*0201	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.379130	0.346054	-4.033076	23940.317844
HLA A*2501	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.447241	0.414162	-4.033079	28005.380795
HLA B*2705	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.476067	0.442960	-4.033107	29927.284603
HLA B*4402	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.400736	0.367626	-4.033110	25161.456440
HLA A*6901	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.336489	0.303321	-4.033168	21701.467797
HLA A*2902	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.275316	0.242067	-4.033248	18850.182868
HLA A*2603	1:54-62	9	LRFRREAQN	1.069423	-0.451534	-4.651160	0.617889	-4.033272	44787.862272
HLA A*3001	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.262168	0.228841	-4.033327	18288.068916
HLA A*0101	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.319058	0.285730	-4.033328	20847.706269
HLA A*2602	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.636692	0.603309	-4.033384	43320.374798
HLA B*0801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.383923	0.350532	-4.033391	24205.990663

HLA A*0203	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.350861	0.317460	-4.033401	22431.633906
HLA A*2301	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.537887	0.504447	-4.033440	34505.391802
HLA B*0702	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.459640	0.426183	-4.033456	28816.399379
HLA A*0301	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.336825	0.303321	-4.033504	21718.262855
HLA A*2603	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.538604	0.505009	-4.033595	34562.373255
HLA A*2601	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.386907	0.353175	-4.033732	24372.871982
HLA A*6801	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.647643	0.613866	-4.033777	44426.607911
HLA A*2603	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.619846	0.586005	-4.033841	41672.197040
HLA A*2601	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.401469	0.367626	-4.033843	25203.961957
HLA B*1503	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.448137	0.414162	-4.033974	28063.164113
HLA A*0212	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.436652	0.402654	-4.033998	27330.800580
HLA A*6802	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.429743	0.395731	-4.034011	26899.395349
HLA A*0201	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.387278	0.353175	-4.034103	24393.713905
HLA B*4801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.429933	0.395731	-4.034202	26911.185274
HLA A*6901	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.330171	0.295880	-4.034291	21388.057527
HLA B*1517	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.460478	0.426183	-4.034295	28872.107145
HLA B*1502	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.626836	0.592477	-4.034359	42348.313144
HLA B*0803	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.503458	0.469073	-4.034384	31875.544333
HLA A*2301	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.544964	0.510481	-4.034483	35072.248687
HLA B*0803	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.457325	0.422686	-4.034640	28663.252658
HLA B*5701	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.408010	0.373369	-4.034641	25586.435149
HLA A*6901	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.352116	0.317460	-4.034655	22496.529916
HLA A*0201	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.391279	0.356622	-4.034657	24619.492654
HLA A*2501	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.429771	0.395099	-4.034672	26901.141679
HLA B*0801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.009678	-0.025025	-4.034703	10225.347932
HLA A*1101	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.408092	0.373369	-4.034723	25591.280300
HLA A*2601	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.245148	0.210423	-4.034725	17585.235158
HLA B*3801	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.539755	0.505009	-4.034746	34654.114314
HLA B*5701	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.380831	0.346054	-4.034777	24034.270191
HLA B*4403	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.575267	0.540402	-4.034865	37606.876985
HLA A*1101	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.485952	0.451064	-4.034888	30616.221916
HLA A*2602	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.503561	0.468482	-4.035079	31883.132736
HLA A*2301	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.534544	0.499448	-4.035095	34240.779737
HLA B*5701	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.369323	0.334125	-4.035198	23405.782318
HLA A*2402	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.577652	0.542449	-4.035203	37813.945747
HLA A*0301	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.298594	0.263371	-4.035223	19888.144426
HLA B*4001	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.388408	0.353175	-4.035233	24457.272830
HLA B*5801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.352696	0.317460	-4.035236	22526.610831
HLA A*0250	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.593896	0.558588	-4.035308	39255.122419
HLA B*0702	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.403029	0.367626	-4.035403	25294.661589
HLA B*7301	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.515266	0.479739	-4.035527	32754.134005
HLA A*3001	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.304195	0.268569	-4.035627	20146.306522
HLA A*3001	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.283969	0.248296	-4.035673	19229.532278
HLA B*3501	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-3.883046	-0.152648	-4.035693	7639.159041
HLA A*0250	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.546223	0.510481	-4.035742	35174.095297
HLA B*2705	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.454262	0.418508	-4.035754	28461.759425
HLA B*4801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.409173	0.373369	-4.035804	25655.044763
HLA A*2902	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.444843	0.409024	-4.035818	27851.119586
HLA A*3301	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.579830	0.543984	-4.035846	38004.057750
HLA B*0802	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.461980	0.426123	-4.035856	28972.088400
HLA A*6802	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.299207	0.263202	-4.036005	19916.245944
HLA A*6901	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.360308	0.324299	-4.036009	22924.938943
HLA B*4403	1:368-376	9	QSSADAIAT	0.890983	-0.298902	-4.628147	0.592081	-4.036066	42476.343912
HLA A*3101	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.252584	0.216497	-4.036087	17888.927350
HLA B*4002	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.649708	0.613540	-4.036168	44638.372532
HLA A*2301	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.501101	0.464928	-4.036173	31703.052247
HLA B*1503	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.487333	0.451064	-4.036270	30713.767636
HLA B*5301	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.594937	0.558588	-4.036349	39349.313318
HLA A*0219	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.459229	0.422686	-4.036543	28789.130922
HLA B*0803	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.524290	0.487735	-4.036555	33441.865311
HLA B*0802	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.465805	0.429083	-4.036721	29228.381227
HLA A*0301	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.361246	0.324517	-4.036729	22974.476919
HLA A*6802	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.149238	0.112336	-4.036901	14100.597099
HLA A*0202	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.495054	0.458095	-4.036959	31264.645019
HLA B*1509	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.558006	0.521039	-4.036967	36141.452550

HLA A*3301	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.569831	0.532852	-4.036979	37139.030391
HLA A*2601	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.393624	0.356622	-4.037002	24752.774478
HLA A*3301	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.561175	0.524138	-4.037037	36406.175510
HLA B*3801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.545499	0.508438	-4.037062	35115.535408
HLA B*4801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.344938	0.307875	-4.037063	22127.780604
HLA B*4601	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.390323	0.353175	-4.037148	24565.344477
HLA A*0216	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.439852	0.402654	-4.037198	27532.925010
HLA A*6901	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.362672	0.325463	-4.037208	23050.044575
HLA B*1509	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.543857	0.506563	-4.037294	34982.996329
HLA A*0202	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.179240	0.141914	-4.037327	15109.163715
HLA B*4501	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.637117	0.599665	-4.037453	43362.814448
HLA A*2501	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.463725	0.426183	-4.037542	29088.777451
HLA B*7301	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.591819	0.554273	-4.037547	39067.839182
HLA B*4501	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.651435	0.613866	-4.037569	44816.220037
HLA A*3002	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.432701	0.395099	-4.037602	27083.233843
HLA A*2601	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.388211	0.350532	-4.037679	24446.161219
HLA B*1801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.528672	0.490880	-4.037793	33780.982990
HLA B*3501	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.417706	0.379878	-4.037828	26164.118430
HLA B*1501	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.186054	0.148101	-4.037953	15348.075733
HLA A*3301	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.447728	0.409720	-4.038008	28036.760105
HLA B*4501	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.654504	0.616392	-4.038111	45133.981981
HLA A*0206	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.464367	0.426183	-4.038183	29131.770399
HLA A*0212	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.180157	0.141914	-4.038243	15141.075539
HLA B*4801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.398739	0.360485	-4.038254	25046.019470
HLA B*0801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.394879	0.356622	-4.038256	24824.385681
HLA B*0801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.433389	0.395099	-4.038290	27126.197452
HLA A*8001	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.433504	0.395099	-4.038405	27133.389141
HLA A*2603	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.599559	0.561125	-4.038434	39770.275083
HLA A*2501	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.447577	0.409024	-4.038553	28027.054536
HLA B*0802	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.467146	0.428564	-4.038582	29318.808657
HLA A*2602	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.457217	0.418508	-4.038710	28656.120554
HLA A*0301	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.363019	0.324299	-4.038720	23068.507297
HLA A*6901	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.324584	0.285730	-4.038854	21114.668540
HLA A*3002	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.529932	0.490880	-4.039052	33879.079884
HLA A*3002	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.538512	0.499448	-4.039063	34555.081858
HLA B*7301	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.613374	0.574191	-4.039182	41055.709972
HLA A*3301	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.619125	0.579907	-4.039218	41603.043798
HLA B*1517	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.475268	0.436027	-4.039241	29872.288079
HLA A*0101	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.373416	0.334125	-4.039291	23627.401673
HLA A*0216	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.490397	0.451064	-4.039333	30931.203820
HLA B*3501	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-3.803304	-0.236114	-4.039418	6357.758553
HLA A*2602	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.547870	0.508438	-4.039432	35307.740408
HLA B*0802	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.461468	0.421976	-4.039492	28937.940139
HLA B*0802	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.474716	0.435191	-4.039525	29834.334854
HLA A*0201	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.387983	0.348457	-4.039525	24433.336236
HLA B*4402	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.390118	0.350532	-4.039586	24553.785263
HLA A*2601	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.374551	0.334871	-4.039679	23689.220247
HLA B*1502	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.561480	0.521798	-4.039682	36431.788454
HLA A*6801	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.656144	0.616392	-4.039751	45304.734716
HLA B*0802	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.442820	0.403047	-4.039773	27721.693114
HLA B*4402	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.446819	0.407006	-4.039813	27978.122987
HLA A*2403	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.413193	0.373369	-4.039823	25893.618529
HLA B*4403	1:601-609	9	NRVVYQNPP	0.431976	0.173522	-4.645352	0.605498	-4.039854	44192.890393
HLA A*3001	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.261167	0.221286	-4.039881	18245.970528
HLA A*2603	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.618730	0.578823	-4.039907	41565.249576
HLA B*4601	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.411245	0.371335	-4.039910	25777.750894
HLA A*0211	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.512863	0.472905	-4.039957	32573.362942
HLA A*0203	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.188107	0.148101	-4.040007	15420.817001
HLA B*4402	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.386174	0.346054	-4.040119	24331.768066
HLA A*8001	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.425546	0.385288	-4.040258	26640.743291
HLA A*2301	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.535942	0.495678	-4.040264	34351.174415
HLA B*3901	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.306446	0.266144	-4.040302	20250.989291
HLA A*2301	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.545408	0.505009	-4.040399	35108.127315
HLA A*0301	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.303617	0.263202	-4.040415	20119.512990
HLA B*1517	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-3.991827	-0.048602	-4.040428	9813.562831

HLA B*1801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.483428	0.442960	-4.040468	30438.850684
HLA A*0203	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.386571	0.346054	-4.040516	24354.024075
HLA A*0212	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.422339	0.381799	-4.040541	26444.739344
HLA B*5301	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.584588	0.543984	-4.040603	38422.682005
HLA B*1509	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.443703	0.403047	-4.040656	27778.139707
HLA A*3201	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.386712	0.346054	-4.040657	24361.930513
HLA B*7301	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.466881	0.426183	-4.040697	29300.891034
HLA A*0250	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.499273	0.458556	-4.040717	31569.897882
HLA A*0211	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.545318	0.504447	-4.040871	35100.910676
HLA A*6802	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.422739	0.381799	-4.040940	26469.071259
HLA A*6802	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.436044	0.395099	-4.040945	27292.532536
HLA B*5101	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.462964	0.421976	-4.040989	29037.835182
HLA A*3002	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.255791	0.214737	-4.041054	18021.517062
HLA A*2602	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.583547	0.542449	-4.041097	38330.709194
HLA B*1801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.389564	0.348457	-4.041107	24522.456618
HLA A*2402	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.499673	0.458556	-4.041117	31598.945477
HLA A*2402	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.504341	0.463212	-4.041129	31940.448951
HLA B*2705	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.470217	0.429083	-4.041134	29526.848523
HLA B*0802	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.492225	0.451064	-4.041161	31061.664325
HLA A*2603	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.657586	0.616392	-4.041194	45455.472394
HLA B*4402	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.421632	0.380356	-4.041276	26401.712390
HLA B*0802	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.464019	0.422686	-4.041333	29108.454986
HLA A*0301	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.366807	0.325463	-4.041343	23270.561532
HLA B*0702	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.455559	0.414162	-4.041396	28546.880638
HLA B*4801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.426747	0.385288	-4.041459	26714.492274
HLA A*2602	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.546510	0.505009	-4.041501	35197.318091
HLA B*0803	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.506925	0.465424	-4.041501	32131.089345
HLA B*0702	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.412885	0.371335	-4.041549	25875.274340
HLA A*2402	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.582332	0.540737	-4.041595	38223.651333
HLA B*1509	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.529976	0.488312	-4.041664	33882.562422
HLA B*0802	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.467915	0.426183	-4.041731	29370.720523
HLA A*2403	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.409405	0.367626	-4.041779	25668.788747
HLA A*0216	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.468030	0.426183	-4.041846	29378.507279
HLA A*2301	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.535944	0.494046	-4.041898	34351.360251
HLA B*1503	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.445768	0.403854	-4.041914	27910.547458
HLA B*1501	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.367469	0.325463	-4.042006	23306.089932
HLA B*0802	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.445970	0.403854	-4.042116	27923.535874
HLA A*6801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.305323	0.263202	-4.042121	20198.689362
HLA B*0802	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.451207	0.409024	-4.042183	28262.294199
HLA B*1503	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.444955	0.402654	-4.042301	27858.352756
HLA A*2902	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.451069	0.408739	-4.042330	28253.274782
HLA B*3801	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.538094	0.495678	-4.042416	34521.822703
HLA B*5701	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.402902	0.360485	-4.042417	25287.273237
HLA B*5401	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.551902	0.509478	-4.042424	35637.041364
HLA A*0206	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.427717	0.385288	-4.042429	26774.246772
HLA A*2402	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.549045	0.506563	-4.042482	35403.375174
HLA B*4501	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.656144	0.613540	-4.042604	45304.734716
HLA A*0203	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.403123	0.360485	-4.042638	25300.135834
HLA A*3101	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.367319	0.324517	-4.042803	23298.021994
HLA B*4501	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.635308	0.592477	-4.042832	43182.557374
HLA B*4002	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.601469	0.558588	-4.042880	39945.579526
HLA B*4001	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.391368	0.348457	-4.042911	24624.554346
HLA B*5801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.338832	0.295880	-4.042951	21818.834358
HLA A*0250	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.586965	0.543984	-4.042981	38633.615689
HLA A*0206	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.524326	0.481266	-4.043060	33444.579173
HLA B*4403	1:246-254	9	DLDAVVLKA	0.985824	-0.369309	-4.659604	0.616515	-4.043089	45667.199860
HLA A*0211	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.492681	0.449508	-4.043173	31094.281229
HLA B*3501	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.372434	0.329236	-4.043198	23574.032600
HLA A*0211	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.512588	0.469073	-4.043515	32552.751926
HLA B*1503	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.400186	0.356622	-4.043564	25129.624351
HLA A*3301	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.552036	0.508438	-4.043598	35648.032228
HLA A*2603	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.614882	0.571232	-4.043650	41198.550472
HLA A*0101	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.368052	0.324299	-4.043753	23337.379592
HLA A*2902	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.439486	0.395731	-4.043755	27509.698601
HLA B*0803	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.465817	0.421976	-4.043841	29229.171850

HLA A*0301	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.329596	0.285730	-4.043865	21359.728086
HLA B*3901	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.493547	0.449508	-4.044039	31156.415156
HLA A*6801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.472752	0.428564	-4.044188	29699.708747
HLA B*4002	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.636711	0.592477	-4.044234	43322.249706
HLA A*0202	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.192773	0.148535	-4.044238	15587.392115
HLA A*0203	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.340145	0.295880	-4.044265	21884.917177
HLA B*1503	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.415620	0.371335	-4.044284	26038.727916
HLA A*0301	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.260838	0.216497	-4.044341	18232.156545
HLA B*4402	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.447432	0.403047	-4.044385	28017.655470
HLA B*3501	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.439512	0.395099	-4.044413	27511.335718
HLA A*2902	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.424834	0.380356	-4.044478	26597.109653
HLA A*2402	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.565623	0.521039	-4.044584	36780.923855
HLA B*0801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.415946	0.371335	-4.044611	26058.315741
HLA B*3501	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.440473	0.395731	-4.044742	27572.275923
HLA A*2501	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.502877	0.458095	-4.044783	31832.979318
HLA A*0202	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.587254	0.542449	-4.044805	38659.331684
HLA B*5701	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.416367	0.371335	-4.045031	26083.562059
HLA A*2902	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.369373	0.324299	-4.045073	23408.441545
HLA B*3901	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.453966	0.408739	-4.045227	28442.365190
HLA A*0202	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.477611	0.432298	-4.045313	30033.844327
HLA B*5801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.353257	0.307875	-4.045382	22555.755755
HLA A*3002	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.454238	0.408739	-4.045499	28460.219717
HLA B*4601	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.413132	0.367626	-4.045505	25889.976663
HLA B*1801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.418911	0.373369	-4.045542	26236.831858
HLA A*2902	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.339003	0.293372	-4.045631	21827.452795
HLA A*2301	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.533475	0.487735	-4.045739	34156.599720
HLA A*3201	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.589752	0.543984	-4.045768	38882.290845
HLA A*0203	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.402453	0.356622	-4.045831	25261.157675
HLA B*4001	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.392132	0.346054	-4.046078	24667.887665
HLA B*1801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.363588	0.317460	-4.046128	23098.728207
HLA B*4002	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.645841	0.599665	-4.046176	44242.646739
HLA A*0202	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.508617	0.462438	-4.046179	32256.487862
HLA A*3301	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.511166	0.464928	-4.046238	32446.381494
HLA B*5801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.349580	0.303321	-4.046260	22365.594114
HLA B*3801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.552823	0.506563	-4.046260	35712.696193
HLA B*5401	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.534579	0.488312	-4.046267	34243.558432
HLA B*4402	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.450134	0.403854	-4.046279	28192.507087
HLA A*8001	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.399467	0.353175	-4.046292	25088.058530
HLA B*4403	1:533-541	9	EVTGTNPPA	0.882185	-0.288794	-4.639709	0.593391	-4.046318	43622.338567
HLA B*4501	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.649699	0.603309	-4.046390	44637.406587
HLA B*4801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.426275	0.379878	-4.046397	26685.459052
HLA A*0206	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.474975	0.428564	-4.046411	29852.094187
HLA A*2601	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.392484	0.346054	-4.046430	24687.913370
HLA B*1503	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.449596	0.403047	-4.046549	28157.602013
HLA A*3002	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.475722	0.429083	-4.046639	29903.494280
HLA A*2501	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.258035	0.211378	-4.046657	18114.865154
HLA A*2603	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.587059	0.540402	-4.046657	38641.976736
HLA B*1517	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.511686	0.464928	-4.046758	32485.197116
HLA B*1517	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.455824	0.409024	-4.046800	28564.337180
HLA A*0211	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.315372	0.268569	-4.046803	20671.497417
HLA A*8001	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.455848	0.409024	-4.046823	28565.882521
HLA B*1801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.453902	0.407006	-4.046897	28438.211002
HLA A*3301	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.632987	0.586005	-4.046982	42952.363618
HLA A*2403	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.313215	0.266144	-4.047071	20569.091508
HLA A*0206	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.551521	0.504447	-4.047074	35605.822670
HLA A*0216	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.475694	0.428564	-4.047129	29901.553048
HLA A*2902	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.400374	0.353175	-4.047199	25140.502583
HLA A*1101	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.432569	0.385288	-4.047281	27075.030118
HLA A*0219	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.427637	0.380356	-4.047281	26769.322471
HLA B*0803	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.473431	0.426123	-4.047308	29746.179311
HLA B*1509	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.482568	0.435191	-4.047377	30378.640797
HLA A*0250	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.553974	0.506563	-4.047411	35807.490627
HLA B*1501	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.322575	0.275124	-4.047452	21017.229110
HLA A*0202	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.573508	0.525884	-4.047623	37454.801970
HLA B*4402	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.429477	0.381799	-4.047678	26882.956304

HLA B*3501	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.264273	0.216497	-4.047776	18376.931149
HLA A*1101	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.451682	0.403854	-4.047828	28293.196049
HLA B*4402	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.355781	0.307875	-4.047906	22687.191144
HLA A*0250	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.587567	0.539629	-4.047938	38687.157672
HLA B*0801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.433281	0.385288	-4.047993	27119.447804
HLA A*1101	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.477129	0.429083	-4.048046	30000.554437
HLA A*3101	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.382967	0.334871	-4.048095	24152.751943
HLA B*3901	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.415890	0.367626	-4.048264	26054.932619
HLA B*0801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.290965	0.242669	-4.048296	19541.841537
HLA A*0250	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.590978	0.542619	-4.048359	38992.248146
HLA B*0702	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.428253	0.379878	-4.048375	26807.291969
HLA B*1501	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.344369	0.295880	-4.048489	22098.830020
HLA B*1501	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.313596	0.264968	-4.048628	20587.126204
HLA A*0201	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.399164	0.350532	-4.048632	25070.556291
HLA B*5101	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.422154	0.373369	-4.048784	26433.439773
HLA B*1502	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.569861	0.521039	-4.048823	37141.642418
HLA A*3002	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.313793	0.264968	-4.048826	20596.483752
HLA B*5301	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.570695	0.521798	-4.048897	37213.041877
HLA A*0301	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.366382	0.317460	-4.048921	23247.786385
HLA A*3001	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.303798	0.254868	-4.048930	20127.895750
HLA B*4001	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.399502	0.350532	-4.048970	25090.094466
HLA A*3101	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.378209	0.329236	-4.048973	23889.601968
HLA A*0212	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.324133	0.275124	-4.049010	21092.748147
HLA A*2402	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.574936	0.525884	-4.049052	37578.201609
HLA B*4403	1:305-313	9	SGPRTDPLP	0.650895	-0.034503	-4.665490	0.616392	-4.049098	46290.283764
HLA B*0801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.318459	0.269282	-4.049178	20818.966234
HLA B*5301	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.591974	0.542619	-4.049355	39081.790949
HLA B*0802	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.452081	0.402654	-4.049427	28319.228737
HLA B*1801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.478532	0.429083	-4.049449	30097.603979
HLA B*5101	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.500530	0.451064	-4.049467	31661.402700
HLA A*0211	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.540429	0.490880	-4.049549	34707.961407
HLA A*2602	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.608202	0.558588	-4.049614	40569.751752
HLA B*4001	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.417246	0.367626	-4.049619	26136.390317
HLA B*0803	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.481943	0.432298	-4.049646	30334.956445
HLA A*0202	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.434949	0.385288	-4.049661	27223.814490
HLA B*2705	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.434949	0.385288	-4.049661	27223.814490
HLA B*5701	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.417295	0.367626	-4.049669	26139.359780
HLA A*2501	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.430083	0.380356	-4.049727	26920.504426
HLA A*3002	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.482164	0.432298	-4.049866	30350.386590
HLA A*0206	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.331384	0.281512	-4.049872	21447.845760
HLA A*3301	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.628258	0.578365	-4.049893	42487.145524
HLA B*0801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.309047	0.259153	-4.049894	20372.631226
HLA A*2501	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.501035	0.451064	-4.049972	31698.250331
HLA A*0216	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.403160	0.353175	-4.049986	25302.325863
HLA A*2902	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.374541	0.324517	-4.050025	23688.707629
HLA A*3002	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.459088	0.409024	-4.050063	28779.787678
HLA B*3801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.531348	0.481266	-4.050083	33989.779431
HLA B*0802	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.458855	0.408739	-4.050116	28764.377954
HLA B*2705	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.486234	0.436027	-4.050207	30636.104013
HLA B*4601	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.410721	0.360485	-4.050236	25746.671230
HLA A*0216	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.472950	0.422686	-4.050264	29713.208273
HLA A*6801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.464480	0.414162	-4.050317	29139.336164
HLA B*5801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.364234	0.313851	-4.050383	23133.118211
HLA B*4402	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.384670	0.334125	-4.050545	24247.669152
HLA B*5401	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.476843	0.426183	-4.050659	29980.760410
HLA B*1503	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.515614	0.464928	-4.050686	32780.369550
HLA B*3901	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.424073	0.373369	-4.050704	26550.530964
HLA A*0250	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.560242	0.509478	-4.050765	36328.068927
HLA B*4002	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.629230	0.578365	-4.050865	42582.410375
HLA A*0212	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.418496	0.367626	-4.050869	26211.720794
HLA B*1517	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.431298	0.380356	-4.050942	26995.904120
HLA A*3001	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.267457	0.216497	-4.050959	18512.136350
HLA B*1503	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.432811	0.381799	-4.051012	27090.121031
HLA A*0216	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.459774	0.408739	-4.051035	28825.286680
HLA A*0206	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.519523	0.468482	-4.051041	33076.792463

HLA B*7301	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.559486	0.508438	-4.051048	36264.841088
HLA B*4403	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.646006	0.594934	-4.051071	44259.404259
HLA A*2403	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.318680	0.267585	-4.051095	20829.555986
HLA A*0211	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.509280	0.458095	-4.051185	32305.735553
HLA A*3101	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.321142	0.269799	-4.051344	20947.985889
HLA A*2603	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.326469	0.275124	-4.051345	21206.478434
HLA A*0250	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.577274	0.525884	-4.051390	37781.024436
HLA B*4501	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.637418	0.586005	-4.051413	43392.852113
HLA A*0206	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.454487	0.403047	-4.051440	28476.544860
HLA B*5301	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.575582	0.524138	-4.051444	37634.149039
HLA B*5301	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.605724	0.554273	-4.051451	40338.862131
HLA B*1501	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.324333	0.272858	-4.051474	21102.449679
HLA A*0201	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.385650	0.334125	-4.051525	24302.431792
HLA B*1501	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.220873	0.169330	-4.051543	16629.274460
HLA B*5701	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.386449	0.334871	-4.051577	24347.173905
HLA A*0219	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.454861	0.403047	-4.051814	28501.050135
HLA A*0203	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.433657	0.381799	-4.051858	27142.932080
HLA B*4402	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.412392	0.360485	-4.051907	25845.894735
HLA A*1101	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.432292	0.380356	-4.051936	27057.751830
HLA A*8001	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.266679	0.214737	-4.051942	18479.016823
HLA B*1509	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.520449	0.468482	-4.051967	33147.370716
HLA A*6801	1:382-390	9	FKIRTLQKP	0.544614	0.041391	-4.638142	0.586005	-4.052137	43465.215544
HLA B*3501	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.461186	0.409024	-4.052161	28919.160110
HLA B*3901	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.447925	0.395731	-4.052194	28049.503764
HLA A*3002	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.562761	0.510481	-4.052280	36539.362066
HLA A*8001	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.432637	0.380356	-4.052281	27079.278165
HLA B*3501	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.262708	0.210423	-4.052285	18310.838457
HLA B*4501	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.630689	0.578365	-4.052324	42725.708308
HLA A*1101	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.475052	0.422686	-4.052366	29857.424048
HLA B*3801	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.517348	0.464928	-4.052420	32911.506724
HLA A*2601	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.263841	0.211378	-4.052463	18358.647493
HLA A*0101	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.366351	0.313851	-4.052500	23246.151459
HLA A*6801	1:600-608	9	HNRVVYQNP	0.656871	-0.061937	-4.647495	0.594934	-4.052561	44411.468881
HLA B*5101	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.447695	0.395099	-4.052596	28034.636724
HLA A*6802	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.355931	0.303321	-4.052610	22695.047556
HLA A*1101	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.484920	0.432298	-4.052622	30543.596460
HLA B*1517	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.448393	0.395731	-4.052662	28079.717221
HLA A*0203	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.294795	0.242067	-4.052728	19714.925845
HLA A*3002	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.415491	0.362756	-4.052734	26030.981404
HLA A*6801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.138886	0.086012	-4.052874	13768.469682
HLA B*1501	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.285343	0.232368	-4.052975	19290.486018
HLA B*0803	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.481556	0.428564	-4.052991	30307.890582
HLA A*3301	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.592668	0.539629	-4.053039	39144.212052
HLA A*2602	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.593786	0.540737	-4.053049	39245.142493
HLA A*2603	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.656477	0.603309	-4.053169	45339.551378
HLA A*0203	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.406349	0.353175	-4.053174	25488.759280
HLA A*2301	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.544071	0.490880	-4.053191	35000.222695
HLA A*6901	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.321845	0.268569	-4.053276	20981.897867
HLA B*4403	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.632186	0.578823	-4.053363	42873.199334
HLA A*2501	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.295570	0.242192	-4.053378	19750.153617
HLA A*0212	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.377906	0.324517	-4.053389	23872.935812
HLA B*1503	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.388265	0.334871	-4.053393	24449.203182
HLA A*3201	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.596086	0.542619	-4.053467	39453.547212
HLA A*0219	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.322200	0.268569	-4.053631	20999.044841
HLA B*4002	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.560219	0.506563	-4.053656	36326.103672
HLA B*5101	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.511772	0.458095	-4.053678	32491.700196
HLA A*3201	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.607996	0.554273	-4.053723	40550.442297
HLA A*1101	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.489821	0.436027	-4.053794	30890.234053
HLA A*2403	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.313922	0.260101	-4.053821	20602.613022
HLA B*5401	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.517085	0.463212	-4.053872	32891.571432
HLA A*6801	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.657191	0.603309	-4.053883	45414.178439
HLA B*1517	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.462668	0.408742	-4.053926	29018.048401
HLA B*1509	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.496910	0.442960	-4.053949	31398.550186
HLA B*5801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.366454	0.312328	-4.054126	23251.685518
HLA B*4601	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.410749	0.356622	-4.054127	25748.342724

HLA B*1517	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.461188	0.407006	-4.054182	28919.316559
HLA A*0211	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.534008	0.479739	-4.054269	34198.571322
HLA A*6801	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.633107	0.578823	-4.054284	42964.215996
HLA A*2403	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.407566	0.353175	-4.054391	25560.287181
HLA A*3002	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.463187	0.408742	-4.054445	29052.762707
HLA A*2403	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.400654	0.346054	-4.054599	25156.692667
HLA A*3301	1:452-460	9	FKQANSPST	0.861933	-0.283110	-4.633457	0.578823	-4.054634	42998.862273
HLA A*2402	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.519653	0.464928	-4.054725	33086.635725
HLA B*4402	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.403217	0.348457	-4.054759	25305.611263
HLA A*0206	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.403229	0.348457	-4.054771	25306.295775
HLA B*3801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.487136	0.432298	-4.054838	30699.813529
HLA A*0301	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.368708	0.313851	-4.054857	23372.630674
HLA B*1502	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.598936	0.543984	-4.054952	39713.300446
HLA B*1517	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.436756	0.381799	-4.054957	27337.307045
HLA B*1509	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.542772	0.487735	-4.055036	34895.670095
HLA B*4403	1:177-185	9	IGTAQYLSP	0.671261	-0.057395	-4.668946	0.613866	-4.055080	46660.129038
HLA B*3901	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.469242	0.414162	-4.055080	29460.632037
HLA A*0216	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.490343	0.435191	-4.055151	30927.355368
HLA B*0801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.296144	0.240938	-4.055206	19776.241290
HLA A*2603	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.550913	0.495678	-4.055235	35555.968105
HLA B*5401	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.546249	0.490880	-4.055369	35176.188527
HLA B*5701	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.303751	0.248296	-4.055456	20125.718074
HLA B*4002	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.630027	0.574537	-4.055489	42660.576144
HLA A*3201	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.528416	0.472905	-4.055511	33761.068963
HLA B*5101	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.474066	0.418508	-4.055558	29789.660413
HLA A*0101	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.384806	0.329236	-4.055570	24255.278623
HLA A*2403	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.426925	0.371335	-4.055590	26725.478238
HLA B*0802	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.498580	0.442960	-4.055620	31519.555118
HLA A*2402	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.579774	0.524138	-4.055635	37999.123724
HLA B*1801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.477731	0.421976	-4.055755	30042.131938
HLA A*2602	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.617015	0.561125	-4.055891	41401.423006
HLA A*3002	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.565414	0.509478	-4.055936	36763.218834
HLA A*6801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-3.992174	-0.063767	-4.055941	9821.423339
HLA A*3201	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.617083	0.561125	-4.055959	41407.918852
HLA A*2301	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.535763	0.479739	-4.056024	34337.053778
HLA A*3002	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.510175	0.454147	-4.056028	32372.391765
HLA B*3801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.546909	0.490880	-4.056029	35229.703291
HLA B*1503	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.284873	0.228841	-4.056033	19269.625427
HLA B*0801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.331287	0.275124	-4.056164	21443.089039
HLA A*0203	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.364091	0.307875	-4.056216	23125.485466
HLA A*8001	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.391096	0.334871	-4.056225	24609.106125
HLA A*0216	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.391105	0.334871	-4.056234	24609.638661
HLA A*3001	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.228843	0.172544	-4.056299	16937.244402
HLA B*1801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.515123	0.458556	-4.056567	32743.326818
HLA A*6901	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.168945	0.112336	-4.056609	14755.196031
HLA A*0250	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.599096	0.542449	-4.056646	39727.912563
HLA A*0301	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.369008	0.312328	-4.056680	23388.821026
HLA B*4801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.438480	0.381799	-4.056682	27446.075435
HLA B*3901	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.491900	0.435191	-4.056709	31038.483437
HLA A*2403	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.381042	0.324299	-4.056743	24045.975087
HLA B*5101	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.485489	0.428564	-4.056924	30583.610115
HLA B*0803	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.506439	0.449508	-4.056931	32095.127578
HLA A*2501	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.460793	0.403854	-4.056939	28893.044850
HLA B*4002	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.556523	0.499448	-4.057075	36018.288978
HLA B*1517	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.461021	0.403854	-4.057167	28908.210721
HLA B*1501	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.424809	0.367626	-4.057182	26595.526938
HLA B*3901	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.479162	0.421976	-4.057186	30141.272647
HLA B*2705	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.464207	0.407006	-4.057202	29121.055594
HLA A*2501	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.459868	0.402654	-4.057213	28831.525019
HLA A*2301	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.523536	0.466242	-4.057294	33383.841419
HLA A*3201	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.108211	0.050897	-4.057314	12829.531471
HLA B*1503	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.231195	0.173777	-4.057418	17029.213440
HLA B*1801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.461374	0.403854	-4.057519	28931.678774
HLA A*2601	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.330413	0.272858	-4.057555	21399.978671
HLA A*1101	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.464651	0.407006	-4.057646	29150.846199

HLA A*3301	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.618815	0.561125	-4.057690	41573.345447
HLA A*0250	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.510429	0.452683	-4.057746	32391.311445
HLA A*0101	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-3.991916	-0.065831	-4.057747	9815.580469
HLA B*4601	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.408416	0.350532	-4.057884	25610.392980
HLA A*6901	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.338491	0.280603	-4.057888	21801.725635
HLA A*0206	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.520372	0.462438	-4.057934	33141.453565
HLA A*2501	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.493237	0.435191	-4.058046	31134.174135
HLA A*2501	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.465145	0.407006	-4.058139	29183.982616
HLA A*0203	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.213425	0.155271	-4.058154	16346.524653
HLA A*0219	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.420920	0.362756	-4.058164	26358.470249
HLA B*1503	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.029611	-0.028622	-4.058233	10705.602776
HLA A*6802	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.287112	0.228841	-4.058272	19369.228916
HLA A*0216	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.375768	0.317460	-4.058307	23755.698187
HLA B*5101	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.493576	0.435191	-4.058384	31158.437855
HLA A*2301	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.539689	0.481266	-4.058423	34648.865414
HLA A*3001	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.281800	0.223276	-4.058524	19133.752252
HLA B*4501	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.591446	0.532852	-4.058594	39034.248555
HLA A*0216	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.387832	0.329236	-4.058596	24424.878075
HLA A*0211	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.521116	0.462438	-4.058678	33198.337762
HLA A*1101	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.440538	0.381799	-4.058740	27576.452802
HLA A*2301	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.484878	0.426123	-4.058754	30540.622330
HLA A*0211	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.546517	0.487735	-4.058781	35197.889336
HLA B*0803	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.516986	0.458095	-4.058891	32884.098812
HLA B*5101	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.467797	0.408742	-4.059055	29362.776980
HLA A*3002	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.494344	0.435191	-4.059153	31213.606967
HLA B*4501	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.630400	0.571232	-4.059168	42697.287380
HLA B*5301	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.565745	0.506563	-4.059182	36791.272308
HLA B*1503	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.444549	0.385288	-4.059261	27832.292019
HLA B*2705	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.494457	0.435191	-4.059265	31221.713403
HLA B*5801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.352684	0.293372	-4.059312	22526.001507
HLA B*4403	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.610303	0.550986	-4.059317	40766.440211
HLA A*0301	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.367263	0.307875	-4.059388	23294.997237
HLA B*3801	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.553436	0.494046	-4.059390	35763.157461
HLA B*4601	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.388824	0.329236	-4.059588	24480.703117
HLA A*3001	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.276610	0.216943	-4.059668	18906.456245
HLA A*2301	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.528228	0.468482	-4.059746	33746.460633
HLA B*1801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.462452	0.402654	-4.059798	29003.609428
HLA A*0301	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.215108	0.155271	-4.059836	16409.965388
HLA A*0202	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.528921	0.469073	-4.059848	33800.360191
HLA B*3801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.512578	0.452683	-4.059896	32552.047507
HLA A*2402	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.565024	0.505009	-4.060015	36730.218754
HLA A*0301	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.233838	0.173777	-4.060061	17133.171396
HLA A*3002	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.602747	0.542619	-4.060128	40063.311712
HLA B*5801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.350593	0.290447	-4.060146	22417.803969
HLA A*2601	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.385629	0.325463	-4.060165	24301.248560
HLA A*2602	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.593074	0.532852	-4.060222	39180.864692
HLA B*4403	1:462-470	9	ELVGKVIGT	0.990844	-0.416307	-4.634796	0.574537	-4.060259	43131.659792
HLA B*1502	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.540041	0.479739	-4.060302	34676.993804
HLA B*5401	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.119897	0.059501	-4.060396	13179.445387
HLA B*1501	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.389665	0.329236	-4.060429	24528.161824
HLA A*0202	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.523724	0.463212	-4.060512	33398.292776
HLA B*3901	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.464393	0.403854	-4.060538	29133.504046
HLA A*6901	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.232167	0.171585	-4.060582	17067.396412
HLA A*3002	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.601363	0.540737	-4.060626	39935.856157
HLA B*0803	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.511697	0.451064	-4.060634	32486.075835
HLA A*3002	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.284004	0.223225	-4.060779	19231.092786
HLA B*4501	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.529918	0.469073	-4.060844	33877.980209
HLA B*1501	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.234669	0.173777	-4.060893	17166.014585
HLA B*0803	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.523358	0.462438	-4.060920	33370.118421
HLA B*5701	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.411499	0.350532	-4.060967	25792.816410
HLA B*4501	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.600609	0.539629	-4.060980	39866.564753
HLA A*0201	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.390227	0.329236	-4.060991	24559.896354
HLA A*3001	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.272564	0.211378	-4.061186	18731.144783
HLA B*4403	1:552-560	9	ELQVSKGNQ	0.736879	-0.137214	-4.660906	0.599665	-4.061241	45804.273354
HLA A*0202	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.463911	0.402654	-4.061257	29101.212105

HLA B*5301	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.594143	0.532852	-4.061291	39277.427169
HLA A*0201	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.277815	0.216497	-4.061318	18958.999703
HLA B*5301	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.602131	0.540737	-4.061395	40006.566561
HLA A*0219	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.336583	0.275124	-4.061459	21706.164407
HLA B*3801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.534504	0.472905	-4.061598	34237.630822
HLA B*1801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.512684	0.451064	-4.061620	32559.973105
HLA B*1502	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.468652	0.407006	-4.061647	29420.655118
HLA B*0802	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.435050	0.373369	-4.061681	27230.148173
HLA A*3201	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.519895	0.458095	-4.061800	33105.077351
HLA B*3501	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.184160	0.122274	-4.061886	15281.298128
HLA A*0206	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.534795	0.472905	-4.061890	34260.606029
HLA A*2603	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.587886	0.525884	-4.062002	38715.632025
HLA A*2403	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.369882	0.307875	-4.062007	23435.937927
HLA B*1517	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.457114	0.395099	-4.062015	28649.300203
HLA B*0802	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.470781	0.408742	-4.062039	29565.210297
HLA B*5101	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.396272	0.334125	-4.062147	24904.151784
HLA B*3801	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.527636	0.465424	-4.062212	33700.485697
HLA A*2601	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.396413	0.334125	-4.062288	24912.236819
HLA A*0219	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.379767	0.317460	-4.062306	23975.442005
HLA A*0211	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.528571	0.466242	-4.062329	33773.125595
HLA A*0212	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.330958	0.268569	-4.062390	21426.854524
HLA B*0702	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.442930	0.380356	-4.062574	27728.742660
HLA A*0206	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.520874	0.458095	-4.062780	33179.844184
HLA A*2402	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.571233	0.508438	-4.062796	37259.172367
HLA A*0250	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.571257	0.508438	-4.062819	37261.188101
HLA A*0301	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.332620	0.269799	-4.062821	21508.964705
HLA A*0101	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.387374	0.324517	-4.062858	24399.125164
HLA B*7301	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.423387	0.360485	-4.062902	26508.622528
HLA B*1509	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.375239	0.312328	-4.062911	23726.799747
HLA A*0101	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.388387	0.325463	-4.062923	24456.082059
HLA A*0212	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.277804	0.214737	-4.063066	18958.486879
HLA B*3901	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.380589	0.317460	-4.063129	24020.881580
HLA B*5101	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.443090	0.379878	-4.063212	27738.945178
HLA A*6802	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.073105	0.009850	-4.063255	11833.270479
HLA B*7301	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.536247	0.472905	-4.063342	34375.341598
HLA A*0301	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.328374	0.264968	-4.063406	21299.724569
HLA A*3201	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.572906	0.509478	-4.063428	37402.965533
HLA B*0803	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.532004	0.468482	-4.063522	34041.120950
HLA A*8001	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.424007	0.360485	-4.063522	26546.509476
HLA B*4501	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.615911	0.552387	-4.063524	41296.287483
HLA B*1517	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.506495	0.442960	-4.063535	32099.294995
HLA A*2301	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.532638	0.469073	-4.063565	34090.880128
HLA A*6802	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.416750	0.353175	-4.063575	26106.572999
HLA A*2601	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.392842	0.329236	-4.063605	24708.222668
HLA A*0201	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.388065	0.324299	-4.063766	24437.963031
HLA B*1502	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.618065	0.554273	-4.063793	41501.661925
HLA A*0219	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.445594	0.381799	-4.063796	27899.376214
HLA A*0250	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.529239	0.465424	-4.063814	33825.054795
HLA B*3901	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.466897	0.403047	-4.063850	29302.000657
HLA B*5301	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.603499	0.539629	-4.063870	40132.727964
HLA A*2402	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.574534	0.510481	-4.064053	37543.454426
HLA B*3801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.533146	0.469073	-4.064073	34130.739835
HLA B*5701	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.420711	0.356622	-4.064089	26345.782224
HLA A*6801	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.336971	0.272858	-4.064112	21725.548668
HLA A*0219	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.424607	0.360485	-4.064122	26583.156235
HLA A*2602	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.618411	0.554273	-4.064138	41534.679402
HLA B*5301	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.287465	0.223276	-4.064188	19384.953102
HLA A*2403	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.388756	0.324517	-4.064239	24476.862719
HLA B*1509	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.372298	0.307875	-4.064423	23566.636852
HLA A*0212	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.415056	0.350532	-4.064524	26004.941863
HLA B*4403	1:393-401	9	TIPPDHVIG	1.155565	-0.542025	-4.678085	0.613540	-4.064546	47652.471705
HLA A*3001	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.275048	0.210423	-4.064625	18838.561029
HLA A*3301	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.617213	0.552387	-4.064826	41420.241359
HLA A*0206	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.460582	0.395731	-4.064851	28878.980539
HLA A*6901	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.355370	0.290447	-4.064922	22665.722650

HLA B*4501	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.575434	0.510481	-4.064953	37621.324641
HLA B*5301	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.569981	0.505009	-4.064972	37151.891372
HLA A*2301	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.523604	0.458556	-4.065048	33389.079313
HLA A*2603	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.644998	0.579907	-4.065091	44156.804260
HLA B*5701	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.418296	0.353175	-4.065121	26199.670352
HLA B*0802	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.472195	0.407006	-4.065190	29661.653853
HLA B*4403	1:464-472	9	VGKVIGTNP	0.628258	-0.024949	-4.668629	0.603309	-4.065320	46626.063952
HLA B*0801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.307522	0.242192	-4.065330	20301.227972
HLA A*2501	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.474108	0.408739	-4.065369	29792.561412
HLA A*0219	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.280146	0.214737	-4.065409	19061.018764
HLA A*3101	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.422111	0.356622	-4.065489	26430.865863
HLA A*2403	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.422189	0.356622	-4.065567	26435.584890
HLA A*0101	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.377927	0.312328	-4.065599	23874.098189
HLA B*3801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.545492	0.479739	-4.065753	35114.965499
HLA A*2301	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.538705	0.472905	-4.065799	34570.414270
HLA B*4001	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.437162	0.371335	-4.065827	27362.904303
HLA A*3201	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.561650	0.495678	-4.065972	36445.981838
HLA B*3901	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.508981	0.442960	-4.066021	32283.547329
HLA B*1801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.451414	0.385288	-4.066126	28275.752240
HLA A*3002	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.178601	0.112336	-4.066265	15086.947084
HLA A*0211	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.331236	0.264968	-4.066268	21440.537086
HLA A*3301	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.076201	0.009850	-4.066352	11917.945985
HLA B*7301	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.610378	0.543984	-4.066394	40773.498164
HLA A*0212	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.419623	0.353175	-4.066449	26279.874447
HLA A*2902	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.448282	0.381799	-4.066484	28072.578445
HLA A*0201	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.391021	0.324517	-4.066504	24604.846253
HLA A*8001	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.448303	0.381799	-4.066505	28073.945304
HLA A*0101	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.374398	0.307875	-4.066523	23680.891568
HLA B*1509	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.520686	0.454147	-4.066539	33165.487349
HLA A*2601	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.384014	0.317460	-4.066554	24211.098319
HLA A*0211	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.547912	0.481266	-4.066646	35311.178773
HLA A*2501	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.238332	0.171585	-4.066747	17311.405299
HLA A*2403	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.380598	0.313851	-4.066748	24021.401386
HLA A*8001	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.417307	0.350532	-4.066775	26140.066845
HLA A*0101	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.362780	0.295880	-4.066900	23055.781405
HLA B*3901	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.475675	0.408742	-4.066933	29900.258964
HLA A*0301	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.347562	0.280603	-4.066959	22261.900203
HLA A*2603	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.609422	0.542449	-4.066972	40683.820824
HLA B*1517	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.502203	0.435191	-4.067012	31783.592568
HLA A*0301	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.363034	0.295880	-4.067153	23069.256097
HLA A*3101	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.363041	0.295880	-4.067160	23069.630507
HLA A*2601	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.238899	0.171585	-4.067314	17333.990339
HLA B*4801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.430078	0.362756	-4.067322	26920.213153
HLA A*0206	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.496428	0.429083	-4.067345	31363.747639
HLA B*1517	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.518436	0.451064	-4.067372	32994.046092
HLA A*2602	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.576851	0.509478	-4.067373	37744.251935
HLA B*1502	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.577908	0.510481	-4.067427	37836.250371
HLA B*4801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.130047	0.062590	-4.067456	13491.085978
HLA A*2301	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.517042	0.449508	-4.067534	32888.368673
HLA A*2602	1:566-574	9	LSGMFWVDA	0.883436	-0.343034	-4.607949	0.540402	-4.067547	40546.055067
HLA B*3901	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.476572	0.409024	-4.067548	29962.114063
HLA B*4601	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.375552	0.307875	-4.067677	23743.877685
HLA A*3001	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.314120	0.246391	-4.067729	20611.977609
HLA B*4501	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.591942	0.524138	-4.067803	39078.831067
HLA B*1502	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.567352	0.499448	-4.067903	36927.665611
HLA A*6801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.441349	0.373369	-4.067980	27627.969879
HLA A*0202	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.476735	0.408742	-4.067993	29973.300479
HLA A*6802	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.435663	0.367626	-4.068037	27268.623783
HLA B*1502	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.533522	0.465424	-4.068098	34160.295588
HLA A*2402	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.534356	0.466242	-4.068113	34225.963837
HLA A*3002	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.453470	0.385288	-4.068182	28409.917134
HLA A*2601	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.310459	0.242192	-4.068267	20438.977444
HLA A*2301	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.531480	0.463212	-4.068267	34000.078324
HLA A*0203	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.435919	0.367626	-4.068293	27284.708230
HLA B*0702	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-3.959385	-0.109105	-4.068490	9107.203028

HLA B*5101	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.482723	0.414162	-4.068561	30389.489509
HLA B*5401	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.562756	0.494046	-4.068710	36538.966721
HLA B*3901	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.497934	0.429083	-4.068851	31472.697724
HLA B*5801	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.341841	0.272858	-4.068983	21970.565510
HLA A*0211	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.292246	0.223225	-4.069021	19599.543521
HLA B*1501	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.217720	0.148535	-4.069185	16508.981938
HLA B*0702	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.454483	0.385288	-4.069194	28476.236752
HLA A*3201	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.332603	0.263371	-4.069232	21508.150193
HLA B*4402	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.442639	0.373369	-4.069270	27710.147729
HLA A*8001	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.344397	0.275124	-4.069274	22100.264693
HLA B*5701	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.393683	0.324299	-4.069383	24756.122448
HLA B*4001	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.403539	0.334125	-4.069414	25324.373591
HLA A*2602	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.532666	0.463212	-4.069454	34093.093335
HLA B*4002	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.620551	0.550986	-4.069566	41739.884542
HLA B*4402	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.449445	0.379878	-4.069567	28147.854612
HLA A*0216	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.418059	0.348457	-4.069601	26185.358794
HLA A*0101	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.387130	0.317460	-4.069670	24385.401383
HLA B*4002	1:220-228	9	SPVSVAYQH	0.938605	-0.367373	-4.640914	0.571232	-4.069682	43743.570619
HLA A*2501	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.492403	0.422686	-4.069717	31074.438003
HLA B*7301	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.574795	0.505009	-4.069786	37566.005954
HLA A*2402	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.535211	0.465424	-4.069787	34293.427997
HLA A*0211	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.465605	0.395731	-4.069874	29214.943921
HLA A*3002	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.465720	0.395731	-4.069989	29222.689379
HLA A*3002	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.549740	0.479739	-4.070001	35460.112977
HLA A*0201	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.395473	0.325463	-4.070009	24858.386129
HLA A*0216	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.373371	0.303321	-4.070050	23624.973187
HLA B*5401	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.528169	0.458095	-4.070075	33741.896826
HLA A*2603	1:124-132	9	QALNFSHQN	1.086993	-0.536007	-4.621115	0.550986	-4.070130	41794.113695
HLA B*4001	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.383991	0.313851	-4.070140	24209.788561
HLA A*3001	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.299487	0.229302	-4.070185	19929.071689
HLA B*0803	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.505377	0.435191	-4.070186	32016.742205
HLA A*0216	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.430711	0.360485	-4.070226	26959.417587
HLA A*2501	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.416327	0.346054	-4.070273	26081.163313
HLA B*1801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.345405	0.275124	-4.070282	22151.615491
HLA A*6901	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.378200	0.307875	-4.070325	23889.085013
HLA B*7301	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.523099	0.452683	-4.070417	33350.266178
HLA A*0219	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.394756	0.324299	-4.070457	24817.403210
HLA B*0803	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.513434	0.442960	-4.070473	32616.212143
HLA A*6901	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.312762	0.242192	-4.070570	20547.626351
HLA A*8001	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.427212	0.356622	-4.070590	26743.123049
HLA B*0803	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.506636	0.436027	-4.070609	32109.715904
HLA B*1501	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.351357	0.280603	-4.070753	22457.253936
HLA A*2601	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.334034	0.263202	-4.070832	21579.128287
HLA B*4801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.419337	0.348457	-4.070879	26262.535282
HLA B*4601	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.405754	0.334871	-4.070883	25453.896629
HLA B*4402	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.427513	0.356622	-4.070891	26761.648161
HLA B*2705	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.466110	0.395099	-4.071011	29248.944357
HLA B*1801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.485183	0.414162	-4.071021	30562.108664
HLA B*2705	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.451480	0.380356	-4.071124	28280.035688
HLA B*0801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.395461	0.324299	-4.071162	24857.713733
HLA B*4002	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.645505	0.574191	-4.071314	44208.433237
HLA B*4402	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.434094	0.362756	-4.071337	27170.258113
HLA B*0702	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.395936	0.324517	-4.071419	24884.893031
HLA A*0206	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.288362	0.216943	-4.071420	19425.055036
HLA A*2601	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.395816	0.324299	-4.071517	24878.028128
HLA B*3901	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.396124	0.324517	-4.071607	24895.665323
HLA A*0203	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.314296	0.242669	-4.071627	20620.342444
HLA A*0212	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.420229	0.348457	-4.071772	26316.580228
HLA B*5401	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.194352	0.122274	-4.072078	15644.162360
HLA A*0211	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.406988	0.334871	-4.072116	25526.293339
HLA B*1509	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.341583	0.269402	-4.072181	21957.494983
HLA B*0803	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.498390	0.426183	-4.072206	31505.746242
HLA B*4601	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.396737	0.324517	-4.072220	24930.842359
HLA B*5801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.347435	0.275124	-4.072312	22255.397694
HLA B*1509	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.535044	0.462438	-4.072606	34280.258347

HLA A*6801	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.651008	0.578365	-4.072643	44772.115711
HLA B*1502	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.612354	0.539629	-4.072725	40959.428677
HLA A*2402	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.577189	0.504447	-4.072742	37773.667071
HLA B*4601	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.398255	0.325463	-4.072791	25018.122802
HLA B*4002	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.531414	0.458556	-4.072858	33994.928488
HLA A*0203	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.296153	0.223276	-4.072877	19776.669243
HLA B*3801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.531532	0.458556	-4.072976	34004.125171
HLA B*0702	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.353582	0.280603	-4.072978	22572.601373
HLA B*5301	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.598910	0.525884	-4.073026	39710.937226
HLA B*1503	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.452986	0.379878	-4.073108	28378.273702
HLA B*7301	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.340768	0.267585	-4.073182	21916.314346
HLA A*6802	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.397555	0.324299	-4.073255	24977.822405
HLA A*0301	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.366656	0.293372	-4.073285	23262.505892
HLA A*2501	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.482040	0.408742	-4.073298	30341.685650
HLA B*1501	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.429942	0.356622	-4.073320	26911.767627
HLA A*0219	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.426510	0.353175	-4.073335	26699.899495
HLA A*0201	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.390800	0.317460	-4.073339	24592.337141
HLA A*3001	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.242672	0.169330	-4.073342	17485.249073
HLA A*3002	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.332511	0.259153	-4.073358	21503.612760
HLA A*3002	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.594754	0.521039	-4.073715	39332.712538
HLA B*0802	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.468864	0.395099	-4.073765	29434.983229
HLA A*6802	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.434258	0.360485	-4.073773	27180.549227
HLA A*0203	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.343592	0.269799	-4.073793	22059.293644
HLA A*2902	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.445146	0.371335	-4.073810	27870.562989
HLA B*5801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.186190	0.112336	-4.073854	15352.892310
HLA B*3801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.509089	0.435191	-4.073898	32291.582248
HLA A*0216	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.349094	0.275124	-4.073970	22340.562088
HLA A*2301	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.536416	0.462438	-4.073978	34388.733815
HLA B*1509	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.496715	0.422686	-4.074029	31384.454748
HLA B*0803	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.469761	0.395731	-4.074030	29495.875806
HLA B*3901	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.454405	0.380356	-4.074049	28471.153447
HLA A*2902	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.441873	0.367626	-4.074247	27661.320521
HLA B*3501	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.297549	0.223276	-4.074272	19840.323279
HLA A*3002	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.496973	0.422686	-4.074287	31403.136813
HLA A*2403	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.408475	0.334125	-4.074350	25613.856949
HLA B*5401	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.562105	0.487735	-4.074370	36484.252649
HLA A*2301	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.517416	0.442960	-4.074456	32916.670509
HLA A*0211	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.316692	0.242192	-4.074500	20734.441802
HLA A*3002	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.547482	0.472905	-4.074577	35276.237662
HLA A*0301	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.365047	0.290447	-4.074600	23176.459833
HLA B*4403	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.667083	0.592477	-4.074606	46460.383884
HLA B*0801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.355243	0.280603	-4.074639	22659.102188
HLA B*3801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.469797	0.395099	-4.074698	29498.269444
HLA A*0211	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.510840	0.436027	-4.074813	32421.991811
HLA A*1101	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.470628	0.395731	-4.074897	29554.815731
HLA A*0203	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.399197	0.324299	-4.074898	25072.455168
HLA A*0219	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.420965	0.346054	-4.074910	26361.179720
HLA A*3101	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.382873	0.307875	-4.074998	24147.525960
HLA A*2601	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.399629	0.324517	-4.075113	25097.425207
HLA A*2603	1:270-278	9	RADLVRVHN	1.093401	-0.500924	-4.667597	0.592477	-4.075121	46515.461175
HLA B*5801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.342739	0.267585	-4.075153	22016.016337
HLA A*1101	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.470436	0.395099	-4.075337	29541.707800
HLA A*3101	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.428554	0.353175	-4.075379	26825.861531
HLA B*4801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.443196	0.367626	-4.075569	27745.698907
HLA B*0803	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.529793	0.454147	-4.075646	33868.267967
HLA B*5101	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.482719	0.407006	-4.075713	30389.160703
HLA A*2602	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.508025	0.432298	-4.075727	32212.542810
HLA B*4001	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.432367	0.356622	-4.075745	27062.436377
HLA B*1501	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.366201	0.290447	-4.075754	23238.104269
HLA B*3801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.563532	0.487735	-4.075796	36604.256664
HLA A*6801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.357357	0.281512	-4.075845	22769.696113
HLA A*2602	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.615479	0.539629	-4.075850	41255.200802
HLA A*0202	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.345713	0.269799	-4.075915	22167.319805
HLA A*2603	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.555677	0.479739	-4.075938	35948.209460
HLA A*2402	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.494485	0.418508	-4.075977	31223.740341

HLA A*3201	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.542271	0.466242	-4.076029	34855.482750
HLA A*0212	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.400362	0.324299	-4.076063	25139.822556
HLA B*4001	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.411003	0.334871	-4.076132	25763.391053
HLA B*5101	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.461437	0.385288	-4.076149	28935.905047
HLA B*5401	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.557421	0.481266	-4.076155	36092.800535
HLA A*2403	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.438917	0.362756	-4.076161	27473.706657
HLA B*1501	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.400816	0.324517	-4.076299	25166.084969
HLA A*2601	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.384174	0.307875	-4.076299	24220.006554
HLA B*0801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.258698	0.182373	-4.076325	18142.522080
HLA A*1101	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.439108	0.362756	-4.076351	27485.748301
HLA A*2402	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.498376	0.421976	-4.076400	31504.723603
HLA B*4001	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.400971	0.324517	-4.076454	25175.072192
HLA A*0206	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.047843	-0.028622	-4.076465	11164.598992
HLA B*4001	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.384362	0.307875	-4.076487	24230.491026
HLA A*0216	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.471599	0.395099	-4.076500	29620.923413
HLA A*3301	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.581515	0.505009	-4.076506	38151.757600
HLA B*4801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.427055	0.350532	-4.076523	26733.431425
HLA A*2403	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.388854	0.312328	-4.076526	24482.424870
HLA B*1502	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.549453	0.472905	-4.076548	35436.716794
HLA B*0801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.301348	0.224721	-4.076626	20014.643623
HLA A*0250	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.570810	0.494046	-4.076764	37222.907788
HLA B*4601	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.344383	0.267585	-4.076798	22099.547345
HLA A*2601	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.390666	0.313851	-4.076815	24584.754927
HLA A*8001	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.422934	0.346054	-4.076879	26480.959092
HLA A*6802	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.411022	0.334125	-4.076897	25764.506094
HLA B*5701	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.402399	0.325463	-4.076936	25258.014689
HLA A*2603	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.162991	0.086012	-4.076980	14554.302218
HLA A*0202	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.218308	0.141319	-4.076989	16531.324984
HLA A*3002	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.483994	0.407006	-4.076989	30478.562231
HLA A*2402	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.545523	0.468482	-4.077041	35117.435171
HLA A*0211	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.505666	0.428564	-4.077102	32038.053759
HLA A*2301	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.529892	0.452683	-4.077209	33875.964232
HLA B*4801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.433979	0.356622	-4.077356	27163.056651
HLA B*5801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.358069	0.280603	-4.077466	22807.050724
HLA A*2603	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.636236	0.558588	-4.077648	43274.933113
HLA B*0803	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.506780	0.429083	-4.077696	32120.313963
HLA A*6802	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.391577	0.313851	-4.077727	24636.413434
HLA B*0801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.385605	0.307875	-4.077730	24299.933925
HLA A*6801	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.620384	0.542449	-4.077935	41723.855242
HLA B*5801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.359453	0.281512	-4.077941	22879.839581
HLA B*4001	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.403475	0.325463	-4.078012	25320.674806
HLA A*0202	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.457990	0.379878	-4.078113	28707.169668
HLA B*3801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.514199	0.436027	-4.078172	32673.785627
HLA B*5401	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.544700	0.466242	-4.078458	35051.004582
HLA A*6802	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.129361	0.050897	-4.078464	13469.791100
HLA B*4002	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.619214	0.540737	-4.078478	41611.597256
HLA B*4801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.431657	0.353175	-4.078483	27018.258232
HLA B*0801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.381829	0.303321	-4.078509	24089.593430
HLA B*3801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.536736	0.458095	-4.078641	34414.044461
HLA A*0203	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.404255	0.325463	-4.078792	25366.193710
HLA B*1509	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.542093	0.463212	-4.078880	34841.154809
HLA B*5301	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.588403	0.509478	-4.078925	38761.737858
HLA B*5101	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.482808	0.403854	-4.078954	30395.408621
HLA B*5301	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.587496	0.508438	-4.079059	38680.879384
HLA A*3201	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.621613	0.542449	-4.079164	41842.074716
HLA B*5701	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.403783	0.324517	-4.079267	25338.625814
HLA B*4501	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.637895	0.558588	-4.079307	43440.532645
HLA B*1501	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.387384	0.307875	-4.079509	24399.653156
HLA A*0101	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.352437	0.272858	-4.079579	22513.209508
HLA B*5801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.349395	0.269799	-4.079596	22356.037521
HLA B*2705	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.482646	0.403047	-4.079599	30384.064668
HLA A*3001	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.251398	0.171585	-4.079813	17840.121606
HLA A*2501	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.405334	0.325463	-4.079870	25429.259766
HLA B*5101	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.475623	0.395731	-4.079892	29896.700520
HLA A*0203	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.451311	0.371335	-4.079975	28269.022419

HLA B*7301	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.543335	0.463212	-4.080123	34941.007131
HLA A*1101	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.488893	0.408739	-4.080154	30824.294998
HLA B*5801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.328482	0.248296	-4.080186	21305.025769
HLA A*3301	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.634463	0.554273	-4.080190	43098.538591
HLA B*4601	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.404495	0.324299	-4.080196	25380.194859
HLA B*1501	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.350205	0.269799	-4.080407	22397.802055
HLA B*1801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.503352	0.422686	-4.080666	31867.785336
HLA B*4601	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.321664	0.240938	-4.080726	20973.159437
HLA B*1503	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.443499	0.362756	-4.080742	27765.068714
HLA A*0202	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.549256	0.468482	-4.080774	35420.616921
HLA B*4801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.393159	0.312328	-4.080830	24726.274539
HLA A*3201	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.193187	0.112336	-4.080851	15602.240570
HLA B*1801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.516056	0.435191	-4.080864	32813.726085
HLA A*0212	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.410160	0.329236	-4.080924	25713.403235
HLA B*4801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.398469	0.317460	-4.081008	25030.442254
HLA A*2902	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.346066	0.264968	-4.081098	22185.315517
HLA B*1503	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.371548	0.290447	-4.081101	23526.001692
HLA B*4402	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.406581	0.325463	-4.081118	25502.414181
HLA B*1503	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.384473	0.303321	-4.081152	24236.652770
HLA A*2501	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.351077	0.269799	-4.081279	22442.801129
HLA A*0250	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.510410	0.429083	-4.081326	32389.909608
HLA B*4403	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.569650	0.488312	-4.081338	37123.562924
HLA B*1502	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.572234	0.490880	-4.081354	37345.139354
HLA A*6801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.507600	0.426183	-4.081416	32181.016050
HLA A*2402	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.591129	0.509478	-4.081651	39005.750883
HLA A*3201	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.306373	0.224721	-4.081652	20247.593352
HLA B*1502	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.588260	0.506563	-4.081697	38748.948469
HLA B*1501	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.406158	0.324299	-4.081859	25477.592527
HLA A*0219	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.438541	0.356622	-4.081919	27449.936193
HLA A*2601	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.394312	0.312328	-4.081984	24792.041152
HLA B*1503	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.394376	0.312328	-4.082047	24795.662715
HLA B*1509	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.548467	0.466242	-4.082225	35356.290541
HLA A*0206	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.223655	0.141319	-4.082336	16736.131960
HLA B*0802	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.478069	0.395731	-4.082338	30065.544599
HLA A*0212	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.390278	0.307875	-4.082403	24562.819587
HLA A*3002	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.442991	0.360485	-4.082506	27732.643180
HLA B*1517	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.411821	0.329236	-4.082585	25811.939966
HLA B*1509	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.350454	0.267585	-4.082869	22410.649719
HLA A*0101	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.325005	0.242067	-4.082938	21135.125258
HLA A*2902	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.429000	0.346054	-4.082946	26853.449445
HLA A*0219	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.454295	0.371335	-4.082959	28463.915156
HLA A*2501	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.478720	0.395731	-4.082989	30110.632774
HLA B*4403	1:277-285	9	HNGEPPEAP	0.690487	-0.112122	-4.661385	0.578365	-4.083020	45854.851651
HLA A*2301	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.534107	0.451064	-4.083043	34206.342645
HLA B*4002	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.637322	0.554273	-4.083049	43383.228409
HLA A*0101	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.342278	0.259153	-4.083125	21992.684284
HLA B*4002	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.635532	0.552387	-4.083145	43204.756299
HLA A*3002	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.552334	0.469073	-4.083261	35672.532835
HLA A*0216	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.407888	0.324517	-4.083371	25579.238333
HLA B*0802	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.465309	0.381799	-4.083510	29195.036456
HLA B*3901	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.486210	0.402654	-4.083556	30634.446678
HLA B*3801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.546824	0.463212	-4.083612	35222.842762
HLA B*4501	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.657807	0.574191	-4.083616	45478.593724
HLA A*3101	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.325867	0.242192	-4.083675	21177.129239
HLA B*4402	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.353123	0.269402	-4.083722	22548.801451
HLA B*5401	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.546169	0.462438	-4.083731	35169.718947
HLA B*0803	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.493486	0.409720	-4.083767	31152.033093
HLA B*0803	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.478889	0.395099	-4.083790	30122.363512
HLA A*6802	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.440430	0.356622	-4.083808	27569.591120
HLA A*3201	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.563562	0.479739	-4.083823	36606.831079
HLA B*1502	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.492890	0.409024	-4.083865	31109.256112
HLA A*8001	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.451501	0.367626	-4.083875	28281.412648
HLA B*4002	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.645016	0.561125	-4.083892	44158.715369
HLA B*4501	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.590478	0.506563	-4.083915	38947.343007
HLA B*2705	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.298653	0.214737	-4.083916	19890.834424

HLA B*0801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.397794	0.313851	-4.083943	24991.609188
HLA A*2301	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.542048	0.458095	-4.083953	34837.573745
HLA B*1502	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.578131	0.494046	-4.084085	37855.700911
HLA A*0301	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.343239	0.259153	-4.084086	22041.400155
HLA A*3301	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.642749	0.558588	-4.084161	43928.783602
HLA A*0203	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.350365	0.266144	-4.084221	22406.043105
HLA B*1502	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.572612	0.488312	-4.084300	37377.680846
HLA A*2603	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.627052	0.542619	-4.084433	42369.395560
HLA A*0203	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.344649	0.260101	-4.084548	22113.061315
HLA A*0211	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.354423	0.269799	-4.084624	22616.361002
HLA B*1801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.493374	0.408742	-4.084632	31143.944749
HLA A*3201	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.491666	0.407006	-4.084660	31021.696502
HLA B*1517	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.437987	0.353175	-4.084812	27414.912293
HLA A*6801	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.548025	0.463212	-4.084813	35320.349382
HLA A*6901	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.397207	0.312328	-4.084878	24957.831576
HLA A*0206	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.414156	0.329236	-4.084920	25951.115730
HLA A*3201	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.549883	0.464928	-4.084956	35471.816860
HLA A*2402	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.499120	0.414162	-4.084958	31558.798506
HLA B*5401	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.553483	0.468482	-4.085001	35767.027165
HLA A*0201	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.392968	0.307875	-4.085093	24715.441834
HLA B*1509	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.402559	0.317460	-4.085099	25267.308126
HLA A*0211	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.257810	0.172544	-4.085266	18105.459653
HLA A*0301	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.366837	0.281512	-4.085326	23272.198174
HLA A*0216	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.456729	0.371335	-4.085393	28623.893191
HLA B*0803	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.489271	0.403854	-4.085417	30851.154412
HLA A*0216	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.453082	0.367626	-4.085456	28384.568856
HLA B*5301	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.550391	0.464928	-4.085463	35513.291184
HLA B*1501	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.354883	0.269282	-4.085602	22640.354714
HLA B*4601	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.403076	0.317460	-4.085616	25297.398563
HLA B*1509	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.514775	0.429083	-4.085692	32717.120921
HLA A*8001	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.376148	0.290447	-4.085701	23776.526855
HLA A*0211	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.480818	0.395099	-4.085719	30256.450115
HLA A*1101	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.457081	0.371335	-4.085746	28647.130431
HLA B*4501	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.626521	0.540737	-4.085785	42317.624911
HLA B*0801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.381726	0.295880	-4.085846	24083.859943
HLA A*3002	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.543942	0.458095	-4.085847	34989.810141
HLA B*4001	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.415122	0.329236	-4.085886	26008.881309
HLA A*2602	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.328167	0.242192	-4.085975	21289.586817
HLA B*1509	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.494769	0.408742	-4.086027	31244.185986
HLA B*4501	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.647152	0.561125	-4.086027	44376.404606
HLA B*5801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.352177	0.266144	-4.086032	22499.694436
HLA B*1517	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.355327	0.269282	-4.086046	22663.515614
HLA B*0702	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.265643	0.179592	-4.086051	18434.982852
HLA A*0202	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.577018	0.490880	-4.086138	37758.752367
HLA A*2601	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.389484	0.303321	-4.086163	24517.946465
HLA A*2602	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.630304	0.543984	-4.086320	42687.817939
HLA B*4801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.420448	0.334125	-4.086323	26329.823949
HLA A*0250	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.555424	0.469073	-4.086350	35927.212205
HLA B*5801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.354980	0.268569	-4.086411	22645.377025
HLA A*3201	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.607507	0.521039	-4.086468	40504.838293
HLA A*0101	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.355936	0.269282	-4.086654	22695.293112
HLA B*0702	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.420798	0.334125	-4.086673	26351.056279
HLA B*5301	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.421545	0.334871	-4.086674	26396.428196
HLA A*0201	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.399046	0.312328	-4.086718	25063.775762
HLA B*3801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.555207	0.468482	-4.086725	35909.335329
HLA B*7301	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.597228	0.510481	-4.086747	39557.415205
HLA A*3001	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.242056	0.155271	-4.086785	17460.483194
HLA A*0301	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.301533	0.214737	-4.086796	20023.199334
HLA A*0101	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.355405	0.268569	-4.086836	22667.562010
HLA A*2301	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.541167	0.454147	-4.087020	34766.970106
HLA B*5701	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.416275	0.329236	-4.087039	26078.059381
HLA B*7301	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.608085	0.521039	-4.087046	40558.779343
HLA A*3101	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.400982	0.313851	-4.087132	25175.753172
HLA B*4001	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.360118	0.272858	-4.087259	22914.895412
HLA A*0219	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.383143	0.295880	-4.087263	24162.553709

HLA A*2602	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.552212	0.464928	-4.087284	35662.499055
HLA B*4402	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.422231	0.334871	-4.087360	26438.159260
HLA A*0202	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.553614	0.466242	-4.087372	35777.864563
HLA A*0201	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.401281	0.313851	-4.087430	25193.056266
HLA B*0801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.440632	0.353175	-4.087458	27582.420870
HLA B*3801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.575777	0.488312	-4.087465	37651.051350
HLA A*2301	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.516095	0.428564	-4.087531	32816.744040
HLA A*0250	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.591991	0.504447	-4.087544	39083.270974
HLA B*1801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.490683	0.403047	-4.087637	30951.625353
HLA A*0201	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.390969	0.303321	-4.087648	24601.918018
HLA B*7301	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.509634	0.421976	-4.087659	32332.136672
HLA A*0216	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.355372	0.267585	-4.087787	22665.845269
HLA A*0101	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.391204	0.303321	-4.087883	24615.230984
HLA A*3002	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.569370	0.481266	-4.088104	37099.671327
HLA A*0250	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.576419	0.488312	-4.088107	37706.699260
HLA A*3001	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.236704	0.148535	-4.088169	17246.625427
HLA B*5401	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.537690	0.449508	-4.088182	34489.715056
HLA B*7301	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.582318	0.494046	-4.088272	38222.410638
HLA A*3301	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.630786	0.542449	-4.088336	42735.186155
HLA A*0301	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.356958	0.268569	-4.088389	22748.764879
HLA A*0202	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.569680	0.481266	-4.088414	37126.173863
HLA A*0206	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.497203	0.408739	-4.088464	31419.790201
HLA B*1502	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.556972	0.468482	-4.088490	36055.525508
HLA B*0802	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.451247	0.362756	-4.088491	28264.893549
HLA B*5401	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.561426	0.472905	-4.088521	36427.255622
HLA A*0101	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.354738	0.266144	-4.088593	22632.762115
HLA A*2902	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.358661	0.269799	-4.088863	22838.164599
HLA B*5401	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.553852	0.464928	-4.088924	35797.418887
HLA B*1517	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.312151	0.223225	-4.088926	20518.744969
HLA B*1509	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.538458	0.449508	-4.088950	34550.782525
HLA B*4601	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.379478	0.290447	-4.089031	23959.493660
HLA B*4002	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.628725	0.539629	-4.089096	42532.910453
HLA A*3201	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.493089	0.403854	-4.089235	31123.564700
HLA A*3002	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.555501	0.466242	-4.089259	35933.626732
HLA B*0801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.307703	0.218420	-4.089284	20309.686443
HLA B*4501	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.643586	0.554273	-4.089313	44013.468470
HLA B*0803	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.498134	0.408742	-4.089392	31487.173476
HLA A*0301	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.358680	0.269282	-4.089398	22839.153036
HLA A*0301	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.314148	0.224721	-4.089426	20613.315755
HLA B*3901	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.449962	0.360485	-4.089477	28181.375446
HLA B*0801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.211790	0.122274	-4.089516	16285.091094
HLA A*0212	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.446175	0.356622	-4.089553	27936.681469
HLA B*0802	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.461005	0.371335	-4.089669	28907.116011
HLA A*0216	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.471481	0.381799	-4.089683	29612.912201
HLA B*0803	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.492746	0.403047	-4.089699	31098.991651
HLA B*5401	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.543857	0.454147	-4.089710	34982.996329
HLA B*5701	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.364854	0.275124	-4.089731	23166.180783
HLA A*3301	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.632381	0.542619	-4.089762	42892.454615
HLA B*1503	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.330700	0.240938	-4.089762	21414.107458
HLA B*4403	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.648386	0.558588	-4.089797	44502.621262
HLA B*7301	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.463183	0.373369	-4.089813	29052.448364
HLA A*3201	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.589310	0.499448	-4.089862	38842.765358
HLA B*5801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.359296	0.269402	-4.089894	22871.547998
HLA A*3002	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.542609	0.452683	-4.089927	34882.646588
HLA A*2402	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.589397	0.499448	-4.089949	38850.541133
HLA B*7301	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.558457	0.468482	-4.089975	36179.012134
HLA B*5301	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.544155	0.454147	-4.090008	35007.039862
HLA A*3301	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.599509	0.509478	-4.090031	39765.757131
HLA A*0216	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.318992	0.228841	-4.090152	20844.548563
HLA A*2603	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.611254	0.521039	-4.090216	40855.857611
HLA A*2601	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.386221	0.295880	-4.090340	24334.400852
HLA A*2601	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.358924	0.268569	-4.090356	22852.006610
HLA B*5801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.332570	0.242192	-4.090378	21506.521261
HLA A*2301	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.516850	0.426183	-4.090666	32873.782269
HLA B*5801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.354091	0.263371	-4.090720	22599.115947

HLA A*3002	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.238856	0.148101	-4.090755	17332.302472
HLA A*2603	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.526856	0.436027	-4.090829	33640.011146
HLA A*0202	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.578573	0.487735	-4.090838	37894.221984
HLA B*5301	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.556274	0.465424	-4.090850	35997.640274
HLA B*0801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.403233	0.312328	-4.090905	25306.569585
HLA A*0211	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.517092	0.426183	-4.090908	32892.105256
HLA B*0702	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.416428	0.325463	-4.090965	26087.231155
HLA A*0211	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.494048	0.403047	-4.091001	31192.337586
HLA A*3301	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.586681	0.495678	-4.091003	38608.334531
HLA B*5101	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.494083	0.403047	-4.091036	31194.868895
HLA A*0211	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.420377	0.329236	-4.091141	26325.551053
HLA B*4801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.415735	0.324517	-4.091218	26045.631296
HLA B*3501	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.372784	0.281512	-4.091272	23593.042663
HLA B*4001	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.394618	0.303321	-4.091297	24809.483169
HLA A*3002	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.246619	0.155271	-4.091348	17644.890107
HLA A*3001	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.282763	0.191384	-4.091379	19176.239060
HLA B*5801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.354606	0.263202	-4.091404	22625.906472
HLA B*4002	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.635421	0.543984	-4.091437	43193.772247
HLA A*2301	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.527488	0.436027	-4.091461	33689.001753
HLA B*5801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.356434	0.264968	-4.091466	22721.337197
HLA A*1101	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.420871	0.329236	-4.091635	26355.475894
HLA A*2403	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.420908	0.329236	-4.091672	26357.757276
HLA A*0250	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.534675	0.442960	-4.091715	34251.154682
HLA A*0301	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.359317	0.267585	-4.091731	22872.661618
HLA A*0206	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.542920	0.451064	-4.091856	34907.565370
HLA A*6901	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.315170	0.223276	-4.091894	20661.882231
HLA A*0101	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.373414	0.281512	-4.091902	23627.273852
HLA B*1801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.500645	0.408739	-4.091906	31669.796762
HLA A*0250	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.487671	0.395731	-4.091940	30737.703722
HLA B*4402	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.416510	0.324517	-4.091994	26092.171139
HLA A*0101	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.306740	0.214737	-4.092003	20264.688373
HLA B*3801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.543084	0.451064	-4.092020	34920.787097
HLA A*0219	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.421468	0.329236	-4.092232	26391.716159
HLA B*4501	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.597254	0.505009	-4.092245	39559.769288
HLA A*3201	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.600752	0.508438	-4.092315	39879.723020
HLA A*0250	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.591777	0.499448	-4.092329	39064.035019
HLA B*5801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.351540	0.259153	-4.092387	22466.732253
HLA A*0201	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.374032	0.281512	-4.092520	23660.914683
HLA A*2601	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.358687	0.266144	-4.092543	22839.523711
HLA B*0803	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.495253	0.402654	-4.092599	31279.025077
HLA B*3801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.488369	0.395731	-4.092638	30787.130828
HLA A*2403	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.410113	0.317460	-4.092652	25710.621253
HLA B*4403	1:592-600	9	DVDAGGSQH	0.892175	-0.317984	-4.666845	0.574191	-4.092654	46435.004920
HLA A*3101	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.396086	0.303321	-4.092765	24893.510491
HLA A*6801	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.636751	0.543984	-4.092767	43326.234155
HLA A*3101	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.334887	0.242067	-4.092820	21621.546795
HLA A*3101	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.275210	0.182373	-4.092837	18845.594444
HLA B*1501	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.309390	0.216497	-4.092893	20388.728779
HLA B*5401	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.551650	0.458556	-4.093094	35616.418542
HLA A*2301	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.515142	0.421976	-4.093166	32744.743951
HLA A*0211	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.325658	0.232368	-4.093290	21166.935326
HLA B*0802	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.441788	0.348457	-4.093331	27655.933837
HLA A*0206	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.516037	0.422686	-4.093351	32812.305966
HLA A*0216	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.449976	0.356622	-4.093354	28182.290210
HLA B*1503	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.417878	0.324517	-4.093361	26174.453254
HLA B*1801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.456120	0.362756	-4.093364	28583.814585
HLA B*1501	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.318088	0.224721	-4.093367	20801.178566
HLA B*1503	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.500436	0.407006	-4.093431	31654.552054
HLA A*0216	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.045559	-0.047884	-4.093443	11106.045013
HLA B*1501	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.335533	0.242067	-4.093466	21653.737532
HLA A*0202	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.441932	0.348457	-4.093474	27665.061891
HLA A*0301	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.366344	0.272858	-4.093486	23245.774185
HLA B*0802	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.478913	0.385288	-4.093624	30123.993142
HLA A*3301	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.634463	0.540737	-4.093726	43098.538591
HLA A*0206	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.194540	0.100651	-4.093889	15650.934480

HLA A*6801	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.646278	0.552387	-4.093892	44287.187838
HLA B*0803	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.454471	0.360485	-4.093986	28475.466496
HLA A*2402	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.584895	0.490880	-4.094016	38449.921637
HLA B*3501	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.447218	0.353175	-4.094043	28003.865776
HLA A*0202	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.065554	-0.028622	-4.094176	11629.299266
HLA A*0301	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.363579	0.269402	-4.094177	23098.228366
HLA A*6802	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.304621	0.210423	-4.094198	20166.043244
HLA A*2402	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.582107	0.487735	-4.094371	38203.805058
HLA A*3101	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.406795	0.312328	-4.094467	25514.972108
HLA A*6901	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.317797	0.223225	-4.094572	20787.229268
HLA B*2705	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.119977	0.025261	-4.094716	13181.869788
HLA A*2501	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.476598	0.381799	-4.094800	29963.897125
HLA A*2402	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.523407	0.428564	-4.094843	33373.909738
HLA B*5101	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.517545	0.422686	-4.094859	32926.466121
HLA A*3101	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.420345	0.325463	-4.094881	26323.557272
HLA B*1501	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.267438	0.172544	-4.094894	18511.335178
HLA B*1509	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.448106	0.353175	-4.094931	28061.190540
HLA A*3002	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.544449	0.449508	-4.094941	35030.720894
HLA B*2705	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.441098	0.346054	-4.095043	27611.981831
HLA A*0101	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.375768	0.280603	-4.095165	23755.698187
HLA B*4403	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.568108	0.472905	-4.095203	36992.049086
HLA A*0202	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.599693	0.504447	-4.095245	39782.540682
HLA A*3001	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.277658	0.182373	-4.095285	18952.129020
HLA B*2705	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.430168	0.334871	-4.095296	26925.747866
HLA A*0211	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.546371	0.451064	-4.095307	35186.085482
HLA A*3001	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.290590	0.195249	-4.095341	19524.933784
HLA B*5801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.350212	0.254868	-4.095344	22398.165567
HLA B*5401	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.546460	0.451064	-4.095397	35193.319633
HLA B*7301	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.554037	0.458556	-4.095481	35812.721302
HLA A*6802	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.446093	0.350532	-4.095561	27931.392267
HLA B*0702	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.403508	0.307875	-4.095633	25322.592627
HLA A*2602	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.602244	0.506563	-4.095681	40016.956602
HLA B*5101	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.498350	0.402654	-4.095696	31502.848851
HLA A*3002	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.583458	0.487735	-4.095722	38322.830138
HLA A*8001	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.364309	0.268569	-4.095741	23137.123281
HLA B*5401	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.429907	0.334125	-4.095782	26909.583870
HLA B*4801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.430668	0.334871	-4.095797	26956.792460
HLA B*0702	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.363471	0.267585	-4.095885	23092.480974
HLA A*3201	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.561365	0.465424	-4.095941	36422.132229
HLA A*0203	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.446511	0.350532	-4.095979	27958.302043
HLA A*0250	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.475879	0.379878	-4.096001	29914.335143
HLA B*7301	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.600480	0.504447	-4.096032	39854.704465
HLA A*2902	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.456548	0.360485	-4.096063	28611.972063
HLA B*1501	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.377622	0.281512	-4.096110	23857.313783
HLA A*2301	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.476004	0.379878	-4.096126	29922.913534
HLA B*2705	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.444629	0.348457	-4.096171	27837.411857
HLA A*2301	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.528614	0.432298	-4.096316	33776.414515
HLA A*0301	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.338526	0.242192	-4.096334	21803.494881
HLA A*6801	1:259-267	9	PENRYQTAA	1.058125	-0.478218	-4.676279	0.579907	-4.096372	47454.639462
HLA B*1509	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.505457	0.409024	-4.096433	32022.631786
HLA B*4601	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.410362	0.313851	-4.096511	25725.369192
HLA A*2602	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-3.685675	-0.410971	-4.096646	4849.251565
HLA B*1501	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.362836	0.266144	-4.096692	23058.775101
HLA A*0201	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.392623	0.295880	-4.096743	24695.794601
HLA A*2601	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.355952	0.259153	-4.096799	22696.152582
HLA A*8001	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.421113	0.324299	-4.096814	26370.165748
HLA B*4402	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.360212	0.263371	-4.096840	22919.854630
HLA B*4601	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.378425	0.281512	-4.096913	23901.495017
HLA A*2402	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.569871	0.472905	-4.096965	37142.446155
HLA A*2403	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.315410	0.218420	-4.096990	20673.286783
HLA B*5801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.245583	0.148535	-4.097048	17602.843790
HLA B*3501	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.311787	0.214737	-4.097049	20501.546539
HLA B*5701	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.414513	0.317460	-4.097053	25972.464190
HLA A*6801	1:207-215	9	YEVLTGEPP	0.511594	0.031025	-4.639674	0.542619	-4.097054	43618.798830
HLA A*2602	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.566149	0.469073	-4.097076	36825.522554

HLA B*4601	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.311827	0.214737	-4.097089	20503.432115
HLA B*7301	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.233088	0.135996	-4.097092	17103.629245
HLA A*3301	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.618174	0.521039	-4.097135	41511.991102
HLA B*1503	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.519944	0.422686	-4.097258	33108.838555
HLA A*2902	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.383051	0.285730	-4.097321	24157.456294
HLA B*0801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.422793	0.325463	-4.097329	26472.364943
HLA A*3201	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.591396	0.494046	-4.097351	39029.814216
HLA B*0802	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.477834	0.380356	-4.097478	30049.283872
HLA B*5101	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.477867	0.380356	-4.097511	30051.559844
HLA B*0801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.426806	0.329236	-4.097570	26718.105580
HLA A*0101	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.362587	0.264968	-4.097620	23045.555877
HLA B*1517	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.393530	0.295880	-4.097650	24747.418667
HLA B*3801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.563959	0.466242	-4.097717	36640.314957
HLA B*4402	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.319009	0.221286	-4.097723	20845.337945
HLA B*4002	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.621862	0.524138	-4.097724	41866.075861
HLA B*0803	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.483052	0.385288	-4.097764	30412.514755
HLA B*3901	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.483088	0.385288	-4.097799	30414.982780
HLA A*0101	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.372953	0.275124	-4.097829	23602.234227
HLA B*5401	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.526398	0.428564	-4.097834	33604.542055
HLA B*4402	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.344264	0.246391	-4.097873	22093.450825
HLA A*8001	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.469364	0.371335	-4.098029	29468.920898
HLA B*5301	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.597489	0.499448	-4.098040	39581.176475
HLA B*4801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.427287	0.329236	-4.098051	26747.753125
HLA B*5701	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.393955	0.295880	-4.098075	24771.662958
HLA B*5101	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.507146	0.409024	-4.098122	32147.433109
HLA A*2602	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.624071	0.525884	-4.098187	42079.519493
HLA A*0212	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.432381	0.334125	-4.098256	27063.314820
HLA B*5101	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.379856	0.281512	-4.098344	23980.371282
HLA B*7301	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.469688	0.371335	-4.098353	29490.929569
HLA B*0801	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.371226	0.272858	-4.098368	23508.571743
HLA B*5301	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.592522	0.494046	-4.098476	39131.084771
HLA B*4601	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.394383	0.295880	-4.098503	24796.065144
HLA B*1517	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.466183	0.367626	-4.098557	29253.850008
HLA A*8001	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.427995	0.329236	-4.098758	26791.344022
HLA A*3101	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.416320	0.317460	-4.098860	26080.740028
HLA B*5101	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.394787	0.295880	-4.098907	24819.148644
HLA A*3002	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.272773	0.173777	-4.098997	18740.165629
HLA A*0212	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.412857	0.313851	-4.099006	25873.594606
HLA B*1502	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.580370	0.481266	-4.099105	38051.374661
HLA A*0101	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.389564	0.290447	-4.099117	24522.456618
HLA B*1501	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.316114	0.216943	-4.099172	20706.866082
HLA B*4601	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.364157	0.264968	-4.099189	23128.988709
HLA B*5101	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.020011	-0.079239	-4.099250	10471.553826
HLA A*0202	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.548897	0.449508	-4.099389	35391.310945
HLA B*4001	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.367063	0.267585	-4.099478	23284.287715
HLA B*4001	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.385260	0.285730	-4.099529	24280.616994
HLA A*0219	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.467308	0.367626	-4.099682	29329.754894
HLA B*2705	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.424414	0.324517	-4.099897	26571.366272
HLA B*0803	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.506989	0.407006	-4.099983	32135.782979
HLA B*5401	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.381522	0.281512	-4.100010	24072.527292
HLA A*2603	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.644020	0.543984	-4.100036	44057.540498
HLA B*5801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.340991	0.240938	-4.100053	21927.580900
HLA B*1509	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.485578	0.385288	-4.100290	30589.898011
HLA B*4601	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.412655	0.312328	-4.100326	25861.559704
HLA A*2301	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.535523	0.435191	-4.100332	34318.111520
HLA B*3801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.543366	0.442960	-4.100406	34943.464568
HLA A*0250	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.591324	0.490880	-4.100444	39023.269209
HLA A*0206	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.370279	0.269799	-4.100481	23457.374529
HLA B*4403	1:400-408	9	IGTDPAANT	0.969409	-0.408284	-4.661623	0.561125	-4.100498	45879.913533
HLA A*0201	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.391028	0.290447	-4.100581	24605.245584
HLA A*2501	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.468239	0.367626	-4.100613	29392.655853
HLA B*7301	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.626514	0.525884	-4.100630	42316.938116
HLA A*0250	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.563849	0.463212	-4.100636	36630.999799
HLA A*0301	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.366788	0.266144	-4.100644	23269.554424
HLA A*0206	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.472083	0.371335	-4.100747	29653.952472

HLA B*0802	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.480679	0.379878	-4.100801	30246.794298
HLA B*4501	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.600296	0.499448	-4.100848	39837.890469
HLA B*3801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.550457	0.449508	-4.100949	35518.671035
HLA B*4501	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.496759	0.395731	-4.101028	31387.680856
HLA A*0212	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.324258	0.223225	-4.101033	21098.796814
HLA A*1101	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.333552	0.232368	-4.101184	21555.209711
HLA B*1501	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.364490	0.263202	-4.101288	23146.763323
HLA A*3201	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.627181	0.525884	-4.101297	42382.004191
HLA B*1502	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.550842	0.449508	-4.101334	35550.197958
HLA A*3001	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.277757	0.176401	-4.101355	18956.435724
HLA B*1509	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.505267	0.403854	-4.101412	32008.602510
HLA A*0216	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.273998	0.172544	-4.101454	18793.060273
HLA B*0801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.333825	0.232368	-4.101457	21568.740866
HLA A*3101	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.370103	0.268569	-4.101535	23447.858825
HLA A*0203	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.316354	0.214737	-4.101617	20718.295463
HLA B*2705	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.452185	0.350532	-4.101653	28325.970510
HLA B*1801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.436575	0.334871	-4.101703	27325.921748
HLA B*5101	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.510473	0.408739	-4.101734	32394.641050
HLA A*0219	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.452307	0.350532	-4.101775	28333.940130
HLA A*0202	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.574717	0.472905	-4.101812	37559.300031
HLA A*6901	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.330778	0.228841	-4.101937	21417.930781
HLA A*6801	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.642679	0.540737	-4.101942	43921.654685
HLA B*3501	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.462478	0.360485	-4.101993	29005.335448
HLA B*1501	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.414337	0.312328	-4.102008	25961.928216
HLA A*2603	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.601459	0.499448	-4.102011	39944.715130
HLA A*3002	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.313445	0.211378	-4.102067	20579.999497
HLA A*3101	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.383660	0.281512	-4.102148	24191.328512
HLA B*4801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.427623	0.325463	-4.102160	26768.453571
HLA A*1101	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.469797	0.367626	-4.102170	29498.269444
HLA A*3301	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.450634	0.348457	-4.102177	28225.012217
HLA A*0101	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.365656	0.263371	-4.102284	23208.956553
HLA A*2403	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.388098	0.285730	-4.102368	24439.813995
HLA B*1501	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.416242	0.313851	-4.102392	26076.084344
HLA A*0201	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.388150	0.285730	-4.102419	24442.722935
HLA B*4403	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.531059	0.428564	-4.102495	33967.169599
HLA B*7301	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.552073	0.449508	-4.102565	35651.117992
HLA A*6801	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.609147	0.506563	-4.102584	40658.077862
HLA B*1503	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.377755	0.275124	-4.102632	23864.671646
HLA A*6802	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.282371	0.179592	-4.102779	19158.922082
HLA B*1801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.483160	0.380356	-4.102804	30420.084000
HLA A*2902	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.370446	0.267585	-4.102861	23466.386288
HLA A*0201	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.370458	0.267585	-4.102873	23467.021049
HLA A*2301	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.517103	0.414162	-4.102941	32892.994981
HLA A*3101	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.091999	-0.010996	-4.102995	12359.455834
HLA B*4402	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.432282	0.329236	-4.103046	27057.166318
HLA B*1801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.437240	0.334125	-4.103115	27367.789738
HLA A*0212	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.428582	0.325463	-4.103118	26827.603087
HLA A*2601	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.393575	0.290447	-4.103127	24749.962532
HLA A*0201	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.396587	0.293372	-4.103215	24922.211976
HLA A*1101	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.427541	0.324299	-4.103242	26763.385548
HLA B*4403	1:539-547	9	PPAGTTVPV	0.689073	-0.136686	-4.655629	0.552387	-4.103242	45251.091003
HLA B*5801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.363421	0.260101	-4.103320	23089.857640
HLA A*3001	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.260737	0.157340	-4.103397	18227.915779
HLA A*3301	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.609990	0.506563	-4.103427	40737.118685
HLA B*1501	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.389174	0.285730	-4.103444	24500.444318
HLA B*0803	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.512207	0.408739	-4.103468	32524.235126
HLA A*2602	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.583209	0.479739	-4.103470	38300.860278
HLA A*2402	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.583439	0.479739	-4.103700	38321.171596
HLA B*5301	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.592068	0.488312	-4.103757	39090.248991
HLA A*6801	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.612319	0.508438	-4.103881	40956.105022
HLA B*4801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.428190	0.324299	-4.103890	26803.376594
HLA A*3201	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.513624	0.409720	-4.103904	32630.507732
HLA B*4002	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.646443	0.542449	-4.103993	44303.962229
HLA B*0702	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.438938	0.334871	-4.104067	27475.044357
HLA B*5301	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.553579	0.449508	-4.104071	35774.961366

HLA A*6901	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.397451	0.293372	-4.104079	24971.877514
HLA B*7301	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.569525	0.465424	-4.104101	37112.920229
HLA B*4001	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.416444	0.312328	-4.104116	26088.219077
HLA B*1801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.485992	0.381799	-4.104193	30619.037762
HLA A*0206	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.336581	0.232368	-4.104212	21706.046979
HLA B*5801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.373646	0.269282	-4.104365	23639.931513
HLA A*0250	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.592139	0.487735	-4.104404	39096.593723
HLA A*2602	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.540446	0.436027	-4.104419	34709.275796
HLA A*2602	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.533172	0.428564	-4.104607	34132.770974
HLA B*4002	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.626453	0.521798	-4.104655	42310.986356
HLA A*3101	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.363830	0.259153	-4.104677	23111.602834
HLA A*2902	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.438837	0.334125	-4.104712	27468.653711
HLA B*7301	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.592536	0.487735	-4.104801	39132.354960
HLA A*0250	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.485223	0.380356	-4.104867	30564.919533
HLA B*0702	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.418728	0.313851	-4.104877	26225.763002
HLA B*4002	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.615493	0.510481	-4.105012	41256.539940
HLA A*2902	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.461634	0.356622	-4.105012	28949.057398
HLA B*7301	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.567594	0.462438	-4.105156	36948.248126
HLA B*2705	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.417629	0.312328	-4.105300	26159.447863
HLA B*0702	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.422814	0.317460	-4.105354	26473.653888
HLA A*2602	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.571616	0.466242	-4.105374	37292.042440
HLA B*1509	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.512491	0.407006	-4.105486	32545.532349
HLA B*3801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.567925	0.462438	-4.105487	36976.442794
HLA B*4403	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.659806	0.554273	-4.105534	45688.451489
HLA A*6901	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.374941	0.269402	-4.105539	23710.503708
HLA B*1503	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.423056	0.317460	-4.105596	26488.409610
HLA B*1801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.451684	0.346054	-4.105630	28293.349112
HLA A*0219	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.430177	0.324517	-4.105661	26926.330534
HLA A*1101	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.458893	0.353175	-4.105718	28766.867855
HLA A*2601	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.399148	0.293372	-4.105776	25069.606907
HLA A*6802	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.373378	0.267585	-4.105793	23625.356615
HLA B*1501	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.202716	0.096922	-4.105794	15948.376554
HLA A*2501	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.115405	0.009579	-4.105825	13043.823677
HLA B*3801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.514606	0.408739	-4.105867	32704.379691
HLA B*0803	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.486311	0.380356	-4.105955	30641.573853
HLA B*5801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.348089	0.242067	-4.106021	22288.893863
HLA A*0301	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.366137	0.260101	-4.106036	23234.710197
HLA B*1501	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.374635	0.268569	-4.106067	23693.834315
HLA B*4601	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.348352	0.242192	-4.106160	22302.402965
HLA B*5701	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.418507	0.312328	-4.106179	26212.429817
HLA B*5701	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.420070	0.313851	-4.106219	26306.900864
HLA B*3801	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.534905	0.428564	-4.106341	34269.318402
HLA B*4501	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.549343	0.442960	-4.106383	35427.707630
HLA A*2603	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.572751	0.466242	-4.106509	37389.613088
HLA B*2705	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.477940	0.371335	-4.106604	30056.600111
HLA A*0206	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.509305	0.402654	-4.106651	32307.658085
HLA B*1517	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.374262	0.267585	-4.106676	23673.462296
HLA A*0201	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.348904	0.242192	-4.106712	22330.774575
HLA B*5301	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.594451	0.487735	-4.106716	39305.272770
HLA A*2403	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.410073	0.303321	-4.106752	25708.256804
HLA B*4501	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.650759	0.543984	-4.106774	44746.448580
HLA A*6901	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.188902	0.082090	-4.106812	15449.040416
HLA A*1101	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.264123	0.157255	-4.106868	18370.569552
HLA A*0202	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.453000	0.346054	-4.106946	28379.194857
HLA A*6901	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.323945	0.216943	-4.107003	21083.621368
HLA B*2705	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.488804	0.381799	-4.107005	30817.958920
HLA B*1503	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.402949	0.295880	-4.107069	25290.009412
HLA A*2902	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.436335	0.329236	-4.107099	27310.847226
HLA B*1502	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.543129	0.436027	-4.107102	34924.376716
HLA B*1517	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.431620	0.324517	-4.107103	27015.919681
HLA A*2301	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.510974	0.403854	-4.107119	32431.991117
HLA B*4403	1:388-396	9	QKPDSTIPP	0.455242	0.085495	-4.647880	0.540737	-4.107144	44450.889190
HLA A*0211	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.455690	0.348457	-4.107233	28555.530334
HLA A*6801	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.628316	0.521039	-4.107278	42492.892181
HLA B*1509	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.474949	0.367626	-4.107323	29850.317778

HLA B*3501	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.474989	0.367626	-4.107363	29853.063182
HLA A*0201	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.336252	0.228841	-4.107411	21689.613380
HLA B*7301	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.397893	0.290447	-4.107446	24997.288311
HLA B*5301	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.576726	0.469073	-4.107653	37733.431299
HLA B*0801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.319155	0.211378	-4.107777	20852.330917
HLA B*0702	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.460970	0.353175	-4.107795	28904.770341
HLA B*1502	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.411170	0.303321	-4.107849	25773.288727
HLA B*4402	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.403846	0.295880	-4.107966	25342.327221
HLA A*6901	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.374133	0.266144	-4.107988	23666.419449
HLA A*6802	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.403886	0.295880	-4.108006	25344.658014
HLA B*4501	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.534222	0.426183	-4.108038	34215.411420
HLA A*0219	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.456496	0.348457	-4.108039	28608.566939
HLA A*2402	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.534229	0.426123	-4.108105	34215.966729
HLA A*2501	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.461374	0.353175	-4.108199	28931.678774
HLA B*5401	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.516988	0.408742	-4.108246	32884.276711
HLA A*3002	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.456778	0.348457	-4.108321	28627.145270
HLA A*0250	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.589594	0.481266	-4.108329	38868.200024
HLA A*2603	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.662619	0.554273	-4.108346	45985.273348
HLA A*6802	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.349331	0.240938	-4.108394	22352.772280
HLA A*6801	1:274-282	9	VRVHNGEPP	0.343523	0.215065	-4.667003	0.558588	-4.108414	46451.838922
HLA A*2603	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.573909	0.465424	-4.108485	37489.467103
HLA B*1502	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.567093	0.458556	-4.108537	36905.696945
HLA B*4402	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.374706	0.266144	-4.108562	23697.680057
HLA A*3301	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.596922	0.488312	-4.108611	39529.604825
HLA B*4402	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.363518	0.254868	-4.108649	23094.979665
HLA B*7301	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.511319	0.402654	-4.108665	32457.793037
HLA B*2705	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.461848	0.353175	-4.108674	28963.312525
HLA A*2602	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.551667	0.442960	-4.108707	35617.767334
HLA A*1101	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.443635	0.334871	-4.108764	27773.782026
HLA A*3201	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.482138	0.373369	-4.108769	30348.580530
HLA B*4001	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.433083	0.324299	-4.108784	27107.126695
HLA A*0219	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.412293	0.303321	-4.108972	25840.022818
HLA B*0802	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.455140	0.346054	-4.109086	28519.404358
HLA A*6901	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.350032	0.240938	-4.109094	22388.837297
HLA B*5101	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.444124	0.334871	-4.109252	27805.052257
HLA B*3801	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.563402	0.454147	-4.109255	36593.366911
HLA B*0702	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.228396	0.119114	-4.109282	16919.843909
HLA B*4601	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.412826	0.303321	-4.109505	25871.775017
HLA A*3101	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.269609	0.160089	-4.109520	18604.100146
HLA B*5101	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.458061	0.348457	-4.109603	28711.829124
HLA A*0201	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.379410	0.269799	-4.109611	23955.735027
HLA B*0802	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.477303	0.367626	-4.109677	30012.567017
HLA A*0301	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.266944	0.157255	-4.109690	18490.316823
HLA B*3501	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.460288	0.350532	-4.109756	28859.458130
HLA A*0101	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.332988	0.223225	-4.109763	21527.241161
HLA A*2301	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.538900	0.429083	-4.109816	34585.940591
HLA B*5801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.356338	0.246391	-4.109947	22716.298039
HLA A*0211	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.326466	0.216497	-4.109969	21206.363709
HLA A*2501	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.481405	0.371335	-4.110070	30297.398810
HLA B*1503	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.088292	-0.021825	-4.110117	12254.394650
HLA A*8001	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.427619	0.317460	-4.110158	26768.163944
HLA A*0219	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.252105	0.141914	-4.110191	17869.195709
HLA B*3801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.434545	0.324299	-4.110246	27198.494487
HLA A*0202	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.383152	0.272858	-4.110294	24163.076582
HLA A*0216	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.456367	0.346054	-4.110312	28600.055900
HLA B*3801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.536522	0.426123	-4.110398	34397.106599
HLA B*3501	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.373653	0.263202	-4.110451	23640.315185
HLA B*1517	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.353196	0.242669	-4.110527	22552.583350
HLA A*0212	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.375521	0.264968	-4.110554	23742.207871
HLA B*4402	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.378387	0.267585	-4.110802	23899.426235
HLA B*1517	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.471312	0.360485	-4.110827	29601.379862
HLA B*1509	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.482258	0.371335	-4.110923	30356.954990
HLA A*6901	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.374328	0.263371	-4.110956	23677.048550
HLA A*2403	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.325714	0.214737	-4.110977	21169.683763
HLA B*4501	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.653557	0.542449	-4.111107	45035.688724

HLA B*5401	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.459663	0.348457	-4.111206	28817.958356
HLA B*7301	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.520997	0.409720	-4.111277	33189.179460
HLA A*3101	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.377485	0.266144	-4.111341	23849.829163
HLA A*2402	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.580556	0.469073	-4.111483	38067.640581
HLA B*4403	1:73-81	9	AVYDTGEAE	0.977936	-0.453798	-4.635654	0.524138	-4.111515	43216.912122
HLA A*0250	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.561095	0.449508	-4.111587	36399.479711
HLA B*1509	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.533594	0.421976	-4.111619	34166.024974
HLA B*1517	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.268909	0.157255	-4.111654	18574.131765
HLA B*1502	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.525820	0.414162	-4.111658	33559.849776
HLA A*0206	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.546928	0.435191	-4.111736	35231.228034
HLA A*0216	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.393368	0.281512	-4.111856	24738.182616
HLA A*0101	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.405301	0.293372	-4.111929	25427.333866
HLA A*0101	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.379536	0.267585	-4.111951	23962.734335
HLA A*2403	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.402456	0.290447	-4.112009	25261.294335
HLA A*3001	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.298883	0.186843	-4.112040	19901.382727
HLA B*0803	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.493954	0.381799	-4.112155	31185.588432
HLA A*6802	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.429667	0.317460	-4.112207	26894.739024
HLA A*0301	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.360585	0.248296	-4.112290	22939.578138
HLA A*2902	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.415657	0.303321	-4.112337	26040.981879
HLA B*5401	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.492229	0.379878	-4.112352	31062.000407
HLA B*2705	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.475146	0.362756	-4.112390	29863.885761
HLA A*0216	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.462941	0.350532	-4.112409	29036.264310
HLA B*5101	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.465596	0.353175	-4.112421	29214.311730
HLA A*0101	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.372650	0.260101	-4.112549	23585.768547
HLA B*5301	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.593821	0.481266	-4.112555	39248.327300
HLA B*3801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.535286	0.422686	-4.112600	34299.365267
HLA A*0201	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.286530	0.173777	-4.112753	19343.259566
HLA B*1502	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.581966	0.469073	-4.112893	38191.406369
HLA A*3001	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.273112	0.160089	-4.113023	18754.770356
HLA A*0206	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.261155	0.148101	-4.113054	18245.476991
HLA B*4501	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.562662	0.449508	-4.113154	36531.060706
HLA A*0250	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.586108	0.472905	-4.113202	38557.404651
HLA B*4002	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.634246	0.521039	-4.113208	43077.093363
HLA A*3201	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.617685	0.504447	-4.113237	41465.305717
HLA A*8001	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.447486	0.334125	-4.113361	28021.141853
HLA A*0250	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.593112	0.479739	-4.113373	39184.256265
HLA A*0301	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.368318	0.254868	-4.113449	23351.650501
HLA A*2402	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.566170	0.452683	-4.113487	36827.315595
HLA B*4501	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.549609	0.436027	-4.113582	35449.371828
HLA A*3002	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.576043	0.462438	-4.113605	37674.075132
HLA B*4403	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.556584	0.442960	-4.113624	36023.355563
HLA B*0801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.383446	0.269799	-4.113647	24179.422054
HLA B*1801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.438027	0.324299	-4.113727	27417.433707
HLA B*1509	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.495537	0.381799	-4.113739	31299.506923
HLA B*5701	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.417351	0.303321	-4.114030	26142.753866
HLA A*2501	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.105866	-0.008210	-4.114076	12760.450595
HLA B*5101	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.476908	0.362756	-4.114152	29985.302146
HLA A*0201	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.382743	0.268569	-4.114175	24140.342080
HLA B*1502	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.601964	0.487735	-4.114229	39991.202904
HLA B*0801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.379229	0.264968	-4.114261	23945.758069
HLA B*0803	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.487646	0.373369	-4.114276	30735.874613
HLA A*0212	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.356389	0.242067	-4.114322	22719.001838
HLA A*2403	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.395837	0.281512	-4.114325	24879.239443
HLA B*4801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.383761	0.269402	-4.114359	24196.956680
HLA A*6802	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.439014	0.324517	-4.114497	27479.801151
HLA A*0212	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.404967	0.290447	-4.114520	25407.807981
HLA B*3801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.543615	0.429083	-4.114532	34963.508583
HLA A*2403	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.377800	0.263202	-4.114598	23867.124772
HLA A*0212	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.331146	0.216497	-4.114649	21436.129884
HLA B*7301	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.499938	0.385288	-4.114650	31618.268370
HLA A*2601	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.287216	0.172544	-4.114672	19373.840022
HLA A*0216	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.384513	0.269799	-4.114714	24238.881872
HLA B*5301	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.605601	0.490880	-4.114722	40327.515830
HLA A*2402	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.577175	0.462438	-4.114737	37772.440983
HLA B*1801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.523776	0.409024	-4.114752	33402.267996

HLA B*4403	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.654515	0.539629	-4.114887	45135.202847
HLA B*0803	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.494772	0.379878	-4.114894	31244.355014
HLA A*2301	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.524615	0.409720	-4.114895	33466.841149
HLA A*8001	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.440379	0.325463	-4.114915	27566.310050
HLA A*3001	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.294518	0.179592	-4.114926	19702.344504
HLA B*5301	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.557966	0.442960	-4.115006	36138.128842
HLA B*5301	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.581268	0.466242	-4.115026	38130.092092
HLA B*1801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.329936	0.214737	-4.115199	21376.489954
HLA A*0301	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.357872	0.242669	-4.115203	22796.688855
HLA B*1801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.468380	0.353175	-4.115205	29402.198062
HLA B*1503	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.251311	0.135996	-4.115315	17836.550980
HLA A*3201	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.538004	0.422686	-4.115319	34514.726582
HLA A*0201	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.374600	0.259153	-4.115447	23691.911677
HLA B*3901	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.468767	0.353175	-4.115593	29428.455114
HLA B*0802	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.476107	0.360485	-4.115622	29930.037086
HLA A*3101	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.383220	0.267585	-4.115635	24166.867747
HLA B*3901	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.495549	0.379878	-4.115671	31300.353569
HLA A*0203	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.380979	0.264968	-4.116011	24042.463020
HLA B*1801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.440567	0.324517	-4.116050	27578.243087
HLA B*5801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.339304	0.223225	-4.116079	21842.572794
HLA A*0216	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.441544	0.325463	-4.116081	27640.378198
HLA A*3001	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.258110	0.141914	-4.116196	18118.001407
HLA A*0216	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.330994	0.214737	-4.116256	21428.593349
HLA B*1517	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.487686	0.371335	-4.116350	30738.701463
HLA A*3201	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.548767	0.432298	-4.116470	35380.782042
HLA A*2402	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.597785	0.481266	-4.116519	39608.166024
HLA A*0301	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.348937	0.232368	-4.116568	22332.465938
HLA B*5401	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.551772	0.435191	-4.116581	35626.439357
HLA A*2403	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.386474	0.269799	-4.116676	24348.622819
HLA A*0212	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.386484	0.269799	-4.116685	24349.149718
HLA A*2602	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.616174	0.499448	-4.116726	41321.316799
HLA A*2902	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.359108	0.242192	-4.116916	22861.651537
HLA B*1502	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.446177	0.329236	-4.116941	27936.832603
HLA B*0801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.224430	0.107303	-4.117127	16766.037050
HLA B*5801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.359834	0.242669	-4.117164	22899.900308
HLA B*5701	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.387076	0.269799	-4.117277	24382.367358
HLA A*0219	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.398790	0.281512	-4.117279	25049.000563
HLA B*3501	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.385849	0.268569	-4.117281	24313.609606
HLA A*6802	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.332044	0.214737	-4.117307	21480.475117
HLA A*3101	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.386611	0.269282	-4.117329	24356.263972
HLA B*4001	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.413273	0.295880	-4.117392	25898.381742
HLA B*4601	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.387278	0.269799	-4.117479	24393.713905
HLA A*2602	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.527234	0.409720	-4.117515	33669.324095
HLA A*0211	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.540213	0.422686	-4.117527	34690.691213
HLA A*0219	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.381049	0.263371	-4.117678	24046.365348
HLA B*5401	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.413606	0.295880	-4.117726	25918.284633
HLA A*2603	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.626270	0.508438	-4.117832	42293.136098
HLA A*0250	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.539828	0.421976	-4.117852	34659.926524
HLA B*5701	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.408388	0.290447	-4.117941	25608.730441
HLA B*5401	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.525028	0.407006	-4.118023	33498.721458
HLA B*0802	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.474646	0.356622	-4.118024	29829.493234
HLA B*4001	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.386604	0.268569	-4.118035	24355.868681
HLA B*7301	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.560999	0.442960	-4.118039	36391.407004
HLA B*4501	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.643973	0.525884	-4.118089	44052.773828
HLA A*3301	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.584383	0.466242	-4.118141	38404.602227
HLA B*5301	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.432012	0.313851	-4.118161	27040.338282
HLA A*2602	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.606494	0.488312	-4.118182	40410.504712
HLA A*2403	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.387654	0.269402	-4.118252	24414.837812
HLA A*2602	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.527152	0.408742	-4.118410	33662.949543
HLA A*0212	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.430739	0.312328	-4.118410	26961.167813
HLA B*3501	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.266674	0.148101	-4.118573	18478.816886
HLA A*2603	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.399192	0.280603	-4.118589	25072.183891
HLA B*3501	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.383601	0.264968	-4.118633	24188.056923
HLA A*2603	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.658286	0.539629	-4.118658	45528.812397
HLA B*0702	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.469193	0.350532	-4.118661	29457.285273

HLA A*0206	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.513800	0.395099	-4.118701	32643.749976
HLA A*2603	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.568296	0.449508	-4.118788	37008.062382
HLA B*5301	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.577422	0.458556	-4.118866	37793.903273
HLA B*0702	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.448118	0.329236	-4.118882	28061.949590
HLA A*0203	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.359871	0.240938	-4.118934	22901.882569
HLA B*5401	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.499468	0.380356	-4.119112	31584.076605
HLA B*4403	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.640945	0.521798	-4.119147	43746.647149
HLA B*0702	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.412549	0.293372	-4.119177	25855.264602
HLA B*0801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.388622	0.269402	-4.119220	24469.316107
HLA A*0202	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.386822	0.267585	-4.119237	24368.125681
HLA A*6801	1:582-590	9	GWTGMLDKG	1.125625	-0.571352	-4.673525	0.554273	-4.119252	47154.710376
HLA B*4501	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.577422	0.458095	-4.119327	37793.903273
HLA B*5801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.267482	0.148101	-4.119382	18513.238017
HLA A*0211	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.554585	0.435191	-4.119393	35857.891849
HLA A*3002	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.555468	0.436027	-4.119441	35930.905278
HLA A*0219	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.216470	0.096922	-4.119548	16461.536389
HLA B*4601	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.394693	0.275124	-4.119569	24813.778471
HLA A*0211	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.288952	0.169330	-4.119622	19451.449888
HLA A*0219	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.453797	0.334125	-4.119672	28431.288704
HLA A*0203	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.388998	0.269282	-4.119716	24490.505483
HLA B*7301	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.585972	0.466242	-4.119729	38545.308254
HLA A*0206	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.268300	0.148535	-4.119765	18548.124635
HLA A*0250	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.586047	0.466242	-4.119805	38551.981659
HLA B*7301	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.610848	0.490880	-4.119968	40817.638059
HLA A*0206	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.437576	0.317460	-4.120115	27388.970039
HLA B*1501	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.389569	0.269402	-4.120167	24522.721947
HLA A*6901	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.379325	0.259153	-4.120172	23951.069958
HLA A*0211	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.405940	0.285730	-4.120210	25464.777472
HLA B*5301	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.599960	0.479739	-4.120221	39807.083231
HLA A*3001	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.182826	0.062590	-4.120235	15234.413565
HLA A*2603	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.546373	0.426123	-4.120250	35186.275835
HLA A*0301	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.349094	0.228841	-4.120253	22340.562088
HLA A*6901	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.366673	0.246391	-4.120282	23263.386842
HLA B*4002	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.625321	0.505009	-4.120312	42200.801362
HLA B*1501	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.413759	0.293372	-4.120387	25927.400213
HLA B*3501	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.477085	0.356622	-4.120462	29997.470902
HLA A*0211	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.529229	0.408739	-4.120490	33824.322844
HLA A*0203	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.292138	0.171585	-4.120553	19594.666686
HLA B*0702	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.423967	0.303321	-4.120647	26544.068156
HLA A*0301	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.361596	0.240938	-4.120658	22993.003501
HLA A*6802	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.390015	0.269282	-4.120734	24547.941296
HLA A*2601	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.390299	0.269402	-4.120898	24564.015555
HLA A*0203	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.434752	0.313851	-4.120901	27211.445964
HLA A*2402	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.575063	0.454147	-4.120916	37589.181083
HLA A*1101	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.455126	0.334125	-4.121001	28518.478652
HLA B*4001	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.396251	0.275124	-4.121127	24902.939256
HLA A*3301	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.524197	0.403047	-4.121150	33434.629422
HLA A*3201	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.575312	0.454147	-4.121165	37610.742715
HLA B*4801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.424524	0.303321	-4.121203	26578.123294
HLA A*2603	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.631737	0.510481	-4.121256	42828.921816
HLA B*0702	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.364032	0.242669	-4.121363	23122.358020
HLA B*3801	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.506681	0.385288	-4.121393	32113.016563
HLA B*5301	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.574076	0.452683	-4.121393	37503.869653
HLA A*6801	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.631878	0.510481	-4.121397	42842.826055
HLA B*4403	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.630971	0.509478	-4.121493	42753.454275
HLA B*5801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.350372	0.228841	-4.121532	22406.406751
HLA B*4601	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.390995	0.269402	-4.121593	24603.382092
HLA A*2601	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.407641	0.285730	-4.121911	25564.712470
HLA B*4501	1:416-424	9	ITVNVSTGP	0.516307	0.005491	-4.643731	0.521798	-4.121933	44028.233642
HLA A*6901	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.386904	0.264968	-4.121937	24372.740128
HLA B*4402	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.403560	0.281512	-4.122048	25325.606639
HLA A*3301	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.495418	0.373369	-4.122048	31290.872444
HLA A*2402	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.525101	0.403047	-4.122054	33504.339885
HLA B*3801	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.548321	0.426183	-4.122138	35344.433566
HLA A*0301	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.368569	0.246391	-4.122178	23365.171707

HLA B*4403	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.655068	0.532852	-4.122216	45192.620802
HLA A*3101	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.364970	0.242669	-4.122300	23172.322594
HLA B*2705	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.262189	0.139887	-4.122302	18288.959366
HLA B*5701	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.430281	0.307875	-4.122406	26932.740709
HLA A*6802	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.403031	0.280603	-4.122428	25294.798431
HLA A*6802	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.430304	0.307875	-4.122429	26934.197780
HLA A*3001	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.301818	0.179347	-4.122471	20036.310743
HLA B*4002	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.618230	0.495678	-4.122552	41517.381258
HLA B*0801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.388791	0.266144	-4.122647	24478.849057
HLA A*3201	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.531400	0.408742	-4.122658	33993.825053
HLA A*6802	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.386047	0.263371	-4.122675	24324.660967
HLA A*2602	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.208891	0.086012	-4.122879	16176.737108
HLA A*0301	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.334288	0.211378	-4.122910	21591.739966
HLA A*2601	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.390530	0.267585	-4.122944	24577.042091
HLA B*4002	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.631415	0.508438	-4.122978	42797.190715
HLA A*0212	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.295758	0.172544	-4.123215	19758.703158
HLA B*4801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.409034	0.285730	-4.123304	25646.857403
HLA B*1503	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.476528	0.353175	-4.123353	29959.034479
HLA A*3101	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.334736	0.211378	-4.123358	21614.062000
HLA B*5801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.346646	0.223276	-4.123370	22214.980296
HLA A*2501	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.437270	0.313851	-4.123419	27369.714543
HLA B*3501	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.447756	0.324299	-4.123457	28038.580273
HLA A*0203	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.448148	0.324517	-4.123632	28063.923216
HLA B*4002	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.649518	0.525884	-4.123634	44618.816236
HLA B*3901	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.472108	0.348457	-4.123651	29655.717195
HLA B*5301	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.596631	0.472905	-4.123726	39503.096221
HLA B*1502	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.532474	0.408742	-4.123732	34077.972621
HLA A*0201	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.388777	0.264968	-4.123809	24478.054502
HLA B*0702	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.396732	0.272858	-4.123874	24930.572615
HLA B*4403	1:206-214	9	LYEVLTGEP	0.425526	0.118458	-4.667879	0.543984	-4.123895	46545.668197
HLA B*1517	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.404507	0.280603	-4.123903	25380.881388
HLA B*4601	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.396798	0.272858	-4.123940	24934.349307
HLA A*2402	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.582088	0.458095	-4.123993	38202.151667
HLA A*3301	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.634589	0.510481	-4.124108	43111.130980
HLA B*1517	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.399270	0.275124	-4.124146	25076.660336
HLA B*5101	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.480792	0.356622	-4.124170	30254.649644
HLA A*2603	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.612497	0.488312	-4.124185	40972.947651
HLA A*2602	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.597103	0.472905	-4.124198	39546.074765
HLA A*0203	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.076342	-0.047884	-4.124226	11921.815099
HLA B*3801	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.542753	0.418508	-4.124245	34894.159874
HLA A*6801	1:225-233	9	AYQHVREDP	0.311821	0.227808	-4.664066	0.539629	-4.124437	46138.774519
HLA A*3001	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.295124	0.170651	-4.124473	19729.863280
HLA B*1502	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.587715	0.463212	-4.124502	38700.345393
HLA B*4402	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.438400	0.313851	-4.124550	27441.027572
HLA A*2601	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.353506	0.228841	-4.124666	22568.694023
HLA B*3801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.533470	0.408742	-4.124728	34156.230155
HLA B*4801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.438624	0.313851	-4.124773	27455.134224
HLA B*5801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.357167	0.232368	-4.124799	22759.720595
HLA B*4001	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.388053	0.263202	-4.124851	24437.302007
HLA A*0250	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.528017	0.403047	-4.124970	33730.033817
HLA A*1101	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.475543	0.350532	-4.125011	29891.201939
HLA A*0219	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.392600	0.267585	-4.125014	24694.458622
HLA A*2501	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.393607	0.268569	-4.125039	24751.837127
HLA B*5401	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.543575	0.418508	-4.125068	34960.293203
HLA A*0101	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.379995	0.254868	-4.125126	23988.026642
HLA B*5701	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.285486	0.160089	-4.125398	19296.852992
HLA A*0101	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.388655	0.263202	-4.125453	24471.169446
HLA A*2602	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.488224	0.362756	-4.125467	30776.806151
HLA A*0212	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.421395	0.295880	-4.125515	26387.290466
HLA B*1509	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.391707	0.266144	-4.125563	24643.744940
HLA A*6901	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.394904	0.269282	-4.125623	24825.862994
HLA B*4402	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.419052	0.293372	-4.125681	26245.349542
HLA A*0201	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.349035	0.223276	-4.125759	22337.540793
HLA B*3501	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.358196	0.232368	-4.125828	22813.714413
HLA A*3101	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.358257	0.232368	-4.125889	22816.923550

HLA A*3002	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.188573	0.062590	-4.125982	15437.343983
HLA B*5801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.355379	0.229302	-4.126077	22666.213131
HLA B*4601	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.395466	0.269282	-4.126184	24857.982689
HLA A*2402	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.552414	0.426183	-4.126230	35679.094910
HLA A*2602	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.617168	0.490880	-4.126288	41415.984078
HLA A*2301	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.522054	0.395731	-4.126323	33270.075290
HLA A*0203	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.394935	0.268569	-4.126366	24827.609022
HLA A*8001	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.450930	0.324517	-4.126414	28244.258243
HLA A*3201	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.540587	0.414162	-4.126424	34720.544024
HLA B*5701	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.419809	0.293372	-4.126437	26291.108373
HLA A*6901	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.389686	0.263202	-4.126484	24529.356105
HLA A*1101	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.451008	0.324517	-4.126491	28249.301037
HLA B*3501	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.368717	0.242192	-4.126525	23373.136453
HLA B*0801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.386688	0.260101	-4.126587	24360.612595
HLA B*4601	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.419973	0.293372	-4.126602	26301.066497
HLA A*0101	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.368795	0.242192	-4.126602	23377.309546
HLA A*6801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.298193	0.171585	-4.126608	19869.754589
HLA B*3901	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.262647	0.135996	-4.126651	18308.263089
HLA A*2902	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.227334	0.100651	-4.126683	16878.520868
HLA B*2705	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.368755	0.242067	-4.126687	23375.159677
HLA A*0250	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.589266	0.462438	-4.126828	38838.772997
HLA A*6801	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.553032	0.426123	-4.126908	35729.895287
HLA A*2902	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.452457	0.325463	-4.126994	28343.751971
HLA B*0802	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.461186	0.334125	-4.127061	28919.160110
HLA A*2602	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.507428	0.380356	-4.127072	32168.309571
HLA B*5401	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.530956	0.403854	-4.127102	33959.085182
HLA B*5801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.351930	0.224721	-4.127209	22486.917375
HLA A*6901	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.079453	-0.047884	-4.127337	12007.513954
HLA B*0702	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.352064	0.224721	-4.127342	22493.852593
HLA A*2601	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.396631	0.269282	-4.127350	24924.773809
HLA A*3101	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.387454	0.260101	-4.127353	24403.613460
HLA A*2301	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.512665	0.385288	-4.127377	32558.563969
HLA A*2601	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.390795	0.263371	-4.127424	24592.071059
HLA B*5301	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.590668	0.463212	-4.127456	38964.413512
HLA A*0216	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.461585	0.334125	-4.127460	28945.768750
HLA A*0203	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.439798	0.312328	-4.127470	27529.499371
HLA A*3201	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.618460	0.490880	-4.127581	41539.398328
HLA A*0201	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.396991	0.269402	-4.127589	24945.412910
HLA A*0101	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.356906	0.229302	-4.127604	22746.057538
HLA A*0101	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.397439	0.269799	-4.127641	24971.202048
HLA A*6802	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.137410	0.009579	-4.127831	13721.771911
HLA A*0201	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.391204	0.263371	-4.127832	24615.230984
HLA B*4601	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.408456	0.280603	-4.127853	25612.748428
HLA A*3201	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.615591	0.487735	-4.127856	41265.915124
HLA B*1503	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.260006	0.132130	-4.127876	18197.273541
HLA A*6802	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.440226	0.312328	-4.127897	27556.618260
HLA A*2403	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.369993	0.242067	-4.127926	23441.897618
HLA A*0219	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.393020	0.264968	-4.128053	24718.383581
HLA B*1509	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.474167	0.346054	-4.128112	29796.591046
HLA A*0101	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.397543	0.269402	-4.128141	24977.146778
HLA A*0219	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.453613	0.325463	-4.128150	28419.294046
HLA A*6802	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.394340	0.266144	-4.128196	24793.650670
HLA B*4801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.345175	0.216943	-4.128233	22139.874501
HLA B*0802	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.452798	0.324517	-4.128281	28365.994494
HLA A*2403	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.424195	0.295880	-4.128315	26558.001057
HLA B*5101	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.369286	0.240938	-4.128348	23403.756443
HLA A*3101	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.225300	0.096922	-4.128377	16799.630549
HLA A*0301	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.351603	0.223225	-4.128378	22470.014141
HLA A*0219	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.418860	0.290447	-4.128413	26233.709400
HLA A*0219	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.436314	0.307875	-4.128439	27309.517520
HLA B*0801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.445919	0.317460	-4.128458	27920.212681
HLA A*0201	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.394693	0.266144	-4.128549	24813.778471
HLA A*2301	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.537633	0.409024	-4.128609	34485.237293
HLA B*0801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.247737	0.119119	-4.128618	17690.386144
HLA A*0201	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.397996	0.269282	-4.128715	25003.239251

HLA B*4402	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.441086	0.312328	-4.128757	27611.234953
HLA B*4501	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.649823	0.521039	-4.128785	44650.207044
HLA A*0216	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.361201	0.232368	-4.128833	22972.115542
HLA B*5301	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.597392	0.468482	-4.128910	39572.398128
HLA A*0212	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.398250	0.269282	-4.128968	25017.852113
HLA A*8001	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.414720	0.285730	-4.128990	25984.831851
HLA A*3301	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.491799	0.362756	-4.129043	31031.263942
HLA A*0201	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.409777	0.280603	-4.129173	25690.738844
HLA B*4001	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.394207	0.264968	-4.129239	24786.006387
HLA A*2301	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.532293	0.403047	-4.129246	34063.780007
HLA A*0201	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.389482	0.260101	-4.129381	24517.813826
HLA B*5701	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.396984	0.267585	-4.129398	24945.008057
HLA A*0206	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.486041	0.356622	-4.129419	30622.516517
HLA A*2402	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.539285	0.409720	-4.129565	34616.639608
HLA A*6802	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.346559	0.216943	-4.129616	22210.534060
HLA A*1101	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.490108	0.360485	-4.129623	30910.628537
HLA A*2602	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.617398	0.487735	-4.129663	41437.947376
HLA B*4601	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.389808	0.260101	-4.129707	24536.257533
HLA B*4501	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.532389	0.402654	-4.129735	34071.336377
HLA B*4601	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.415542	0.285730	-4.129812	26034.079732
HLA B*4001	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.410423	0.280603	-4.129819	25728.987902
HLA A*6802	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.389923	0.260101	-4.129822	24542.762578
HLA A*0202	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.525594	0.395731	-4.129863	33542.425015
HLA B*5801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.346963	0.216943	-4.130021	22231.210601
HLA B*1509	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.510523	0.380356	-4.130167	32398.321539
HLA B*2705	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.459438	0.329236	-4.130202	28802.995654
HLA B*0702	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.442590	0.312328	-4.130261	27706.999823
HLA A*2402	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.562693	0.432298	-4.130395	36533.629973
HLA A*3101	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.393647	0.263202	-4.130445	24754.113612
HLA A*2402	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.565719	0.435191	-4.130528	36789.082970
HLA A*0216	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.395722	0.264968	-4.130754	24872.645215
HLA A*0250	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.359608	0.228841	-4.130767	22888.010347
HLA B*4402	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.434157	0.303321	-4.130836	27174.227081
HLA A*8001	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.372927	0.242067	-4.130860	23600.829728
HLA B*4801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.406050	0.275124	-4.130927	25471.253092
HLA A*0211	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.448437	0.317460	-4.130977	28082.603624
HLA A*0202	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.371955	0.240938	-4.131017	23548.030238
HLA B*4403	1:536-544	9	GTNPPAGTT	0.935886	-0.430877	-4.636055	0.505009	-4.131047	43256.910198
HLA B*4801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.426998	0.295880	-4.131118	26729.960652
HLA A*3201	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.228091	0.096922	-4.131169	16907.948610
HLA A*3101	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.421656	0.290447	-4.131209	26403.140732
HLA A*3101	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.400625	0.269402	-4.131224	25155.059581
HLA B*5401	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.533959	0.402654	-4.131304	34194.686322
HLA B*4403	1:607-615	9	NPPAGTGVN	1.255096	-0.712647	-4.673849	0.542449	-4.131400	47189.927563
HLA B*4001	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.400731	0.269282	-4.131450	25161.184200
HLA A*3201	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.593901	0.462438	-4.131463	39255.547153
HLA B*4001	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.424987	0.293372	-4.131615	26606.463979
HLA B*1517	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.356340	0.224721	-4.131618	22716.420932
HLA B*1801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.439528	0.307875	-4.131653	27512.377571
HLA B*7301	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.511674	0.379878	-4.131796	32484.318422
HLA B*4601	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.397966	0.266144	-4.131822	25001.480872
HLA A*3301	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.560910	0.429083	-4.131826	36383.926580
HLA A*2402	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.511709	0.379878	-4.131831	32486.954577
HLA A*2602	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.585997	0.454147	-4.131850	38547.602107
HLA A*2902	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.391007	0.259153	-4.131853	24604.047609
HLA A*2902	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.360722	0.228841	-4.131881	22946.777100
HLA B*3901	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.444213	0.312328	-4.131885	27810.768890
HLA A*0101	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.292072	0.160089	-4.131983	19591.698771
HLA A*2501	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.488639	0.356622	-4.132017	30806.290608
HLA A*2301	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.539156	0.407006	-4.132150	34606.341170
HLA B*3501	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.449617	0.317460	-4.132157	28158.973012
HLA B*2705	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.466301	0.334125	-4.132176	29261.764083
HLA B*0803	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.503519	0.371335	-4.132183	31880.028171
HLA B*3901	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.494988	0.362756	-4.132231	31259.909506
HLA A*2301	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.527368	0.395099	-4.132269	33679.708093

HLA A*0212	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.425652	0.293372	-4.132280	26647.229637
HLA A*2601	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.397256	0.264968	-4.132289	24960.667139
HLA B*1801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.528165	0.395731	-4.132434	33741.531748
HLA B*3901	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.467379	0.334871	-4.132508	29334.515402
HLA B*0702	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.423007	0.290447	-4.132559	26485.400495
HLA B*7301	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.535631	0.403047	-4.132585	34326.652813
HLA A*6801	1:510-518	9	KNLNVYGFT	0.828277	-0.339965	-4.620988	0.488312	-4.132676	41781.905996
HLA A*3101	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.397757	0.264968	-4.132789	24989.446053
HLA A*2603	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.639458	0.506563	-4.132895	43597.094728
HLA A*0301	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.302285	0.169330	-4.132955	20057.892808
HLA B*5401	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.542168	0.409024	-4.133143	34847.186909
HLA A*0101	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.365522	0.232368	-4.133153	23201.800857
HLA A*2602	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.489791	0.356622	-4.133169	30888.061664
HLA A*2403	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.408318	0.275124	-4.133194	25604.574567
HLA A*0202	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.555910	0.422686	-4.133224	35967.467724
HLA A*0201	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.396429	0.263202	-4.133227	24913.180244
HLA A*0206	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.458742	0.325463	-4.133279	28756.909543
HLA A*6801	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.585981	0.452683	-4.133298	38546.142367
HLA B*5301	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.559425	0.426123	-4.133301	36259.740538
HLA B*4001	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.403121	0.269799	-4.133322	25299.998963
HLA B*1502	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.561934	0.428564	-4.133370	36469.847063
HLA B*4801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.413975	0.280603	-4.133372	25940.307746
HLA B*5401	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-3.944710	-0.188668	-4.133378	8804.610232
HLA A*2501	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.493954	0.360485	-4.133469	31185.588432
HLA B*5401	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.547642	0.414162	-4.133480	35289.217205
HLA B*5801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.350140	0.216497	-4.133642	22394.409562
HLA B*1503	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.501303	0.367626	-4.133677	31717.805539
HLA A*6901	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.375763	0.242067	-4.133696	23755.441157
HLA B*5801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.354982	0.221286	-4.133696	22645.499534
HLA A*6901	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.363106	0.229302	-4.133804	23073.125287
HLA B*5101	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.505208	0.371335	-4.133872	32004.273728
HLA B*0702	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.345262	0.211378	-4.133884	22144.306592
HLA A*6901	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.382219	0.248296	-4.133924	24111.236603
HLA A*2301	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.542685	0.408742	-4.133943	34888.685871
HLA B*5801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.184865	0.050897	-4.133968	15306.119303
HLA B*5101	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.494485	0.360485	-4.134000	31223.740341
HLA A*6801	1:378-386	9	QNRGFKIRT	0.834848	-0.325370	-4.643503	0.509478	-4.134026	44005.135480
HLA B*5301	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.596481	0.462438	-4.134043	39489.421317
HLA A*3101	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.352508	0.218420	-4.134088	22516.863623
HLA B*3801	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.543819	0.409720	-4.134100	34979.968394
HLA B*4801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.394467	0.260101	-4.134366	24800.894797
HLA A*3002	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.577687	0.442960	-4.134727	37817.014410
HLA A*2601	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.394940	0.260101	-4.134838	24827.877653
HLA B*4001	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.416412	0.281512	-4.134900	26086.243271
HLA A*0202	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.247237	0.112336	-4.134901	17670.013140
HLA A*0212	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.438231	0.303321	-4.134910	27430.341043
HLA B*0801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.425358	0.290447	-4.134911	26629.215909
HLA A*0211	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.497786	0.362756	-4.135030	31461.972932
HLA B*5701	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.416623	0.281512	-4.135111	26098.947495
HLA B*0702	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.367549	0.232368	-4.135181	23310.377161
HLA A*0250	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.593302	0.458095	-4.135207	39201.430609
HLA B*1502	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.597651	0.462438	-4.135213	39595.954188
HLA B*5301	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.543956	0.408742	-4.135214	34990.945905
HLA B*1509	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.537871	0.402654	-4.135216	34504.085135
HLA A*6901	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.390086	0.254868	-4.135217	24551.925668
HLA A*8001	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.443153	0.307875	-4.135278	27742.997218
HLA B*1502	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.544130	0.408739	-4.135390	35004.956698
HLA A*0101	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.101068	-0.034337	-4.135406	12620.261737
HLA B*5301	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.593610	0.458095	-4.135515	39229.222332
HLA B*3901	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.449384	0.313851	-4.135533	28143.895694
HLA B*0702	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.410716	0.275124	-4.135593	25746.392658
HLA B*0801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.398859	0.263202	-4.135656	25052.930729
HLA A*2902	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.088259	-0.047418	-4.135677	12253.466556
HLA A*2402	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.586766	0.451064	-4.135702	38615.854468
HLA A*2403	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.382147	0.246391	-4.135756	24107.193330

HLA B*5401	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.558551	0.422686	-4.135865	36186.841959
HLA A*0216	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.291142	0.155271	-4.135870	19549.772086
HLA A*2501	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.470821	0.334871	-4.135950	29567.929478
HLA B*4002	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.564516	0.428564	-4.135952	36687.323236
HLA B*2705	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.421703	0.285730	-4.135972	26405.997648
HLA B*0801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.421740	0.285730	-4.136010	26408.283403
HLA A*2402	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.585523	0.449508	-4.136015	38505.500388
HLA B*1502	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.291339	0.155271	-4.136068	19558.658121
HLA A*2403	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.377034	0.240938	-4.136097	23825.069237
HLA B*1509	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.449953	0.313851	-4.136102	28180.765620
HLA B*1517	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.327519	0.191384	-4.136134	21257.822429
HLA B*4501	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.631817	0.495678	-4.136139	42836.800331
HLA A*6802	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.322996	0.186843	-4.136153	21037.591425
HLA A*1101	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.378239	0.242067	-4.136172	23891.282149
HLA B*4601	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.378963	0.242669	-4.136294	23931.124082
HLA A*0211	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.258754	0.122446	-4.136308	18144.877809
HLA A*2603	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.605383	0.469073	-4.136310	40307.231366
HLA B*0801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.403901	0.267585	-4.136315	25345.480698
HLA B*0702	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.395499	0.259153	-4.136345	24859.865465
HLA A*2301	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.545102	0.408739	-4.136363	35083.444955
HLA A*2902	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.432301	0.295880	-4.136421	27058.337354
HLA A*0101	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.379116	0.242669	-4.136447	23939.540770
HLA B*0801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.429855	0.293372	-4.136483	26906.381348
HLA B*5401	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.539543	0.403047	-4.136496	34637.245679
HLA B*5701	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.399869	0.263371	-4.136497	25111.278006
HLA A*2403	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.399897	0.263371	-4.136526	25112.908250
HLA B*7301	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.555243	0.418508	-4.136735	35912.249430
HLA A*3301	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.599958	0.463212	-4.136746	39806.867880
HLA A*3201	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.618068	0.481266	-4.136802	41501.886445
HLA B*4403	1:253-261	9	KALAKNPEN	0.977859	-0.471296	-4.643400	0.506563	-4.136837	43994.661959
HLA A*6901	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.396972	0.260101	-4.136871	24944.333318
HLA A*2402	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.471780	0.334871	-4.136908	29633.264919
HLA B*7301	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.618185	0.481266	-4.136920	41513.113993
HLA A*0212	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.422741	0.285730	-4.137011	26469.214455
HLA B*1503	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.462476	0.325463	-4.137012	29005.178533
HLA B*5801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.269219	0.132177	-4.137042	18587.400389
HLA A*1101	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.309637	0.172544	-4.137093	20400.313649
HLA A*0211	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.461653	0.324517	-4.137137	28950.310315
HLA A*2902	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.454602	0.317460	-4.137142	28484.094553
HLA A*0216	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.360494	0.223225	-4.137269	22934.738726
HLA B*3501	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.406755	0.269402	-4.137353	25512.625652
HLA B*5801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.355910	0.218420	-4.137490	22693.942583
HLA A*0301	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.366805	0.229302	-4.137503	23270.435641
HLA B*0702	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.407331	0.269799	-4.137532	25546.463089
HLA A*0101	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.378486	0.240938	-4.137549	23904.857168
HLA A*1101	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.440957	0.303321	-4.137636	27603.020620
HLA A*3001	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.244967	0.107303	-4.137664	17577.911352
HLA B*4501	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.618975	0.481266	-4.137709	41588.641949
HLA A*3002	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.551880	0.414162	-4.137718	35635.306274
HLA A*3001	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.149872	0.012088	-4.137784	14121.208469
HLA A*2601	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.324643	0.186843	-4.137800	21117.524433
HLA B*0802	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.462140	0.324299	-4.137840	28982.748394
HLA A*0206	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.471967	0.334125	-4.137843	29646.092709
HLA B*4402	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.423599	0.285730	-4.137868	26521.532455
HLA B*5101	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.483945	0.346054	-4.137891	30475.099829
HLA A*6802	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.286426	0.148535	-4.137891	19338.655739
HLA B*4801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.431265	0.293372	-4.137893	26993.859569
HLA B*0802	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.491092	0.353175	-4.137918	30980.774476
HLA A*8001	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.410780	0.272858	-4.137921	25750.153631
HLA A*6801	1:577-585	9	RLRALGWTG	1.065349	-0.532497	-4.670783	0.532852	-4.137932	46857.944405
HLA A*8001	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.451823	0.313851	-4.137972	28302.381323
HLA B*3901	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.494626	0.356622	-4.138004	31233.877004
HLA B*0803	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.486508	0.348457	-4.138051	30655.501488
HLA A*3001	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.279373	0.141319	-4.138054	19027.123116
HLA A*6901	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.380779	0.242669	-4.138110	24031.409861

HLA B*1503	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.362958	0.224721	-4.138237	23065.262775
HLA A*0101	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.367218	0.228841	-4.138377	23292.602916
HLA B*4801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.404563	0.266144	-4.138419	25384.176988
HLA A*2902	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.401779	0.263202	-4.138577	25221.966670
HLA A*0211	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.499135	0.360485	-4.138650	31559.822900
HLA A*3301	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.518572	0.379878	-4.138694	33004.400376
HLA A*2601	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.148321	0.009579	-4.138742	14070.878221
HLA B*4801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.429336	0.290447	-4.138889	26874.231691
HLA A*2301	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.519335	0.380356	-4.138979	33062.480218
HLA B*0803	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.501740	0.362756	-4.138984	31749.737307
HLA B*1503	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.294274	0.155271	-4.139002	19691.262522
HLA B*4601	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.398212	0.259153	-4.139059	25015.686706
HLA B*1502	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.492368	0.353175	-4.139193	31071.916466
HLA B*0702	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.380166	0.240938	-4.139228	23997.501910
HLA B*4601	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.356215	0.216943	-4.139273	22709.908520
HLA A*2402	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.575300	0.436027	-4.139273	37609.725379
HLA A*3001	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.276561	0.137283	-4.139278	18904.308449
HLA B*5101	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.261555	0.122274	-4.139281	18262.264731
HLA A*0202	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.590461	0.451064	-4.139398	38945.868129
HLA A*0216	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.356009	0.216497	-4.139511	22699.099581
HLA B*4501	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.598093	0.458556	-4.139536	39636.246102
HLA A*2301	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.542316	0.402654	-4.139662	34859.065656
HLA B*1517	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.496412	0.356622	-4.139789	31362.559941
HLA A*8001	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.403167	0.263371	-4.139796	25302.736515
HLA B*7301	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.485907	0.346054	-4.139853	30613.075101
HLA A*2601	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.394817	0.254868	-4.139949	24820.894200
HLA A*6901	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.361257	0.221286	-4.139972	22975.098374
HLA B*4002	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.598156	0.458095	-4.140061	39642.036072
HLA A*6802	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.372457	0.232368	-4.140089	23575.307963
HLA A*0101	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.388455	0.248296	-4.140159	24459.919196
HLA B*4002	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.297530	0.157340	-4.140190	19839.464626
HLA B*0801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.363449	0.223225	-4.140224	23091.356652
HLA A*2403	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.408799	0.268569	-4.140231	25632.986490
HLA A*2501	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.469468	0.329236	-4.140232	29475.936371
HLA B*1509	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.513603	0.373369	-4.140233	32628.919024
HLA A*0101	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.386641	0.246391	-4.140250	24357.976973
HLA B*1502	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.420869	0.280603	-4.140265	26355.333314
HLA A*2602	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.589806	0.449508	-4.140298	38887.129170
HLA B*4001	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.388650	0.248296	-4.140354	24470.904674
HLA A*0201	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.395250	0.254868	-4.140381	24845.613706
HLA A*0211	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.369281	0.228841	-4.140440	23403.503221
HLA B*5801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.351944	0.211378	-4.140566	22487.647298
HLA B*4601	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.403971	0.263202	-4.140769	25349.594519
HLA B*3801	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.562761	0.421976	-4.140785	36539.362066
HLA A*1101	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.404171	0.263371	-4.140799	25361.253972
HLA B*4403	1:394-402	9	IPPDHVIGT	0.952408	-0.431369	-4.661876	0.521039	-4.140838	45906.727532
HLA B*2705	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.466467	0.325463	-4.141004	29273.005747
HLA B*4501	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.549768	0.408739	-4.141029	35462.415075
HLA B*1801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.512397	0.371335	-4.141062	32538.490402
HLA B*0702	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.383272	0.242192	-4.141080	24169.744200
HLA A*0206	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.296369	0.155271	-4.141098	19786.514735
HLA A*3201	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.520978	0.379878	-4.141100	33187.743092
HLA A*8001	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.406219	0.264968	-4.141252	25481.176383
HLA A*0301	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.362554	0.221286	-4.141268	23043.810509
HLA A*6801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.521173	0.379878	-4.141295	33202.648425
HLA A*0301	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.364580	0.223276	-4.141303	23151.522226
HLA B*0803	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.509040	0.367626	-4.141414	32287.913884
HLA A*2402	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.584411	0.442960	-4.141451	38407.095484
HLA A*3301	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.567730	0.426123	-4.141607	36959.843329
HLA A*6802	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.289737	0.148101	-4.141636	19486.628543
HLA B*0802	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.492199	0.350532	-4.141667	31059.815938
HLA A*3002	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.374050	0.232368	-4.141682	23661.938729
HLA B*1501	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.390010	0.248296	-4.141715	24547.675694
HLA B*1517	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.414694	0.272858	-4.141836	25983.285572
HLA A*3101	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.422499	0.280603	-4.141896	26454.469425

HLA B*5401	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.476779	0.334871	-4.141908	29976.381530
HLA A*3101	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.382863	0.240938	-4.141926	24147.003424
HLA B*0702	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.466249	0.324299	-4.141950	29258.281626
HLA B*7301	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.596121	0.454147	-4.141974	39456.748931
HLA A*0206	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.523795	0.381799	-4.141996	33403.713648
HLA B*0801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.356786	0.214737	-4.142049	22739.782667
HLA A*3301	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.641560	0.499448	-4.142112	43808.697216
HLA A*2603	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.607079	0.464928	-4.142152	40464.976864
HLA A*1101	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.498794	0.356622	-4.142172	31535.076012
HLA B*4601	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.405566	0.263371	-4.142195	25442.882792
HLA B*0702	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.438104	0.295880	-4.142224	27422.328878
HLA A*2902	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.358790	0.216497	-4.142293	22844.960967
HLA B*0802	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.471542	0.329236	-4.142306	29617.077761
HLA B*1501	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.402444	0.260101	-4.142343	25260.611041
HLA A*0202	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.495549	0.353175	-4.142375	31300.353569
HLA B*2705	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.417629	0.275124	-4.142505	26159.447863
HLA B*3801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.551549	0.409024	-4.142525	35608.134228
HLA A*6802	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.435908	0.293372	-4.142536	27283.970204
HLA B*1501	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.352982	0.210423	-4.142559	22541.483448
HLA A*0301	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.359559	0.216943	-4.142616	22885.410242
HLA A*2902	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.302720	0.160089	-4.142631	20077.977388
HLA B*0803	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.495815	0.353175	-4.142640	31319.493872
HLA A*8001	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.436016	0.293372	-4.142644	27290.760799
HLA B*2705	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.460178	0.317460	-4.142717	28852.121119
HLA A*0201	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.384811	0.242067	-4.142744	24255.541062
HLA A*0216	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.428504	0.285730	-4.142774	26822.814080
HLA A*0219	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.455213	0.312328	-4.142885	28524.187650
HLA B*4001	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.412415	0.269402	-4.143013	25847.293007
HLA A*0211	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.514369	0.371335	-4.143033	32686.514938
HLA B*3501	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.455573	0.312328	-4.143244	28547.807266
HLA A*0201	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.389677	0.246391	-4.143286	24528.825306
HLA A*2501	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.460789	0.317460	-4.143328	28892.732235
HLA B*1801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.359923	0.216497	-4.143425	22904.608457
HLA B*5301	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.594512	0.451064	-4.143448	39310.801725
HLA B*5701	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.412852	0.269402	-4.143450	25873.314661
HLA A*0101	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.360426	0.216943	-4.143483	22931.140851
HLA A*0101	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.354867	0.211378	-4.143489	22639.497357
HLA B*1503	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.494024	0.350532	-4.143492	31190.650160
HLA B*4601	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.412100	0.268569	-4.143532	25828.562444
HLA A*0211	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.467835	0.324299	-4.143535	29365.318680
HLA A*6802	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.412960	0.269402	-4.143558	25879.754163
HLA B*5701	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.424202	0.280603	-4.143599	26558.432088
HLA A*2402	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.523957	0.380356	-4.143601	33416.184993
HLA A*0212	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.409840	0.266144	-4.143696	25694.491687
HLA B*5701	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.412375	0.268569	-4.143807	25844.915989
HLA A*3301	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.598046	0.454147	-4.143899	39631.957780
HLA A*8001	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.439850	0.295880	-4.143970	27532.776060
HLA B*4501	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.652420	0.508438	-4.143982	44917.922138
HLA A*3301	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.612476	0.468482	-4.143994	40970.952768
HLA B*3901	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.412674	0.268569	-4.144105	25862.678993
HLA A*0212	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.386301	0.242192	-4.144108	24338.877242
HLA A*0250	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.595311	0.451064	-4.144247	39383.175072
HLA B*0803	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.468589	0.324299	-4.144290	29416.358045
HLA B*0702	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.413693	0.269402	-4.144292	25923.473109
HLA A*0202	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.299621	0.155271	-4.144350	19935.218039
HLA B*4403	1:529-537	9	RPAGEVTGT	0.899106	-0.388625	-4.654873	0.510481	-4.144392	45172.332930
HLA A*6802	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.430161	0.285730	-4.144430	26925.310874
HLA B*0801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.361006	0.216497	-4.144509	22961.802900
HLA A*3301	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.603125	0.458556	-4.144569	40098.221743
HLA A*0212	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.404671	0.260101	-4.144570	25390.494751
HLA B*4403	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.644084	0.499448	-4.144635	44063.976321
HLA A*2902	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.425241	0.280603	-4.144638	26622.013828
HLA B*5701	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.414088	0.269282	-4.144806	25947.044662
HLA A*3002	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.490864	0.346054	-4.144810	30964.521293
HLA B*4001	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.411036	0.266144	-4.144892	25765.342406

HLA A*0211	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.498073	0.353175	-4.144898	31482.744892
HLA B*4601	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.391291	0.246391	-4.144900	24620.158607
HLA B*5701	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.387109	0.242192	-4.144917	24384.214111
HLA B*5701	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.417802	0.272858	-4.144944	26169.922418
HLA A*0203	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.435431	0.290447	-4.144984	27254.023191
HLA A*0101	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.363421	0.218420	-4.145002	23089.857640
HLA A*2902	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.408461	0.263371	-4.145089	25613.025554
HLA B*5301	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.567072	0.421976	-4.145097	36903.900087
HLA B*0702	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.414487	0.269282	-4.145206	25970.918647
HLA B*0803	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.491308	0.346054	-4.145254	30996.197749
HLA B*1801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.495817	0.350532	-4.145285	31319.663307
HLA A*0202	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.426874	0.281512	-4.145362	26722.297626
HLA B*5301	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.571562	0.426183	-4.145379	37287.402575
HLA A*2501	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.469919	0.324517	-4.145402	29506.568895
HLA A*2602	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.571600	0.426183	-4.145416	37290.630246
HLA B*0802	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.480355	0.334871	-4.145484	30224.221536
HLA A*0301	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.363917	0.218420	-4.145497	23116.229452
HLA B*4002	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.649983	0.504447	-4.145536	44666.635647
HLA B*1502	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.567784	0.421976	-4.145808	36964.442434
HLA A*0203	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.431547	0.285730	-4.145817	27011.389313
HLA A*0250	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.581853	0.436027	-4.145826	38181.490316
HLA B*5401	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.369156	0.223276	-4.145880	23396.793833
HLA A*1101	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.463420	0.317460	-4.145960	29068.326925
HLA A*2603	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.555689	0.409720	-4.145969	35949.181852
HLA A*2902	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.318537	0.172544	-4.145993	20822.683300
HLA A*2602	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.604194	0.458095	-4.146100	40197.045075
HLA B*5301	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.581359	0.435191	-4.146168	38138.137844
HLA B*4403	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.650627	0.504447	-4.146180	44732.894527
HLA A*0216	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.454060	0.307875	-4.146185	28448.520658
HLA A*2602	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.282308	0.135996	-4.146311	19156.123800
HLA A*0212	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.427926	0.281512	-4.146414	26787.141144
HLA B*1517	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.470931	0.324299	-4.146632	29575.448517
HLA A*2402	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.576019	0.429083	-4.146936	37672.037061
HLA B*1502	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.601236	0.454147	-4.147089	39924.191239
HLA A*2403	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.304388	0.157255	-4.147133	20155.245626
HLA B*4801	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.420058	0.272858	-4.147200	26306.189286
HLA A*3001	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.279422	0.132177	-4.147246	19029.284866
HLA A*0206	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.229414	0.082090	-4.147324	16959.524797
HLA B*3501	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.307478	0.160089	-4.147389	20299.141359
HLA A*2501	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.422537	0.275124	-4.147413	26456.759376
HLA B*5701	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.413573	0.266144	-4.147429	25916.321696
HLA B*4601	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.376355	0.228841	-4.147515	23787.848847
HLA B*1503	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.295711	0.148101	-4.147611	19756.565426
HLA B*5301	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.583641	0.436027	-4.147614	38339.004687
HLA A*3002	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.527974	0.380356	-4.147619	33726.749414
HLA A*2501	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.481831	0.334125	-4.147706	30327.080247
HLA B*5101	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.515348	0.367626	-4.147722	32760.336461
HLA A*0211	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.493797	0.346054	-4.147742	31174.286872
HLA B*4002	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.620713	0.472905	-4.147808	41755.468213
HLA B*0702	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.433579	0.285730	-4.147849	27138.086784
HLA B*4403	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.616928	0.469073	-4.147855	41393.136682
HLA B*3501	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.455763	0.307875	-4.147888	28560.319685
HLA A*0201	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.380262	0.232368	-4.147894	24002.825277
HLA B*3901	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.498498	0.350532	-4.147966	31513.587577
HLA A*0211	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.498559	0.350532	-4.148027	31518.020499
HLA A*1101	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.433760	0.285730	-4.148030	27149.393820
HLA A*2403	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.317407	0.169330	-4.148077	20768.569852
HLA B*3801	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.551152	0.403047	-4.148105	35575.593612
HLA B*1801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.508643	0.360485	-4.148158	32258.407463
HLA A*2403	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.407350	0.259153	-4.148196	25547.568741
HLA B*4501	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.456289	0.307875	-4.148414	28594.950493
HLA B*1517	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.473903	0.325463	-4.148440	29778.542533
HLA B*5801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.358903	0.210423	-4.148480	22850.893995
HLA B*4403	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.598020	0.449508	-4.148512	39629.599400
HLA A*3201	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.390743	0.242192	-4.148551	24589.144345

HLA	B*4002	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.629825	0.481266	-4.148559	42640.732908
HLA	B*4001	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.380958	0.232368	-4.148590	24041.292445
HLA	B*5401	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.557388	0.408739	-4.148649	36090.067026
HLA	B*5701	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.413641	0.264968	-4.148674	25920.387944
HLA	A*2601	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.397017	0.248296	-4.148721	24946.897425
HLA	A*2601	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.391427	0.242669	-4.148758	24627.884974
HLA	B*4801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.418615	0.269799	-4.148817	26218.953720
HLA	B*3501	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.267950	0.119114	-4.148835	18533.179508
HLA	B*4501	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.603019	0.454147	-4.148872	40088.461219
HLA	A*2902	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.372124	0.223225	-4.148899	23557.204266
HLA	B*3801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.555980	0.407006	-4.148975	35973.305598
HLA	A*2601	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.389914	0.240938	-4.148976	24542.231489
HLA	B*4501	1:232-240	9	DPIPPSARH	1.047890	-0.543443	-4.653437	0.504447	-4.148990	45023.264896
HLA	A*3001	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.268128	0.119119	-4.149009	18540.801021
HLA	B*4002	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.558762	0.409720	-4.149043	36204.465261
HLA	A*1101	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.474512	0.325463	-4.149049	29820.296320
HLA	B*5401	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.495105	0.346054	-4.149051	31268.366282
HLA	B*4403	1:278-286	9	NGEPPEAPK	0.495512	0.030372	-4.674998	0.525884	-4.149114	47314.930757
HLA	B*3901	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.328778	0.179592	-4.149186	21319.553206
HLA	B*3501	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.442683	0.293372	-4.149312	27712.996143
HLA	A*0202	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.558093	0.408739	-4.149353	36148.687561
HLA	B*1517	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.499910	0.350532	-4.149378	31616.215821
HLA	B*1502	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.614330	0.464928	-4.149402	41146.207048
HLA	B*1801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.517047	0.367626	-4.149421	32888.724520
HLA	B*0702	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.281650	0.132130	-4.149520	19127.128664
HLA	A*2601	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.366523	0.216943	-4.149580	23255.333686
HLA	A*0216	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.473915	0.324299	-4.149616	29779.348037
HLA	A*2601	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.391697	0.242067	-4.149630	24643.211666
HLA	B*2705	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.440111	0.290447	-4.149664	27549.314394
HLA	A*2902	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.415822	0.266144	-4.149678	26050.845265
HLA	B*5701	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.409856	0.260101	-4.149755	25695.464736
HLA	A*0211	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.531607	0.381799	-4.149808	34010.012354
HLA	B*1502	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.552931	0.403047	-4.149884	35721.584579
HLA	B*5401	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.545657	0.395731	-4.149926	35128.265782
HLA	A*0201	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.392611	0.242669	-4.149942	24695.126602
HLA	A*3002	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.576294	0.426183	-4.150111	37695.889390
HLA	B*4002	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.644208	0.494046	-4.150162	44076.612338
HLA	A*6801	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.616421	0.466242	-4.150179	41344.795560
HLA	A*0201	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.398487	0.248296	-4.150192	25031.525573
HLA	B*1502	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.545969	0.395731	-4.150238	35153.550201
HLA	A*3002	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.418827	0.268569	-4.150258	26231.722575
HLA	B*1509	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.446172	0.295880	-4.150292	27936.530335
HLA	B*5401	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.291633	0.141319	-4.150314	19571.888866
HLA	A*3301	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.552968	0.402654	-4.150314	35724.676709
HLA	A*2501	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.413540	0.263202	-4.150338	25914.358909
HLA	A*2402	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.500944	0.350532	-4.150412	31691.563160
HLA	B*4403	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.644464	0.494046	-4.150418	44102.611007
HLA	A*0219	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.464346	0.313851	-4.150495	29130.352036
HLA	B*3501	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.420319	0.269799	-4.150520	26321.990836
HLA	A*0203	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.419966	0.269402	-4.150565	26300.639643
HLA	B*4801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.369020	0.218420	-4.150600	23389.453690
HLA	A*0219	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.420403	0.269799	-4.150605	26327.117701
HLA	A*2601	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.365369	0.214737	-4.150632	23193.643545
HLA	A*0219	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.416790	0.266144	-4.150646	26108.974082
HLA	A*0301	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.361182	0.210423	-4.150759	22971.121351
HLA	B*0702	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.416945	0.266144	-4.150801	26118.298026
HLA	B*1503	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.084974	-0.065831	-4.150805	12161.142845
HLA	B*0702	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.414215	0.263371	-4.150843	25954.625784
HLA	A*3002	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.601972	0.451064	-4.150908	39991.851953
HLA	B*4601	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.399213	0.248296	-4.150918	25073.404660
HLA	B*5701	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.414196	0.263202	-4.150994	25953.502515
HLA	A*3201	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.577177	0.426183	-4.150994	37772.645328
HLA	B*3501	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.441473	0.290447	-4.151026	27635.892620
HLA	B*1501	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.372333	0.221286	-4.151047	23568.549323
HLA	A*0216	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.441586	0.290447	-4.151139	27643.069893

HLA A*0202	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.475783	0.324299	-4.151484	29907.700716
HLA A*2902	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.463866	0.312328	-4.151538	29098.221007
HLA B*1501	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.374821	0.223276	-4.151545	23703.962779
HLA B*1517	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.442033	0.290447	-4.151586	27671.498231
HLA A*0101	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.374863	0.223276	-4.151587	23706.271136
HLA B*3901	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.477082	0.325463	-4.151619	29997.308619
HLA A*0202	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.586900	0.435191	-4.151708	38627.764032
HLA B*5701	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.410883	0.259153	-4.151730	25756.283802
HLA A*6802	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.373040	0.221286	-4.151754	23606.959062
HLA A*0212	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.363156	0.211378	-4.151778	23075.746720
HLA B*7301	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.485968	0.334125	-4.151843	30617.381350
HLA B*4403	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.587139	0.435191	-4.151948	38649.085050
HLA B*4001	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.411151	0.259153	-4.151998	25772.173306
HLA B*1502	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.477463	0.325463	-4.151999	30023.609845
HLA B*4002	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.581150	0.429083	-4.152067	38119.779508
HLA A*2902	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.465929	0.313851	-4.152078	29236.762911
HLA B*1509	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.486285	0.334125	-4.152160	30639.750464
HLA A*6802	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.442611	0.290447	-4.152164	27708.348882
HLA B*1502	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.288184	0.135996	-4.152188	19417.070035
HLA B*1509	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.481457	0.329236	-4.152221	30301.004947
HLA A*2902	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.460100	0.307875	-4.152225	28846.970715
HLA B*4601	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.375540	0.223225	-4.152315	23743.235435
HLA A*8001	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.464663	0.312328	-4.152334	29151.634724
HLA B*4402	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.422248	0.269799	-4.152449	26439.160471
HLA A*0101	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.362890	0.210423	-4.152467	23061.644424
HLA B*5101	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.332152	0.179592	-4.152560	21485.821303
HLA B*3801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.556518	0.403854	-4.152664	36017.899270
HLA A*2603	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.640433	0.487735	-4.152697	43695.084697
HLA B*3501	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.294621	0.141914	-4.152707	19707.034913
HLA A*2602	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.634040	0.481266	-4.152774	43056.590522
HLA A*0301	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.325334	0.172544	-4.152790	21151.138737
HLA B*3501	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.456254	0.303321	-4.152933	28592.630154
HLA B*1517	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.470419	0.317460	-4.152959	29540.589100
HLA B*4501	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.619261	0.466242	-4.153019	41616.099782
HLA A*2601	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.399432	0.246391	-4.153041	25086.022758
HLA A*3201	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.367787	0.214737	-4.153049	23323.117403
HLA B*0702	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.421639	0.268569	-4.153071	26402.140884
HLA A*0203	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.433706	0.280603	-4.153103	27146.015900
HLA A*0219	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.376386	0.223276	-4.153109	23789.521871
HLA A*6901	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.323825	0.170651	-4.153174	21077.805107
HLA A*0206	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.477696	0.324517	-4.153179	30039.694168
HLA A*3002	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.335592	0.182373	-4.153219	21656.666338
HLA A*2601	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.322651	0.169330	-4.153321	21020.867853
HLA B*5101	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.482578	0.329236	-4.153342	30379.298184
HLA A*0211	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.510050	0.356622	-4.153428	32363.111149
HLA A*2301	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.526917	0.373369	-4.153548	33644.743185
HLA B*2705	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.413785	0.260101	-4.153684	25928.943167
HLA A*2501	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.370256	0.216497	-4.153759	23456.105546
HLA A*0219	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.377001	0.223225	-4.153776	23823.264832
HLA A*3001	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.293686	0.139887	-4.153799	19664.648637
HLA B*1801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.333517	0.179592	-4.153925	21553.460612
HLA B*0802	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.479408	0.325463	-4.153945	30158.398910
HLA A*0250	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.539259	0.385288	-4.153971	34614.579675
HLA A*0250	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.563055	0.409024	-4.154030	36564.079660
HLA A*3101	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.402331	0.248296	-4.154035	25254.052351
HLA A*2402	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.557984	0.403854	-4.154130	36139.692902
HLA B*5401	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.396396	0.242192	-4.154204	24911.293429
HLA B*4001	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.417593	0.263371	-4.154222	26157.325153
HLA B*4002	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.580410	0.426183	-4.154227	38054.874336
HLA B*1801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.479784	0.325463	-4.154321	30184.514786
HLA B*4002	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.645214	0.490880	-4.154334	44178.787004
HLA A*3201	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.623432	0.469073	-4.154359	42017.645442
HLA B*5701	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.377732	0.223276	-4.154456	23863.380629
HLA A*8001	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.457791	0.303321	-4.154470	28693.971981
HLA A*3301	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.642329	0.487735	-4.154593	43886.264869

HLA A*2601	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.296090	0.141319	-4.154771	19773.780735
HLA B*4801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.436368	0.281512	-4.154856	27312.915785
HLA A*6801	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.623429	0.468482	-4.154947	42017.418131
HLA A*0201	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.395980	0.240938	-4.155043	24887.451028
HLA A*2902	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.378329	0.223276	-4.155052	23896.194123
HLA B*0801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.255709	0.100651	-4.155058	18018.105081
HLA A*0212	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.424491	0.269402	-4.155090	26576.110384
HLA A*0250	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.583655	0.428564	-4.155091	38340.249166
HLA A*2403	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.387499	0.232368	-4.155131	24406.121985
HLA B*5801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.350389	0.195249	-4.155140	22407.255280
HLA B*0702	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.420187	0.264968	-4.155220	26314.017697
HLA A*2402	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.528623	0.373369	-4.155254	33777.145430
HLA A*2603	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.623796	0.468482	-4.155314	42052.893392
HLA B*5301	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.583979	0.428564	-4.155415	38368.883330
HLA B*5101	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.480980	0.325463	-4.155517	30267.746422
HLA A*2501	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.479859	0.324299	-4.155560	30189.740675
HLA A*2501	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.423190	0.267585	-4.155605	26496.578933
HLA A*2403	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.425093	0.269282	-4.155811	26612.941979
HLA A*0202	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.422027	0.266144	-4.155883	26425.718794
HLA A*2301	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.506449	0.350532	-4.155917	32095.822110
HLA A*0219	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.449354	0.293372	-4.155982	28141.916444
HLA B*3801	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.558699	0.402654	-4.156045	36199.177369
HLA B*4402	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.379332	0.223276	-4.156056	23951.458679
HLA A*2403	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.428972	0.272858	-4.156113	26851.706211
HLA A*0216	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.452006	0.295880	-4.156126	28314.326637
HLA B*4002	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.592207	0.436027	-4.156180	39102.727943
HLA A*2603	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.588737	0.432298	-4.156439	38791.526230
HLA B*5401	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.480888	0.324299	-4.156589	30261.361035
HLA B*4002	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.644384	0.487735	-4.156649	44094.499685
HLA A*8001	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.424235	0.267585	-4.156650	26560.443658
HLA B*3801	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.570848	0.414162	-4.156685	37226.129876
HLA A*2902	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.425990	0.269282	-4.156709	26667.996557
HLA A*0203	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.450160	0.293372	-4.156788	28194.184838
HLA A*6802	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.421827	0.264968	-4.156860	26413.569970
HLA A*3001	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.296499	0.139599	-4.156900	19792.402968
HLA B*4501	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.620135	0.463212	-4.156923	41699.935630
HLA A*6901	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.343801	0.186843	-4.156958	22069.917313
HLA A*3001	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.257654	0.100651	-4.157003	18098.996204
HLA A*0250	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.559732	0.402654	-4.157078	36285.446760
HLA A*1101	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.420326	0.263202	-4.157124	26322.418037
HLA B*0802	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.474634	0.317460	-4.157174	29828.686373
HLA A*0206	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.510541	0.353175	-4.157367	32399.723740
HLA A*2403	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.378730	0.221286	-4.157445	23918.310506
HLA A*2501	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.508131	0.350532	-4.157599	32220.385747
HLA B*1801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.460970	0.303321	-4.157649	28904.770341
HLA A*2602	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.586782	0.429083	-4.157699	38617.316849
HLA A*3201	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.586799	0.429083	-4.157715	38618.779284
HLA A*2402	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.566790	0.409024	-4.157766	36879.950341
HLA B*5701	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.382499	0.224721	-4.157778	24126.763856
HLA A*3101	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.381007	0.223225	-4.157782	24044.023875
HLA A*3201	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.607312	0.449508	-4.157804	40486.654861
HLA A*3101	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.430675	0.272858	-4.157817	26957.229964
HLA A*6801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.149623	-0.008210	-4.157833	14113.113008
HLA A*6801	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.607347	0.449508	-4.157839	40489.940419
HLA B*0803	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.492225	0.334125	-4.158100	31061.664325
HLA A*3002	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.454022	0.295880	-4.158142	28446.058311
HLA A*0201	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.330742	0.172544	-4.158199	21416.192822
HLA B*4501	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.623634	0.465424	-4.158210	42037.198719
HLA A*6901	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.349599	0.191384	-4.158215	22366.562098
HLA B*3901	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.487460	0.329236	-4.158224	30722.741483
HLA A*3301	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.649203	0.490880	-4.158324	44586.482656
HLA B*7301	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.593518	0.435191	-4.158327	39220.946401
HLA B*4601	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.376837	0.218420	-4.158417	23814.244854
HLA B*1501	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.209370	0.050897	-4.158474	16194.599892
HLA B*2705	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.417765	0.259153	-4.158612	26167.657294

HLA A*8001	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.439385	0.280603	-4.158782	27503.299895
HLA A*3201	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.609856	0.451064	-4.158793	40724.558774
HLA B*5401	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.318887	0.160089	-4.158798	20839.474679
HLA A*8001	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.400992	0.242192	-4.158800	25176.297970
HLA B*7301	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.623798	0.464928	-4.158870	42053.120895
HLA B*5701	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.401711	0.242669	-4.159042	25218.009987
HLA B*1509	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.509688	0.350532	-4.159156	32336.159928
HLA B*4403	1:103-111	9	IVHTEGPMT	0.780042	-0.284364	-4.654842	0.495678	-4.159164	45169.156137
HLA A*2601	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.380481	0.221286	-4.159195	24014.904609
HLA B*0802	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.434345	0.275124	-4.159222	27185.990391
HLA A*1101	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.467104	0.307875	-4.159229	29315.953789
HLA A*8001	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.314514	0.155271	-4.159243	20630.719555
HLA B*1502	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.509970	0.350532	-4.159438	32357.158948
HLA A*2601	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.391883	0.232368	-4.159515	24653.745963
HLA B*0803	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.510128	0.350532	-4.159596	32368.889333
HLA B*4402	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.434853	0.275124	-4.159729	27217.776769
HLA A*2902	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.333508	0.173777	-4.159731	21552.994210
HLA B*4002	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.626014	0.466242	-4.159772	42268.204121
HLA B*4001	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.374541	0.214737	-4.159804	23688.707629
HLA B*5101	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.484117	0.324299	-4.159817	30487.137491
HLA A*0211	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.463164	0.303321	-4.159843	29051.191027
HLA B*1502	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.522636	0.362756	-4.159880	33314.742127
HLA B*1502	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.589035	0.429083	-4.159952	38818.187336
HLA A*6801	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.589047	0.429083	-4.159964	38819.237361
HLA A*0101	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.384686	0.224721	-4.159965	24248.587410
HLA B*1502	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.545365	0.385288	-4.160077	35104.708722
HLA A*3301	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.582884	0.422686	-4.160198	38272.276879
HLA B*3801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.531567	0.371335	-4.160231	34006.884661
HLA A*8001	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.423761	0.263202	-4.160559	26531.434323
HLA B*5401	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.545946	0.385288	-4.160658	35151.648484
HLA B*5101	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.451130	0.290447	-4.160683	28257.249086
HLA B*4801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.401645	0.240938	-4.160707	25214.190330
HLA A*6802	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.330089	0.169330	-4.160759	21384.008165
HLA B*4001	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.389625	0.228841	-4.160784	24525.906119
HLA A*0101	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.382187	0.221286	-4.160901	24109.410525
HLA B*1801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.347783	0.186843	-4.160940	22273.223916
HLA B*2705	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.430483	0.269402	-4.161081	26945.274094
HLA A*0250	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.509545	0.348457	-4.161088	32325.490651
HLA A*6801	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.623601	0.462438	-4.161163	42034.015007
HLA B*1503	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.420321	0.259153	-4.161168	26322.133236
HLA A*6801	1:465-473	9	GKVIGTNPP	0.458143	0.041305	-4.660690	0.499448	-4.161241	45781.481790
HLA A*3001	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.301909	0.140490	-4.161419	20040.538564
HLA B*3501	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.297422	0.135996	-4.161426	19834.528092
HLA B*3901	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.464766	0.303321	-4.161445	29158.574663
HLA A*0219	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.403576	0.242067	-4.161509	25326.565719
HLA A*0216	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.473856	0.312328	-4.161528	29775.320736
HLA A*6901	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.330944	0.169330	-4.161614	21426.159034
HLA A*2601	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.386362	0.224721	-4.161640	24342.300919
HLA A*0212	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.442343	0.280603	-4.161740	27691.265653
HLA A*0206	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.529445	0.367626	-4.161819	33841.161731
HLA A*3101	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.416719	0.254868	-4.161851	26104.737026
HLA A*0201	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.385145	0.223225	-4.161920	24274.181430
HLA A*6801	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.565945	0.403854	-4.162090	36808.194319
HLA A*2403	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.385328	0.223225	-4.162103	24284.426601
HLA A*3301	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.641903	0.479739	-4.162164	43843.312913
HLA A*2603	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.547560	0.385288	-4.162272	35282.535961
HLA B*5401	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.533656	0.371335	-4.162320	34170.831007
HLA B*4801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.430901	0.268569	-4.162332	26971.233820
HLA B*1501	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.373728	0.211378	-4.162350	23644.408066
HLA B*4402	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.435212	0.272858	-4.162354	27240.314604
HLA A*3201	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.421548	0.259153	-4.162394	26396.570998
HLA A*6901	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.380814	0.218420	-4.162395	24033.360049
HLA A*3101	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.334957	0.172544	-4.162414	21625.056185
HLA A*3301	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.635334	0.472905	-4.162429	43185.127192
HLA B*1503	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.443952	0.281512	-4.162440	27794.073601

HLA B*7301	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.585206	0.422686	-4.162520	38477.388739
HLA A*3201	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.385847	0.223225	-4.162622	24313.478073
HLA A*3002	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.332025	0.169330	-4.162695	21479.545481
HLA A*6801	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.635614	0.472905	-4.162708	43212.937726
HLA B*1509	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.525482	0.362756	-4.162725	33533.716027
HLA A*0219	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.448562	0.285730	-4.162832	28090.656739
HLA B*4501	1:219-227	9	DSPVSVAYQ	0.680513	-0.186467	-4.656994	0.494046	-4.162948	45393.545531
HLA B*7301	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.592057	0.429083	-4.162973	39089.191635
HLA A*0250	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.598170	0.435191	-4.162979	39643.322847
HLA A*0301	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.358269	0.195249	-4.163020	22817.540743
HLA A*2403	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.405244	0.242192	-4.163052	25424.032663
HLA B*1501	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.418080	0.254868	-4.163211	26186.633764
HLA B*4001	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.405409	0.242192	-4.163217	25433.662370
HLA A*0206	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.453674	0.290447	-4.163227	28423.291703
HLA A*2602	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.625668	0.462438	-4.163231	42234.603538
HLA A*2601	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.386514	0.223276	-4.163238	24350.862219
HLA A*2902	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.345664	0.182373	-4.163291	22164.801571
HLA A*3301	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.249361	0.086012	-4.163349	17756.640697
HLA B*5801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.350227	0.186843	-4.163384	22398.892608
HLA A*0201	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.380448	0.216943	-4.163505	24013.085827
HLA A*0101	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.380011	0.216497	-4.163514	23988.935067
HLA B*7301	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.543871	0.380356	-4.163515	34984.131872
HLA A*3201	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.598755	0.435191	-4.163564	39696.760861
HLA A*0201	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.392954	0.229302	-4.163652	24714.639600
HLA A*0211	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.531431	0.367626	-4.163804	33996.215874
HLA A*0212	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.422964	0.259153	-4.163811	26482.821525
HLA B*7301	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.570876	0.407006	-4.163871	37228.546625
HLA A*2902	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.436836	0.272858	-4.163977	27342.335828
HLA B*4601	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.418874	0.254868	-4.164006	26234.560943
HLA B*4501	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.654894	0.490880	-4.164014	45174.532380
HLA A*0216	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.424118	0.260101	-4.164017	26553.260177
HLA B*4402	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.424120	0.260101	-4.164019	26553.403828
HLA A*3301	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.645331	0.481266	-4.164065	44190.738738
HLA A*2403	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.444720	0.280603	-4.164117	27843.285772
HLA A*2501	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.467473	0.303321	-4.164152	29340.863948
HLA A*0250	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.590337	0.426183	-4.164153	38934.703010
HLA A*0216	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.423357	0.259153	-4.164203	26506.758281
HLA A*2402	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.489668	0.325463	-4.164205	30879.373634
HLA B*0803	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.520846	0.356622	-4.164224	33177.690263
HLA A*2501	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.454710	0.290447	-4.164263	28491.183842
HLA B*0803	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.499219	0.334871	-4.164348	31565.969964
HLA A*0206	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.306301	0.141914	-4.164387	20244.197982
HLA A*2501	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.351305	0.186843	-4.164462	22454.581287
HLA A*1101	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.375890	0.211378	-4.164512	23762.381943
HLA B*0803	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.427995	0.263371	-4.164623	26791.344022
HLA A*3301	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.549949	0.385288	-4.164661	35477.190427
HLA A*3001	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.215643	0.050897	-4.164747	16430.218826
HLA B*0802	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.450543	0.285730	-4.164812	28219.057772
HLA B*7301	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.578994	0.414162	-4.164831	37930.935391
HLA A*6801	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.623441	0.458556	-4.164885	42018.554695
HLA B*1801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.478767	0.313851	-4.164916	30113.890854
HLA B*4601	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.407131	0.242067	-4.165064	25534.718489
HLA A*0250	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.587764	0.422686	-4.165078	38704.742299
HLA A*3301	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.593661	0.428564	-4.165097	39233.891577
HLA B*5701	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.407204	0.242067	-4.165137	25539.001188
HLA A*3002	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.494403	0.329236	-4.165167	31217.828806
HLA A*0201	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.307142	0.141914	-4.165228	20283.443728
HLA A*6801	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.601255	0.436027	-4.165228	39925.919160
HLA B*4403	1:273-281	9	LVRVHNGEP	0.441596	0.066842	-4.673697	0.508438	-4.165259	47173.336482
HLA A*3101	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.388547	0.223276	-4.165270	24465.080433
HLA A*2403	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.430264	0.264968	-4.165297	26931.720806
HLA A*2403	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.322639	0.157340	-4.165299	21020.299258
HLA A*2601	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.394620	0.229302	-4.165318	24809.617386
HLA A*2902	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.455873	0.290447	-4.165426	28567.582492
HLA A*0203	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.428629	0.263202	-4.165427	26830.505931

HLA B*4002	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.614962	0.449508	-4.165454	41206.129075
HLA B*5701	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.420333	0.254868	-4.165465	26322.845244
HLA B*3901	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.499640	0.334125	-4.165515	31596.552312
HLA B*1502	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.623622	0.458095	-4.165527	42036.061651
HLA A*2301	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.514016	0.348457	-4.165559	32660.001134
HLA B*4402	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.434244	0.268569	-4.165676	27179.666979
HLA A*2403	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.337279	0.171585	-4.165694	21740.950923
HLA A*3301	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.598050	0.432298	-4.165752	39632.386591
HLA B*4002	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.618437	0.452683	-4.165754	41537.151154
HLA B*3901	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.398123	0.232368	-4.165755	25010.544615
HLA B*5101	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.516326	0.350532	-4.165794	32834.147078
HLA B*5801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.357212	0.191384	-4.165827	22762.060139
HLA A*3101	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.387149	0.221286	-4.165863	24386.456784
HLA A*2603	1:474-482	9	ANQTSAITN	1.122561	-0.649656	-4.638821	0.472905	-4.165916	43533.224732
HLA B*3801	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.539440	0.373369	-4.166071	34629.001779
HLA B*1509	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.514648	0.348457	-4.166191	32707.564533
HLA B*1801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.435659	0.269402	-4.166257	27268.328745
HLA B*1517	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.376787	0.210423	-4.166364	23811.539527
HLA A*0212	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.412807	0.246391	-4.166416	25870.655334
HLA B*4501	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.595611	0.429083	-4.166528	39410.456019
HLA A*0201	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.387858	0.221286	-4.166572	24426.331613
HLA A*2301	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.501479	0.334871	-4.166608	31730.677386
HLA A*0250	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.348988	0.182373	-4.166616	22335.124051
HLA A*3101	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.377058	0.210423	-4.166634	23826.358182
HLA B*5401	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.529410	0.362756	-4.166654	33838.415688
HLA A*0301	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.349080	0.182373	-4.166707	22339.836940
HLA A*2301	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.548819	0.381799	-4.167021	35384.993227
HLA B*4001	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.407967	0.240938	-4.167030	25583.943714
HLA A*6801	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.654894	0.487735	-4.167158	45174.532380
HLA B*4403	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.569932	0.402654	-4.167277	37147.670872
HLA A*2603	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.658176	0.490880	-4.167296	45517.237495
HLA A*0203	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.384240	0.216943	-4.167298	24223.675603
HLA A*1101	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.341096	0.173777	-4.167320	21932.919710
HLA A*3201	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.603348	0.436027	-4.167321	40118.835098
HLA A*6802	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.264346	0.096922	-4.167424	18380.013339
HLA B*1517	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.475330	0.307875	-4.167455	29876.490124
HLA A*3301	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.571341	0.403854	-4.167487	37268.445648
HLA A*6802	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.268213	0.100651	-4.167562	18544.412305
HLA B*2705	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.385995	0.218420	-4.167575	24321.766078
HLA A*2402	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.562698	0.395099	-4.167599	36534.025261
HLA A*0211	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.475543	0.307875	-4.167668	29891.201939
HLA B*4001	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.409746	0.242067	-4.167679	25688.932115
HLA B*1509	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.303827	0.135996	-4.167830	20129.202469
HLA A*3002	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.492133	0.324299	-4.167834	31055.111450
HLA A*2403	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.410505	0.242669	-4.167836	25733.860048
HLA A*2301	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.530594	0.362756	-4.167838	33930.804872
HLA A*0201	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.392654	0.224721	-4.167932	24697.531482
HLA A*3002	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.535617	0.367626	-4.167991	34325.538611
HLA A*0216	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.434162	0.266144	-4.168018	27174.521102
HLA B*4402	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.386439	0.218420	-4.168020	24346.647049
HLA B*4601	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.392846	0.224721	-4.168125	24708.490007
HLA A*0212	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.409098	0.240938	-4.168160	25650.603837
HLA B*1502	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.619313	0.451064	-4.168250	41621.053124
HLA A*2602	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.571015	0.402654	-4.168361	37240.431258
HLA B*4801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.433368	0.264968	-4.168400	27124.876736
HLA A*2402	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.577234	0.408742	-4.168492	37777.549946
HLA B*0702	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.325829	0.157255	-4.168575	21175.296264
HLA A*2403	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.397545	0.228841	-4.168705	24977.281902
HLA B*1502	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.611712	0.442960	-4.168752	40898.980356
HLA B*0801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.410841	0.242067	-4.168774	25753.775828
HLA A*3301	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.604857	0.436027	-4.168830	40258.416036
HLA B*0803	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.301002	0.132130	-4.168872	19998.733231
HLA B*4402	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.449497	0.280603	-4.168894	28151.204901
HLA A*2602	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.433983	0.264968	-4.169016	27163.350551
HLA A*0212	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.401401	0.232368	-4.169032	25200.008099

HLA B*0802	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.476944	0.307875	-4.169069	29987.735502
HLA A*0212	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.411778	0.242669	-4.169109	25809.426573
HLA B*4002	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.604464	0.435191	-4.169273	40222.060935
HLA B*4403	1:560-568	9	QFVMPDLSG	0.897973	-0.431731	-4.635550	0.466242	-4.169308	43206.626203
HLA A*0250	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.442289	0.272858	-4.169430	27687.820314
HLA A*2402	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.565181	0.395731	-4.169450	36743.534497
HLA A*2902	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.417840	0.248296	-4.169544	26172.187738
HLA A*3001	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.313199	0.143550	-4.169649	20568.312588
HLA A*1101	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.435837	0.266144	-4.169693	27279.542466
HLA A*3001	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.298700	0.128996	-4.169704	19892.986685
HLA B*5801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.339062	0.169330	-4.169732	21830.405097
HLA B*4001	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.380204	0.210423	-4.169780	23999.579181
HLA A*3101	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.343559	0.173777	-4.169782	22057.622971
HLA B*3501	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.393029	0.223225	-4.169804	24718.918482
HLA A*0216	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.433250	0.263202	-4.170048	27117.540600
HLA B*4801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.433419	0.263202	-4.170217	27128.105265
HLA B*0802	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.473563	0.303321	-4.170242	29755.192394
HLA B*1502	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.550132	0.379878	-4.170255	35492.163945
HLA B*4403	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.592294	0.421976	-4.170318	39110.555759
HLA A*3301	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.516610	0.346054	-4.170556	32855.647234
HLA B*0802	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.461021	0.290447	-4.170574	28908.210721
HLA B*1517	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.484427	0.313851	-4.170576	30508.916294
HLA A*6802	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.417008	0.246391	-4.170617	26122.113326
HLA B*0801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.344407	0.173777	-4.170630	22100.742939
HLA A*2902	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.387647	0.216943	-4.170704	24414.441571
HLA B*3501	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.456531	0.285730	-4.170801	28610.888571
HLA B*7301	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.574666	0.403854	-4.170811	37554.830081
HLA B*0702	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.419165	0.248296	-4.170869	26252.165679
HLA A*0212	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.387837	0.216943	-4.170895	24425.142348
HLA B*1509	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.474228	0.303321	-4.170907	29800.782443
HLA B*3801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.496374	0.325463	-4.170910	31359.845371
HLA A*3001	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.307022	0.135996	-4.171026	20277.848210
HLA A*3301	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.640104	0.469073	-4.171031	43662.003247
HLA B*1503	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.500300	0.329236	-4.171064	31644.621250
HLA A*6802	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.419395	0.248296	-4.171100	26266.087457
HLA B*5801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.343688	0.172544	-4.171144	22064.187059
HLA B*0801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.343749	0.172544	-4.171205	22067.290762
HLA B*2705	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.467167	0.295880	-4.171287	29320.236196
HLA A*2402	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.578308	0.407006	-4.171302	37871.063664
HLA A*3101	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.400658	0.229302	-4.171356	25156.964858
HLA B*4403	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.597576	0.426183	-4.171392	39589.100070
HLA A*2902	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.403842	0.232368	-4.171474	25342.053024
HLA B*1517	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.389916	0.218420	-4.171497	24542.364260
HLA A*2402	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.495805	0.324299	-4.171506	31318.816139
HLA B*4402	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.400938	0.229302	-4.171636	25173.165543
HLA A*0203	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.341282	0.169330	-4.171952	21942.295432
HLA A*2603	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.635283	0.463212	-4.172070	43179.987709
HLA B*3901	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.284479	0.112336	-4.172143	19252.119965
HLA A*3001	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.294509	0.122274	-4.172235	19701.918159
HLA B*1509	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.552254	0.379878	-4.172376	35665.971967
HLA A*8001	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.415103	0.242669	-4.172434	26007.755692
HLA A*8001	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.442479	0.269799	-4.172681	27699.955804
HLA A*2403	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.346479	0.173777	-4.172702	22206.449114
HLA B*4501	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.660650	0.487735	-4.172915	45777.271547
HLA B*2705	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.476244	0.303321	-4.172923	29939.429814
HLA B*1517	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.389501	0.216497	-4.173003	24518.874958
HLA A*2402	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.558351	0.385288	-4.173063	36170.205606
HLA A*6901	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.352416	0.179347	-4.173070	22512.113389
HLA B*4601	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.396368	0.223276	-4.173092	24909.676274
HLA A*0206	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.415204	0.242067	-4.173137	26013.806456
HLA B*5301	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.587355	0.414162	-4.173193	38668.325866
HLA B*4001	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.433323	0.260101	-4.173222	27122.088771
HLA B*1501	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.419792	0.246391	-4.173401	26290.112768
HLA A*2301	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.530120	0.356622	-4.173497	33893.745622
HLA A*1101	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.485867	0.312328	-4.173539	30610.259803

HLA A*3002	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.421872	0.248296	-4.173576	26416.285105
HLA B*4402	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.368952	0.195249	-4.173703	23385.784481
HLA B*1801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.530498	0.356622	-4.173876	33923.279669
HLA A*0203	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.392332	0.218420	-4.173912	24679.233569
HLA A*2402	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.576637	0.402654	-4.173983	37725.675016
HLA A*0301	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.365409	0.191384	-4.174025	23195.776719
HLA B*1501	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.296501	0.122446	-4.174055	19792.510043
HLA B*5801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.356476	0.182373	-4.174103	22723.549863
HLA A*0206	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.433474	0.259153	-4.174320	27131.480956
HLA A*2501	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.482204	0.307875	-4.174329	30353.177987
HLA B*1509	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.530970	0.356622	-4.174348	33960.187489
HLA B*4001	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.391296	0.216943	-4.174353	24620.424993
HLA B*4001	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.385737	0.211378	-4.174359	24307.296797
HLA B*7301	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.583162	0.408742	-4.174419	38296.716434
HLA A*3101	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.322606	0.148101	-4.174505	21018.707274
HLA B*4403	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.632653	0.458095	-4.174559	42919.380100
HLA A*8001	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.456071	0.281512	-4.174559	28580.567429
HLA B*4801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.429505	0.254868	-4.174637	26884.701566
HLA A*8001	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.306855	0.132177	-4.174678	20270.060941
HLA B*4601	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.403990	0.229302	-4.174688	25350.691651
HLA A*0202	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.535178	0.360485	-4.174693	34290.830764
HLA A*2501	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.403539	0.228841	-4.174698	25324.373591
HLA A*6801	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.665579	0.490880	-4.174699	46299.800903
HLA A*2301	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.542342	0.367626	-4.174715	34861.140138
HLA A*3001	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.271700	0.096922	-4.174777	18693.891181
HLA A*3002	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.527960	0.353175	-4.174786	33725.654684
HLA A*0216	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.444079	0.269282	-4.174798	27802.194382
HLA A*3301	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.637468	0.462438	-4.175030	43397.782154
HLA A*2902	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.444486	0.269402	-4.175084	27828.226936
HLA B*1502	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.570265	0.395099	-4.175166	37176.218835
HLA A*6901	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.399944	0.224721	-4.175223	25115.625558
HLA A*2403	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.385772	0.210423	-4.175349	24309.269374
HLA B*4402	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.434533	0.259153	-4.175380	27197.758793
HLA B*3801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.557249	0.381799	-4.175451	36078.549511
HLA A*3101	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.347041	0.171585	-4.175456	22235.179812
HLA A*6802	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.307586	0.132130	-4.175456	20304.193528
HLA B*4002	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.641062	0.465424	-4.175638	43758.481976
HLA B*0802	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.489513	0.313851	-4.175663	30868.350039
HLA B*0803	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.443261	0.267585	-4.175676	27749.902058
HLA A*0211	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.457217	0.281512	-4.175705	28656.120554
HLA A*3101	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.355334	0.179592	-4.175742	22663.883438
HLA A*2602	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.457302	0.281512	-4.175790	28661.702049
HLA B*0802	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.471693	0.295880	-4.175812	29627.333944
HLA A*0212	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.404706	0.228841	-4.175866	25392.555231
HLA B*3501	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.439272	0.263371	-4.175901	27496.158912
HLA A*2301	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.547264	0.371335	-4.175928	35258.493956
HLA B*2705	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.489828	0.313851	-4.175977	30890.735395
HLA A*2603	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.657384	0.481266	-4.176118	45434.329133
HLA B*4801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.405031	0.228841	-4.176190	25411.519495
HLA B*3501	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.445498	0.269282	-4.176217	27893.188667
HLA A*0201	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.387640	0.211378	-4.176262	24414.045336
HLA B*5801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.355856	0.179592	-4.176264	22691.119010
HLA B*5801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.352719	0.176401	-4.176318	22527.829529
HLA A*0250	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.571419	0.395099	-4.176320	37275.099641
HLA A*0212	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.399683	0.223276	-4.176407	25100.548210
HLA B*1517	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.435588	0.259153	-4.176435	27263.903545
HLA A*0203	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.431486	0.254868	-4.176618	27007.590236
HLA B*5801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.317966	0.141319	-4.176647	20795.327721
HLA B*5301	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.595287	0.418508	-4.176780	39381.044544
HLA B*1502	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.602979	0.426183	-4.176796	40084.774528
HLA B*4601	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.393335	0.216497	-4.176837	24736.309055
HLA A*3301	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.603090	0.426183	-4.176906	40094.967971
HLA A*2603	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.151892	-0.025025	-4.176917	14187.060527
HLA B*4002	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.631065	0.454147	-4.176918	42762.706934
HLA A*2603	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.572650	0.395731	-4.176919	37380.916332

HLA B*1503	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.490808	0.313851	-4.176957	30960.501203
HLA B*4501	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.629717	0.452683	-4.177034	42630.122872
HLA B*4402	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.241624	0.064589	-4.177035	17443.111335
HLA B*5401	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.391874	0.214737	-4.177136	24653.212473
HLA A*2602	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.168945	-0.008210	-4.177155	14755.196031
HLA B*3801	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.557068	0.379878	-4.177190	36063.523708
HLA A*2501	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.470614	0.293372	-4.177242	29553.856417
HLA A*0250	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.540067	0.362756	-4.177311	34679.057451
HLA A*3002	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.527845	0.350532	-4.177313	33716.715718
HLA B*1503	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.123060	-0.054260	-4.177319	13275.764556
HLA A*0219	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.393845	0.216497	-4.177347	24765.365197
HLA A*0301	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.357150	0.179592	-4.177558	22758.858718
HLA A*3301	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.572659	0.395099	-4.177560	37381.725247
HLA A*0201	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.396027	0.218420	-4.177608	24890.143941
HLA A*0206	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.485573	0.307875	-4.177698	30589.567037
HLA B*5301	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.600421	0.422686	-4.177735	39849.314591
HLA B*2705	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.441112	0.263371	-4.177740	27612.878113
HLA B*4601	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.410110	0.232368	-4.177742	25710.482161
HLA A*2602	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.613014	0.435191	-4.177823	41021.741685
HLA B*4402	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.441079	0.263202	-4.177877	27610.786835
HLA A*0301	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.338042	0.160089	-4.177953	21779.209790
HLA B*2705	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.446555	0.268569	-4.177987	27961.175965
HLA A*0202	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.495451	0.317460	-4.177990	31293.242456
HLA B*4801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.441410	0.263371	-4.178039	27631.856223
HLA B*5401	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.453327	0.275124	-4.178203	28400.543316
HLA A*3301	1:241-249	9	EGLSADLDA	0.887610	-0.438102	-4.627837	0.449508	-4.178329	42446.022154
HLA B*4402	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.420528	0.242192	-4.178336	26334.667403
HLA B*0802	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.490714	0.312328	-4.178386	30953.802213
HLA B*3801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.546051	0.367626	-4.178425	35160.207019
HLA B*4801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.447735	0.269282	-4.178453	28037.215136
HLA A*2601	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.264546	0.086012	-4.178534	18388.467159
HLA B*1503	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.443710	0.264968	-4.178743	27778.590541
HLA B*4403	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.641960	0.463212	-4.178747	43849.005782
HLA B*4002	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.611073	0.432298	-4.178776	40838.842179
HLA A*0216	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.459402	0.280603	-4.178799	28800.658433
HLA B*0702	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.400137	0.221286	-4.178851	25126.769595
HLA A*0212	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.442127	0.263202	-4.178924	27677.486868
HLA B*1517	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.351486	0.172544	-4.178942	22463.936949
HLA B*4801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.427250	0.248296	-4.178954	26745.437987
HLA B*4002	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.647554	0.468482	-4.179072	44417.475815
HLA B*4501	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.647671	0.468482	-4.179189	44429.492121
HLA B*5701	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.395745	0.216497	-4.179248	24873.990834
HLA A*0216	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.493172	0.313851	-4.179321	31129.458384
HLA A*3201	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.542118	0.362756	-4.179362	34843.228226
HLA A*6801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.359101	0.179592	-4.179508	22861.280503
HLA B*0702	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.461101	0.281512	-4.179589	28913.528478
HLA A*2601	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.402815	0.223225	-4.179590	25282.212094
HLA B*4403	1:385-393	9	RTLQKPDST	0.656751	-0.198195	-4.638208	0.458556	-4.179652	43471.800018
HLA B*1517	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.449060	0.269402	-4.179658	28122.892297
HLA B*5801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.353455	0.173777	-4.179678	22566.008112
HLA B*0702	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.394578	0.214737	-4.179841	24807.201593
HLA B*4402	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.421935	0.242067	-4.179868	26420.143934
HLA A*0301	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.366750	0.186843	-4.179907	23267.540340
HLA A*1101	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.445038	0.264968	-4.180070	27863.628126
HLA A*0203	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.404822	0.224721	-4.180100	25399.287298
HLA B*5101	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.497589	0.317460	-4.180128	31447.678894
HLA B*1517	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.280849	0.100651	-4.180197	19091.875995
HLA A*0219	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.439352	0.259153	-4.180199	27501.216917
HLA B*1501	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.367065	0.186843	-4.180222	23284.413680
HLA A*1101	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.439390	0.259153	-4.180236	27503.597476
HLA A*3201	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.242841	0.062590	-4.180250	17492.061114
HLA A*1101	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.494130	0.313851	-4.180279	31198.244293
HLA B*4801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.423002	0.242669	-4.180333	26485.113930
HLA B*5801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.350995	0.170651	-4.180344	22438.552074
HLA A*3201	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.623310	0.442960	-4.180349	42005.826942

HLA A*8001	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.428662	0.248296	-4.180366	26832.538109
HLA B*5301	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.584268	0.403854	-4.180414	38394.423109
HLA B*1501	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.409762	0.229302	-4.180461	25689.904953
HLA B*4501	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.589397	0.408742	-4.180655	38850.541133
HLA B*2705	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.423399	0.242669	-4.180730	26509.339582
HLA B*4002	1:170-178	9	VTQTAAVIG	1.041766	-0.578554	-4.643992	0.463212	-4.180780	44054.680434
HLA A*6801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.561140	0.380356	-4.180784	36403.221329
HLA B*4402	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.421761	0.240938	-4.180824	26409.569227
HLA A*2601	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.399244	0.218420	-4.180824	25075.168099
HLA A*2602	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.631906	0.451064	-4.180843	42845.607445
HLA A*0206	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.449455	0.268569	-4.180886	28148.463726
HLA B*4501	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.561267	0.380356	-4.180911	36413.857502
HLA B*3901	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.466904	0.285730	-4.181174	29302.476223
HLA A*2301	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.506641	0.325463	-4.181178	32110.063326
HLA B*4403	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.662478	0.481266	-4.181212	45970.349256
HLA B*1502	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.563012	0.381799	-4.181214	36560.519296
HLA B*1502	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.616444	0.435191	-4.181253	41347.032328
HLA B*3501	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.322578	0.141319	-4.181259	21017.342812
HLA A*0203	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.404537	0.223225	-4.181312	25382.666452
HLA A*0219	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.353864	0.172544	-4.181320	22587.259963
HLA B*5701	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.399777	0.218420	-4.181358	25105.980445
HLA B*0803	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.422304	0.240938	-4.181366	26442.593484
HLA A*8001	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.392834	0.211378	-4.181456	24707.821665
HLA A*6802	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.085313	-0.096147	-4.181460	12170.620359
HLA B*3501	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.423624	0.242067	-4.181557	26523.110766
HLA A*3301	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.639664	0.458095	-4.181570	43617.854949
HLA A*0211	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.440724	0.259153	-4.181571	27588.240980
HLA A*0250	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.590332	0.408739	-4.181593	38934.281747
HLA B*0801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.336910	0.155271	-4.181638	21722.493029
HLA B*4001	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.402996	0.221286	-4.181710	25292.745883
HLA A*0101	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.294062	0.112336	-4.181726	19681.677377
HLA A*0211	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.472179	0.290447	-4.181732	29660.530610
HLA A*0203	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.430032	0.248296	-4.181736	26917.300603
HLA A*2501	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.477649	0.295880	-4.181768	30036.444115
HLA B*5801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.361203	0.179347	-4.181857	22972.239819
HLA A*3002	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.475330	0.293372	-4.181958	29876.490124
HLA A*2602	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.590720	0.408739	-4.181981	38969.051238
HLA A*3101	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.410827	0.228841	-4.181986	25752.939892
HLA A*2601	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.373461	0.191384	-4.182076	23629.830409
HLA A*2602	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.489983	0.307875	-4.182108	30901.766984
HLA B*4001	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.244721	0.062590	-4.182130	17567.929260
HLA B*5401	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.535324	0.353175	-4.182149	34302.334288
HLA A*3001	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.301381	0.119114	-4.182266	20016.159558
HLA B*1509	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.452150	0.269799	-4.182351	28323.671998
HLA A*0219	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.442571	0.260101	-4.182470	27705.800714
HLA A*3002	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.564305	0.381799	-4.182506	36669.464893
HLA A*3101	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.351838	0.169330	-4.182508	22482.173458
HLA A*0202	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.516774	0.334125	-4.182650	32868.091769
HLA A*8001	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.452063	0.269402	-4.182661	28318.003132
HLA A*6802	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.424750	0.242067	-4.182683	26591.930210
HLA A*6901	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.377936	0.195249	-4.182687	23874.614820
HLA B*1801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.323233	0.140490	-4.182743	21049.089481
HLA B*3501	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.369591	0.186843	-4.182748	23420.221756
HLA A*8001	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.442850	0.260101	-4.182749	27723.642809
HLA B*3801	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.545565	0.362756	-4.182809	35120.855003
HLA A*2902	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.464350	0.281512	-4.182839	29130.667222
HLA B*3501	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.353492	0.170651	-4.182841	22567.961470
HLA B*3901	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.442000	0.259153	-4.182846	27669.402514
HLA B*4801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.397602	0.214737	-4.182864	24980.525097
HLA B*0801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.393340	0.210423	-4.182916	24736.576698
HLA A*2403	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.412399	0.229302	-4.183097	25846.314208
HLA B*4601	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.404422	0.221286	-4.183136	25375.938790
HLA A*6901	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.331276	0.148101	-4.183175	21442.509023
HLA B*0803	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.500688	0.317460	-4.183227	31672.880854
HLA B*0802	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.453094	0.269799	-4.183296	28385.336653

HLA A*2301	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.536508	0.353175	-4.183333	34395.990110
HLA A*3002	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.425474	0.242067	-4.183406	26636.275839
HLA B*1501	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.365872	0.182373	-4.183499	23220.510753
HLA B*0802	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.456447	0.272858	-4.183588	28605.316971
HLA A*0219	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.464303	0.280603	-4.183700	29127.515519
HLA B*1509	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.459059	0.275124	-4.183936	28777.919393
HLA B*3901	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.459092	0.275124	-4.183969	28780.099070
HLA A*2403	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.196072	0.012088	-4.183984	15706.236678
HLA A*1101	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.452596	0.268569	-4.184027	28352.800272
HLA B*7301	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.537215	0.353175	-4.184040	34452.045364
HLA A*2602	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.606821	0.422686	-4.184135	40440.903813
HLA B*4402	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.398938	0.214737	-4.184201	25057.539294
HLA B*4403	1:343-351	9	TVVVTIAIN	0.929296	-0.463872	-4.649654	0.465424	-4.184230	44632.818638
HLA A*1101	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.451844	0.267585	-4.184259	28303.759371
HLA A*1101	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.480167	0.295880	-4.184287	30211.143591
HLA A*0301	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.355877	0.171585	-4.184292	22692.223844
HLA B*4001	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.407526	0.223225	-4.184301	25557.936558
HLA A*0216	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.426564	0.242192	-4.184372	26703.221902
HLA B*0801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.407721	0.223276	-4.184444	25569.415180
HLA A*0301	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.363926	0.179347	-4.184580	23116.729683
HLA B*1501	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.355318	0.170651	-4.184667	22663.025191
HLA B*4403	1:490-498	9	SGPATKDIP	0.559394	-0.068514	-4.675595	0.490880	-4.184715	47379.991454
HLA A*6802	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.439615	0.254868	-4.184747	27517.885162
HLA A*2501	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.470494	0.285730	-4.184764	29545.703504
HLA B*5301	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.518941	0.334125	-4.184816	33032.444657
HLA B*0801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.433248	0.248296	-4.184952	27117.393897
HLA A*0212	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.247587	0.062590	-4.184996	17684.262211
HLA B*1801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.247599	0.062590	-4.185008	17684.740567
HLA B*0803	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.514249	0.329236	-4.185013	32677.497831
HLA A*2603	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.558433	0.373369	-4.185064	36177.054942
HLA B*5801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.342363	0.157255	-4.185108	21996.967909
HLA A*2301	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.545596	0.360485	-4.185111	35123.325089
HLA A*3101	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.402075	0.216943	-4.185132	25239.164984
HLA A*3301	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.399928	0.214737	-4.185190	25114.674467
HLA B*5701	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.414595	0.229302	-4.185293	25977.382441
HLA A*6802	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.408578	0.223225	-4.185353	25619.954672
HLA B*5701	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.431761	0.246391	-4.185370	27024.690292
HLA A*2602	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.594418	0.409024	-4.185394	39302.295962
HLA B*4402	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.433711	0.248296	-4.185415	27146.309616
HLA B*0803	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.493350	0.307875	-4.185475	31142.259942
HLA A*3301	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.628455	0.442960	-4.185495	42506.457374
HLA B*5801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.357087	0.171585	-4.185502	22755.534642
HLA A*0203	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.406823	0.221286	-4.185537	25516.628560
HLA A*0206	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.499409	0.313851	-4.185559	31579.805235
HLA B*0803	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.451715	0.266144	-4.185571	28295.339013
HLA A*6801	1:532-540	9	GEVTGTNPP	0.472046	0.007693	-4.665391	0.479739	-4.185652	46279.767096
HLA A*8001	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.454938	0.269282	-4.185657	28506.138778
HLA B*3901	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.481542	0.295880	-4.185661	30306.906824
HLA B*3801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.471467	0.285730	-4.185737	29611.951002
HLA A*3002	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.453341	0.267585	-4.185755	28401.465194
HLA A*0219	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.427990	0.242192	-4.185798	26791.054147
HLA A*2402	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.594557	0.408739	-4.185817	39314.842607
HLA B*1517	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.427980	0.242067	-4.185913	26790.474407
HLA B*4601	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.396359	0.210423	-4.185936	24909.137245
HLA B*3801	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.566320	0.380356	-4.185964	36840.068632
HLA B*4801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.445120	0.259153	-4.185967	27868.904495
HLA A*0202	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.581160	0.395099	-4.186061	38120.604412
HLA A*0202	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.138674	-0.047418	-4.186092	13761.767583
HLA B*2705	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.396641	0.210423	-4.186217	24925.313176
HLA B*3901	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.446356	0.260101	-4.186255	27948.321238
HLA B*4002	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.608238	0.421976	-4.186262	40573.044054
HLA B*1503	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.373141	0.186843	-4.186298	23612.451275
HLA B*4002	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.595196	0.408739	-4.186456	39372.736584
HLA B*3501	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.359030	0.172544	-4.186486	22857.570494
HLA B*5301	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.589627	0.403047	-4.186580	38871.143952

HLA B*5101	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.409859	0.223276	-4.186582	25695.603746
HLA A*8001	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.445780	0.259153	-4.186627	27911.302433
HLA B*4001	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.433102	0.246391	-4.186711	27108.299893
HLA B*1503	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.459640	0.272858	-4.186781	28816.399379
HLA A*2403	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.378185	0.191384	-4.186801	23888.309602
HLA B*3901	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.456715	0.269799	-4.186916	28622.964094
HLA B*4002	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.651851	0.464928	-4.186923	44859.154379
HLA B*5701	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.415775	0.228841	-4.186934	26048.026774
HLA B*4402	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.451903	0.264968	-4.186935	28307.587635
HLA A*0206	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.490263	0.303321	-4.186942	30921.667230
HLA B*2705	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.456874	0.269799	-4.187076	28633.495631
HLA A*8001	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.411832	0.224721	-4.187111	25812.638174
HLA B*3501	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.453308	0.266144	-4.187164	28399.314192
HLA A*6801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.533343	0.346054	-4.187289	34146.253415
HLA B*2705	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.468826	0.281512	-4.187314	29432.435500
HLA A*2501	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.499680	0.312328	-4.187351	31599.458321
HLA B*1501	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.329389	0.141914	-4.187475	21349.561775
HLA A*0211	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.483447	0.295880	-4.187567	30440.168079
HLA A*0250	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.462692	0.275124	-4.187568	29019.618288
HLA B*3501	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.446816	0.259153	-4.187663	27977.971629
HLA B*5101	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.500072	0.312328	-4.187744	31628.019799
HLA A*2402	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.536280	0.348457	-4.187823	34377.945231
HLA A*2602	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.522735	0.334871	-4.187864	33322.312607
HLA A*0301	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.336045	0.148101	-4.187944	21679.290058
HLA B*2705	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.457255	0.269282	-4.187973	28658.601084
HLA B*4601	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.399373	0.211378	-4.187995	25082.630172
HLA B*0801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.367608	0.179592	-4.188016	23313.530038
HLA B*4402	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.405214	0.216943	-4.188271	25422.244691
HLA A*2603	1:371-379	9	ADAIATLQN	1.071952	-0.609514	-4.650770	0.462438	-4.188332	44747.658963
HLA B*7301	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.523301	0.334871	-4.188430	33365.786015
HLA B*2705	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.404979	0.216497	-4.188482	25408.495258
HLA A*0201	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.399000	0.210423	-4.188576	25061.064063
HLA A*2603	1:142-150	9	ANIMISATN	1.034069	-0.605505	-4.617177	0.428564	-4.188613	41416.880311
HLA A*2301	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.513013	0.324299	-4.188714	32584.642864
HLA A*0206	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.360320	0.171585	-4.188735	22925.559058
HLA A*0216	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.270960	0.082090	-4.188870	18662.061768
HLA B*5301	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.591591	0.402654	-4.188937	39047.343350
HLA A*3002	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.464144	0.275124	-4.189020	29116.802279
HLA A*0212	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.437327	0.248296	-4.189031	27373.268384
HLA A*0211	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.514568	0.325463	-4.189105	32701.548980
HLA A*3001	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.271258	0.082090	-4.189168	18674.888053
HLA A*0301	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.311641	0.122446	-4.189195	20494.671205
HLA A*2602	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.405712	0.216497	-4.189215	25451.418100
HLA A*2403	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.444093	0.254868	-4.189225	27803.096837
HLA B*4001	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.413982	0.224721	-4.189261	25940.728752
HLA B*0803	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.513784	0.324517	-4.189267	32642.513806
HLA B*2705	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.462133	0.272858	-4.189274	28982.278017
HLA B*4801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.414020	0.224721	-4.189298	25942.974233
HLA A*2902	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.449405	0.260101	-4.189304	28145.266026
HLA B*5301	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.596316	0.407006	-4.189311	39474.469810
HLA A*3301	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.640383	0.451064	-4.189320	43690.120882
HLA B*5801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.344609	0.155271	-4.189338	22111.027712
HLA A*8001	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.412664	0.223225	-4.189439	25862.119342
HLA B*5701	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.337579	0.148101	-4.189478	21756.011002
HLA A*2403	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.437806	0.248296	-4.189510	27403.494675
HLA A*2602	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.535617	0.346054	-4.189563	34325.538611
HLA A*0202	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.557341	0.367626	-4.189714	36086.162372
HLA B*4001	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.406222	0.216497	-4.189724	25481.314234
HLA B*0803	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.493061	0.303321	-4.189740	31121.544265
HLA B*5401	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.557406	0.367626	-4.189780	36091.629005
HLA B*1517	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.493129	0.303321	-4.189808	31126.427208
HLA A*2301	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.514514	0.324517	-4.189998	32697.480263
HLA B*4403	1:422-430	9	TGPEQREIP	0.551955	-0.064220	-4.677766	0.487735	-4.190031	47617.424535
HLA B*5401	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.546705	0.356622	-4.190082	35213.125968
HLA B*7301	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.571938	0.381799	-4.190139	37319.691862

HLA B*0702	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.408618	0.218420	-4.190199	25622.310999
HLA B*4402	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.459515	0.269282	-4.190234	28808.138206
HLA B*5401	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.550760	0.360485	-4.190275	35543.467303
HLA B*3501	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.450472	0.260101	-4.190371	28214.478284
HLA B*3501	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.302795	0.112336	-4.190459	20081.453517
HLA A*0216	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.459936	0.269402	-4.190534	28836.048659
HLA A*2301	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.536811	0.346054	-4.190756	34420.002614
HLA A*0203	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.402164	0.211378	-4.190786	25244.354079
HLA B*4002	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.641915	0.451064	-4.190852	43844.498866
HLA A*0101	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.370235	0.179347	-4.190888	23454.963519
HLA B*1501	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.382283	0.191384	-4.190899	24114.758717
HLA A*2402	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.553671	0.362756	-4.190914	35782.510167
HLA B*1502	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.539377	0.348457	-4.190919	34623.943994
HLA B*4403	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.645143	0.454147	-4.190996	44171.617516
HLA B*0801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.445938	0.254868	-4.191069	27921.421069
HLA A*0212	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.445966	0.254868	-4.191097	27923.233749
HLA B*3501	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.439467	0.248296	-4.191171	27508.508031
HLA A*0219	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.460502	0.269282	-4.191220	28873.669137
HLA B*1517	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.503561	0.312328	-4.191233	31883.132736
HLA A*1101	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.461244	0.269799	-4.191446	28923.071610
HLA B*4001	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.327479	0.135996	-4.191483	21255.867477
HLA A*0301	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.367885	0.176401	-4.191484	23328.417376
HLA B*4403	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.642561	0.451064	-4.191498	43909.775728
HLA B*1801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.484899	0.293372	-4.191527	30542.109359
HLA B*4801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.433786	0.242067	-4.191719	27151.009495
HLA B*4403	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.600463	0.408739	-4.191724	39853.195226
HLA B*1503	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.433974	0.242067	-4.191907	27162.762755
HLA A*2403	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.292645	0.100651	-4.191994	19617.577144
HLA A*0212	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.349261	0.157255	-4.192006	22349.144794
HLA A*0101	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.387278	0.195249	-4.192029	24393.713905
HLA B*4801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.438433	0.246391	-4.192042	27443.105991
HLA B*0802	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.459630	0.267585	-4.192045	28815.775811
HLA A*0206	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.452215	0.260101	-4.192114	28327.962705
HLA A*0219	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.455451	0.263202	-4.192248	28539.777491
HLA A*0101	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.364932	0.172544	-4.192388	23170.316926
HLA A*0216	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.415674	0.223276	-4.192397	26041.968050
HLA B*4801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.434636	0.242192	-4.192444	27204.233585
HLA B*4402	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.368994	0.176401	-4.192593	23388.061853
HLA A*0219	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.438995	0.246391	-4.192604	27478.611875
HLA A*3002	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.500486	0.307875	-4.192611	31658.148458
HLA A*3301	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.601767	0.409024	-4.192743	39973.033803
HLA A*2403	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.340941	0.148101	-4.192841	21925.089900
HLA B*5101	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.460516	0.267585	-4.192931	28874.606372
HLA A*3201	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.275045	0.082090	-4.192956	18838.459115
HLA B*1502	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.539055	0.346054	-4.193000	34598.291798
HLA A*6801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.435240	0.242192	-4.193048	27242.083066
HLA B*5101	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.500930	0.307875	-4.193055	31690.534489
HLA A*0212	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.341639	0.148535	-4.193104	21960.346071
HLA B*4001	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.447996	0.254868	-4.193127	28054.056475
HLA A*2601	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.372831	0.179592	-4.193239	23595.595516
HLA A*2402	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.462034	0.268569	-4.193465	28975.693547
HLA A*0203	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.439864	0.246391	-4.193473	27533.669770
HLA B*0702	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.435548	0.242067	-4.193481	27261.396250
HLA A*2301	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.527702	0.334125	-4.193577	33705.590928
HLA A*0203	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.422938	0.229302	-4.193636	26481.245611
HLA B*1501	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.351028	0.157340	-4.193688	22440.251600
HLA B*0801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.306028	0.112336	-4.193692	20231.497779
HLA B*5301	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.602780	0.409024	-4.193755	40066.346160
HLA B*1502	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.574198	0.380356	-4.193842	37514.421510
HLA B*1502	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.596521	0.402654	-4.193867	39493.053251
HLA B*1801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.523123	0.329236	-4.193887	33352.070440
HLA B*3501	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.351164	0.157255	-4.193909	22447.293862
HLA A*2603	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.636920	0.442960	-4.193960	43343.113531
HLA A*0212	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.415263	0.221286	-4.193977	26017.324989
HLA A*3101	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.389364	0.195249	-4.194115	24511.182790

HLA B*0702	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.457349	0.263202	-4.194147	28664.803350
HLA A*0101	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.385532	0.191384	-4.194148	24295.859008
HLA B*0803	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.508142	0.313851	-4.194292	32221.257302
HLA A*6802	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.368170	0.173777	-4.194393	23343.693077
HLA B*5701	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.417718	0.223225	-4.194493	26164.826165
HLA A*2602	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.576379	0.381799	-4.194580	37703.231606
HLA B*4801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.406010	0.211378	-4.194632	25468.910656
HLA B*1503	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.351930	0.157255	-4.194675	22486.917375
HLA B*0803	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.520184	0.325463	-4.194720	33127.113342
HLA B*4801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.424059	0.229302	-4.194757	26549.669165
HLA A*8001	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.460930	0.266144	-4.194785	28902.112146
HLA B*4403	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.580110	0.385288	-4.194821	38028.531758
HLA A*2403	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.411360	0.216497	-4.194863	25784.585083
HLA A*1101	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.443196	0.248296	-4.194900	27745.698907
HLA B*0801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.374316	0.179347	-4.194969	23676.408108
HLA B*4402	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.427358	0.232368	-4.194990	26752.094548
HLA B*2705	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.488428	0.293372	-4.195056	30791.294983
HLA A*0301	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.365733	0.170651	-4.195082	23213.100333
HLA A*0216	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.488456	0.293372	-4.195084	30793.293978
HLA A*6802	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.437764	0.242669	-4.195095	27400.826308
HLA A*6801	1:531-539	9	AGEVTGTNP	0.616075	-0.134809	-4.676361	0.481266	-4.195095	47463.625665
HLA B*5701	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.416477	0.221286	-4.195191	26090.195033
HLA A*0219	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.424134	0.228841	-4.195294	26554.265748
HLA B*5701	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.427694	0.232368	-4.195325	26772.798354
HLA B*4001	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.352665	0.157255	-4.195411	22525.026623
HLA B*0803	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.485916	0.290447	-4.195469	30613.737561
HLA B*2705	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.437684	0.242192	-4.195492	27395.786766
HLA A*0301	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.327632	0.132130	-4.195502	21263.343264
HLA B*4501	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.660518	0.464928	-4.195591	45763.405250
HLA B*5701	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.387001	0.191384	-4.195616	24378.146734
HLA A*2602	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.337029	0.141319	-4.195710	21728.487186
HLA B*4601	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.365066	0.169330	-4.195736	23177.462912
HLA B*0802	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.489116	0.293372	-4.195745	30840.140891
HLA B*0802	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.464336	0.268569	-4.195768	29129.721675
HLA A*1101	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.465058	0.269282	-4.195776	29178.141562
HLA B*4402	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.407202	0.211378	-4.195823	25538.863025
HLA A*0206	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.438560	0.242669	-4.195891	27451.124227
HLA A*8001	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.442373	0.246391	-4.195982	27693.213209
HLA B*3901	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.461017	0.264968	-4.196049	28907.897943
HLA B*4002	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.503963	0.307875	-4.196088	31912.641183
HLA A*8001	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.425412	0.229302	-4.196110	26632.529520
HLA A*2603	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.654215	0.458095	-4.196120	45103.959081
HLA B*1502	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.618928	0.422686	-4.196242	41584.142394
HLA B*0802	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.477049	0.280603	-4.196446	29995.036756
HLA B*0801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.365778	0.169330	-4.196448	23215.486481
HLA B*3501	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.345060	0.148535	-4.196525	22134.006340
HLA B*0702	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.425424	0.228841	-4.196584	26633.249925
HLA B*4001	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.354042	0.157340	-4.196702	22596.548660
HLA A*8001	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.413204	0.216497	-4.196707	25894.318947
HLA B*1801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.464339	0.267585	-4.196753	29129.879264
HLA A*0201	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.388173	0.191384	-4.196789	24444.045295
HLA B*5701	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.407486	0.210423	-4.197063	25555.586150
HLA B*4801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.413599	0.216497	-4.197102	25917.863991
HLA A*8001	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.452027	0.254868	-4.197159	28315.705267
HLA A*8001	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.426127	0.228841	-4.197286	26676.365583
HLA A*0203	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.429663	0.232368	-4.197294	26894.448031
HLA B*4402	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.413874	0.216497	-4.197377	25934.274078
HLA B*3901	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.260018	0.062590	-4.197428	18197.765774
HLA A*6901	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.373891	0.176401	-4.197489	23653.235754
HLA A*3201	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.186505	-0.010996	-4.197501	15364.026042
HLA B*1517	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.490958	0.293372	-4.197587	30971.222603
HLA B*5701	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.414729	0.216943	-4.197787	25985.394158
HLA B*5301	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.606555	0.408739	-4.197816	40416.189137
HLA B*4501	1:346-354	9	VTIAINTFG	0.959431	-0.537455	-4.619889	0.421976	-4.197913	41676.255193
HLA A*0219	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.438894	0.240938	-4.197956	27472.220400

HLA B*4801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.430424	0.232368	-4.198056	26941.630067
HLA A*2601	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.371849	0.173777	-4.198072	23542.298286
HLA B*0803	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.510457	0.312328	-4.198128	32393.414314
HLA A*6802	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.427445	0.229302	-4.198143	26757.449941
HLA B*0702	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-3.831667	-0.366558	-4.198225	6786.830669
HLA A*2601	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.368900	0.170651	-4.198249	23383.001328
HLA A*2501	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.441138	0.242669	-4.198468	27614.521370
HLA A*0219	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.467969	0.269402	-4.198567	29374.375274
HLA A*3101	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.321081	0.122446	-4.198635	20945.039613
HLA A*2501	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.467955	0.269282	-4.198673	29373.421817
HLA B*5401	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.549233	0.350532	-4.198701	35418.700757
HLA B*1501	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.340042	0.141319	-4.198722	21879.708418
HLA A*0201	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.394063	0.195249	-4.198814	24777.828275
HLA B*1501	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.394087	0.195249	-4.198838	24779.168764
HLA B*4002	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.607608	0.408742	-4.198866	40514.261837
HLA A*0219	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.453813	0.254868	-4.198945	28432.365395
HLA B*4601	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.331106	0.132130	-4.198976	21434.158534
HLA B*5301	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.594794	0.395731	-4.199063	39336.330060
HLA B*1517	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.465215	0.266144	-4.199071	29188.719464
HLA B*4601	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.394355	0.195249	-4.199106	24794.455469
HLA A*2902	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.356479	0.157255	-4.199224	22723.672795
HLA B*0702	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.381625	0.182373	-4.199252	24078.258081
HLA A*0206	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.462647	0.263371	-4.199276	29016.635576
HLA A*0216	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.447617	0.248296	-4.199322	28029.632250
HLA B*5301	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.579245	0.379878	-4.199367	37952.898378
HLA A*3201	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.467936	0.268569	-4.199367	29372.150589
HLA B*2705	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.424104	0.224721	-4.199382	26552.398290
HLA B*4002	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.454295	0.254868	-4.199426	28463.915156
HLA A*2603	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.634693	0.435191	-4.199501	43121.394164
HLA A*0216	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.356850	0.157255	-4.199595	22743.104442
HLA A*3201	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.533782	0.334125	-4.199657	34180.814927
HLA B*4501	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.650766	0.451064	-4.199702	44747.174806
HLA B*5301	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.594867	0.395099	-4.199768	39342.927574
HLA B*2705	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.464747	0.264968	-4.199780	29157.312733
HLA B*4402	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.410218	0.210423	-4.199795	25716.881137
HLA A*6801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.534720	0.334871	-4.199849	34254.675467
HLA B*5401	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.493289	0.293372	-4.199917	31137.879869
HLA A*2902	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.442632	0.242669	-4.199963	27709.698006
HLA B*5801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.357353	0.157340	-4.200012	22769.449751
HLA B*1502	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.507903	0.307875	-4.200028	32203.482237
HLA B*4001	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.348171	0.148101	-4.200070	22293.114579
HLA A*0211	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.460211	0.260101	-4.200109	28854.306417
HLA A*2902	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.429618	0.229302	-4.200316	26891.683749
HLA B*1517	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.322801	0.122446	-4.200355	21028.147230
HLA B*4403	1:546-554	9	PVDSVIELQ	0.716558	-0.251630	-4.665311	0.464928	-4.200384	46271.255353
HLA B*4403	1:467-475	9	VIGTNPPAN	0.982011	-0.513529	-4.668944	0.468482	-4.200462	46659.876612
HLA A*2601	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.332641	0.132130	-4.200511	21510.011981
HLA B*5401	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-3.860335	-0.340176	-4.200512	7249.956983
HLA A*2902	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.446936	0.246391	-4.200545	27985.691938
HLA A*2501	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.465558	0.264968	-4.200591	29211.783100
HLA B*5301	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.574024	0.373369	-4.200655	37499.406300
HLA B*3501	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.421942	0.221286	-4.200656	26420.572728
HLA A*3301	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.411081	0.210423	-4.200657	25767.990907
HLA A*0206	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.441671	0.240938	-4.200733	27648.454072
HLA A*0212	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.419214	0.218420	-4.200795	26255.148296
HLA A*6801	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.607803	0.407006	-4.200797	40532.457668
HLA A*0250	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.482310	0.281512	-4.200798	30360.568216
HLA A*0101	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.387656	0.186843	-4.200813	24414.969894
HLA A*2601	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.358107	0.157255	-4.200852	22809.024948
HLA A*2501	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.460041	0.259153	-4.200888	28843.069506
HLA A*2603	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.530124	0.329236	-4.200888	33894.112347
HLA A*8001	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.374675	0.173777	-4.200898	23696.013492
HLA A*0216	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.417953	0.216943	-4.201010	26178.984875
HLA B*1503	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.301724	0.100651	-4.201072	20031.975443
HLA B*4403	1:397-405	9	DHVIGTDPA	0.831115	-0.395088	-4.637127	0.436027	-4.201100	43363.752810

HLA A*0219	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.356471	0.155271	-4.201200	22723.304000
HLA A*0211	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.467433	0.266144	-4.201289	29338.165648
HLA B*0803	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.497295	0.295880	-4.201415	31426.420026
HLA B*1503	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.424729	0.223276	-4.201452	26590.635507
HLA A*1101	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.461571	0.260101	-4.201470	28944.829205
HLA A*1101	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.482996	0.281512	-4.201484	30408.566331
HLA B*3901	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.412925	0.211378	-4.201547	25877.654149
HLA B*3801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.558259	0.356622	-4.201637	36162.575016
HLA A*6901	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.298566	0.096922	-4.201644	19886.853356
HLA A*3101	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.448200	0.246391	-4.201809	28067.263515
HLA A*3001	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.275316	0.073404	-4.201911	18850.182868
HLA A*2603	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.631105	0.429083	-4.202022	42766.639920
HLA B*1517	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.470708	0.268569	-4.202140	29560.252432
HLA B*3901	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.492699	0.290447	-4.202252	31095.626991
HLA B*1517	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.425577	0.223276	-4.202301	26642.616962
HLA B*1502	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.573930	0.371335	-4.202595	37491.292472
HLA A*6801	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.611400	0.408742	-4.202658	40869.563500
HLA A*0206	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.359953	0.157255	-4.202699	22906.219362
HLA A*1101	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.493153	0.290447	-4.202706	31128.111158
HLA B*0801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.360134	0.157255	-4.202880	22915.763198
HLA A*2603	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.611665	0.408742	-4.202923	40894.555417
HLA B*4501	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.638128	0.435191	-4.202936	43463.804715
HLA B*1502	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.299872	0.096922	-4.202950	19946.761043
HLA B*0801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.449520	0.246391	-4.203129	28152.727891
HLA B*4501	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.625899	0.422686	-4.203213	42257.000958
HLA B*5101	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.466493	0.263202	-4.203291	29274.747800
HLA B*7301	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.551857	0.348457	-4.203400	35633.378496
HLA B*3901	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.466672	0.263202	-4.203470	29286.786633
HLA A*0101	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.383286	0.179592	-4.203694	24170.528746
HLA A*0201	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.390638	0.186843	-4.203795	24583.158969
HLA A*0203	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.399049	0.195249	-4.203800	25063.911354
HLA A*2602	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.618007	0.414162	-4.203844	41496.049320
HLA B*0801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.425321	0.221286	-4.204035	26626.911031
HLA A*0101	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.386442	0.182373	-4.204069	24346.778762
HLA B*4801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.427417	0.223276	-4.204140	26755.712940
HLA A*3201	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.467417	0.263202	-4.204214	29337.054655
HLA A*0219	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.415613	0.211378	-4.204235	26038.305319
HLA A*2602	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.608155	0.403854	-4.204301	40565.362432
HLA B*5101	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.464407	0.260101	-4.204306	29134.449716
HLA A*3201	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.477221	0.272858	-4.204363	30006.884792
HLA A*0101	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.373724	0.169330	-4.204394	23644.152240
HLA A*0219	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.414819	0.210423	-4.204395	25990.736675
HLA A*8001	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.445444	0.240938	-4.204507	27889.718204
HLA B*4402	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.427757	0.223225	-4.204532	26776.709262
HLA A*0219	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.447333	0.242669	-4.204664	28011.290152
HLA B*5101	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.479883	0.275124	-4.204759	30191.373951
HLA B*0702	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.427997	0.223225	-4.204772	26791.488961
HLA B*1509	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.529290	0.324517	-4.204774	33829.080810
HLA A*2402	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.586629	0.381799	-4.204831	38603.739735
HLA A*8001	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.374196	0.169330	-4.204866	23669.876585
HLA A*2602	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.553344	0.348457	-4.204887	35755.612743
HLA A*2301	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.534201	0.329236	-4.204965	34213.745546
HLA B*5701	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.374530	0.169330	-4.205200	23688.066871
HLA B*1517	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.468420	0.263202	-4.205218	29404.902251
HLA B*0801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.327700	0.122446	-4.205254	21266.679463
HLA A*3101	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.362597	0.157340	-4.205256	23046.054578
HLA B*0802	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.471413	0.266144	-4.205269	29608.266691
HLA A*3301	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.640520	0.435191	-4.205328	43703.831838
HLA B*5301	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.568104	0.362756	-4.205347	36991.648842
HLA B*5301	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.590647	0.385288	-4.205359	38962.516420
HLA A*0101	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.379158	0.173777	-4.205381	23941.872068
HLA A*3001	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.291410	0.086012	-4.205398	19561.832684
HLA B*0802	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.464574	0.259153	-4.205420	29145.642470
HLA B*3901	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.486039	0.280603	-4.205435	30622.350853
HLA A*6801	1:363-371	9	PDVRGQSSA	0.988678	-0.519605	-4.674599	0.469073	-4.205526	47271.436110

HLA A*0206	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.556124	0.350532	-4.205592	35985.178864
HLA A*0211	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.475156	0.269282	-4.205874	29864.532009
HLA B*5401	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.035513	-0.170363	-4.205876	10852.081120
HLA B*1501	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.382306	0.176401	-4.205905	24116.063334
HLA B*0802	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.487521	0.281512	-4.206009	30727.063159
HLA B*1517	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.466162	0.260101	-4.206061	29252.425702
HLA A*8001	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.427445	0.221286	-4.206159	26757.449941
HLA B*0802	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.448888	0.242669	-4.206219	28111.788143
HLA B*4403	1:62-70	9	NAAALNHPA	0.615967	-0.206247	-4.615939	0.409720	-4.206220	41298.968470
HLA A*0212	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.435654	0.229302	-4.206352	27268.033709
HLA A*0219	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.438750	0.232368	-4.206382	27463.155974
HLA B*1517	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.435254	0.228841	-4.206414	27242.967340
HLA A*2902	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.461329	0.254868	-4.206461	28928.705101
HLA B*4402	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.435393	0.228841	-4.206552	27251.664233
HLA B*3901	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.500056	0.293372	-4.206684	31626.822093
HLA B*0702	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.423639	0.216943	-4.206696	26523.971702
HLA A*2603	1:481-489	9	TNVVIIIVG	1.069245	-0.643062	-4.632891	0.426183	-4.206707	42942.837606
HLA A*2902	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.417248	0.210423	-4.206825	26136.531713
HLA B*0702	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.467050	0.260101	-4.206949	29312.306307
HLA A*1101	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.476354	0.269402	-4.206952	29947.043325
HLA B*2705	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.428504	0.221286	-4.207218	26822.814080
HLA A*6901	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.367321	0.160089	-4.207233	23298.148034
HLA A*0101	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.362554	0.155271	-4.207283	23043.810509
HLA B*1801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.449363	0.242067	-4.207296	28142.525430
HLA B*4002	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.633419	0.426123	-4.207296	42995.140529
HLA B*2705	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.381082	0.173777	-4.207306	24048.186651
HLA B*5101	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.510673	0.303321	-4.207352	32409.540846
HLA B*4801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.430699	0.223225	-4.207474	26958.688359
HLA B*0802	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.476965	0.269402	-4.207563	29989.195611
HLA A*2902	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.379177	0.171585	-4.207592	23942.908273
HLA B*3901	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.422349	0.214737	-4.207611	26445.311603
HLA A*2403	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.424607	0.216943	-4.207664	26583.156235
HLA A*0250	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.589573	0.381799	-4.207775	38866.307616
HLA B*4001	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.431136	0.223276	-4.207859	26985.828906
HLA A*0101	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.378604	0.170651	-4.207953	23911.324174
HLA A*2902	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.448933	0.240938	-4.207995	28114.677843
HLA B*5101	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.474282	0.266144	-4.208138	29804.490709
HLA B*5701	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.394987	0.186843	-4.208144	24830.564120
HLA A*0219	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.456454	0.248296	-4.208158	28605.781229
HLA B*4002	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.610942	0.402654	-4.208288	40826.471771
HLA A*2601	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.403602	0.195249	-4.208353	25328.072917
HLA B*1503	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.320867	0.112336	-4.208531	20934.730910
HLA B*4601	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.395438	0.186843	-4.208595	24856.368994
HLA A*0101	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.380190	0.171585	-4.208605	23998.800183
HLA A*2603	1:411-419	9	SAGDEITVN	1.028251	-0.574104	-4.662762	0.454147	-4.208615	46000.451141
HLA A*2402	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.561875	0.353175	-4.208701	36464.914951
HLA A*0203	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.357247	0.148535	-4.208712	22763.907317
HLA A*2501	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.378106	0.169330	-4.208776	23883.916081
HLA A*6802	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.142950	-0.065831	-4.208781	13897.935176
HLA B*0802	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.478121	0.269282	-4.208839	30069.123140
HLA A*6802	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.291024	0.082090	-4.208935	19544.484696
HLA A*3201	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.604847	0.395731	-4.209116	40257.544871
HLA A*8001	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.432397	0.223276	-4.209121	27064.339706
HLA A*3002	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.565775	0.356622	-4.209153	36793.859876
HLA B*0803	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.484305	0.275124	-4.209181	30500.334909
HLA B*5301	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.589665	0.380356	-4.209309	38874.508715
HLA A*2403	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.434120	0.224721	-4.209398	27171.875030
HLA B*5401	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.477059	0.267585	-4.209474	29995.685842
HLA A*3301	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.618256	0.408742	-4.209514	41519.851981
HLA B*3501	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.388901	0.179347	-4.209555	24485.073957
HLA B*3501	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.455979	0.246391	-4.209588	28574.537974
HLA B*4501	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.635813	0.426123	-4.209690	43232.813358
HLA A*2602	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.472921	0.263202	-4.209719	29711.279394
HLA A*0301	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.367211	0.157340	-4.209871	23292.224888
HLA A*3002	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.544912	0.334871	-4.210041	35068.074722

HLA A*6802	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.162634	-0.047418	-4.210052	14542.339088
HLA A*3001	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.269642	0.059501	-4.210141	18605.509245
HLA B*5101	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.452345	0.242192	-4.210153	28336.392772
HLA B*1501	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.381750	0.171585	-4.210165	24085.162888
HLA B*5101	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.483059	0.272858	-4.210201	30413.008344
HLA B*1501	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.389688	0.179347	-4.210342	24529.488806
HLA B*7301	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.181740	-0.028622	-4.210362	15196.384692
HLA B*4801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.431678	0.221286	-4.210393	27019.573756
HLA A*0202	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.479838	0.269282	-4.210557	30188.270802
HLA A*6801	1:430-438	9	PDVSTLTYA	0.978843	-0.535883	-4.653547	0.442960	-4.210587	45034.714182
HLA B*4801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.387050	0.176401	-4.210649	24380.916436
HLA B*4001	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.440019	0.229302	-4.210717	27543.502496
HLA B*5401	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.539978	0.329236	-4.210742	34671.929009
HLA B*4001	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.382412	0.171585	-4.210827	24121.934984
HLA B*5101	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.480278	0.269402	-4.210876	30218.826198
HLA A*3001	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.162315	-0.048602	-4.210916	14531.643571
HLA B*2705	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.427868	0.216943	-4.210925	26783.518502
HLA B*5801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.354625	0.143550	-4.211075	22626.885723
HLA A*0203	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.402491	0.191384	-4.211107	25263.344331
HLA A*0201	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.390727	0.179592	-4.211135	24588.213191
HLA B*4002	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.629695	0.418508	-4.211188	42628.047305
HLA A*0203	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.323616	0.112336	-4.211280	21067.659006
HLA B*3501	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.429721	0.218420	-4.211302	26898.085676
HLA A*0201	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.371391	0.160089	-4.211302	23517.475942
HLA B*4001	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.429733	0.218420	-4.211313	26898.813264
HLA B*1517	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.492915	0.281512	-4.211404	31111.107441
HLA A*2402	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.571959	0.360485	-4.211474	37321.508964
HLA B*1801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.493028	0.281512	-4.211516	31119.187257
HLA A*0202	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.428507	0.216943	-4.211564	26822.959189
HLA A*2501	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.474937	0.263371	-4.211566	29849.510354
HLA B*0802	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.474911	0.263202	-4.211709	29847.734099
HLA A*0202	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.507658	0.295880	-4.211778	32185.368737
HLA A*2602	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.606929	0.395099	-4.211830	40450.968982
HLA A*0202	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.583206	0.371335	-4.211871	38300.653075
HLA A*3101	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.367148	0.155271	-4.211876	23288.822911
HLA B*2705	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.492561	0.280603	-4.211957	31085.703365
HLA B*4801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.422447	0.210423	-4.212024	26451.321066
HLA B*3801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.536571	0.324517	-4.212055	34401.014597
HLA A*0202	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.568679	0.356622	-4.212057	37040.710926
HLA B*5801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.351688	0.139599	-4.212089	22474.390738
HLA B*4501	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.644401	0.432298	-4.212103	44096.169542
HLA A*2603	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.663169	0.451064	-4.212105	46043.523614
HLA A*6901	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.360649	0.148535	-4.212114	22942.929098
HLA A*2602	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.607916	0.395731	-4.212185	40542.984288
HLA B*3801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.546331	0.334125	-4.212206	35182.849633
HLA B*0801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.441532	0.229302	-4.212230	27639.630551
HLA A*0250	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.541479	0.329236	-4.212243	34791.994473
HLA B*5701	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.423634	0.211378	-4.212256	26523.684720
HLA A*6802	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.403656	0.191384	-4.212272	25331.224620
HLA B*1502	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.502725	0.290447	-4.212277	31821.787448
HLA B*5801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.352816	0.140490	-4.212325	22532.826879
HLA B*3801	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.560792	0.348457	-4.212335	36374.086261
HLA A*0202	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.435619	0.223276	-4.212342	27265.821043
HLA B*0801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.383991	0.171585	-4.212406	24209.788561
HLA B*3501	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.441791	0.229302	-4.212489	27656.083453
HLA A*2402	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.569116	0.356622	-4.212494	37078.001506
HLA A*2601	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.394954	0.182373	-4.212581	24828.683563
HLA A*2603	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.575357	0.362756	-4.212600	37614.608843
HLA A*0202	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.541923	0.329236	-4.212687	34827.586404
HLA B*5101	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.506141	0.293372	-4.212769	32073.084004
HLA B*0803	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.455476	0.242669	-4.212807	28541.475909
HLA B*0803	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.455014	0.242192	-4.212822	28511.074086
HLA B*2705	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.360987	0.148101	-4.212886	22960.809155
HLA B*0801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.352891	0.139887	-4.213004	22536.728019
HLA A*2603	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.627252	0.414162	-4.213090	42388.883208

HLA B*5701	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.392729	0.179592	-4.213137	24701.807401
HLA B*0803	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.482552	0.269282	-4.213270	30377.490403
HLA B*1503	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.476601	0.263202	-4.213398	29964.059227
HLA A*0201	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.392881	0.179347	-4.213535	24710.495141
HLA B*0702	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.468453	0.254868	-4.213584	29407.129417
HLA A*2602	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.547802	0.334125	-4.213677	35302.201525
HLA B*4001	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.357270	0.143550	-4.213720	22765.138852
HLA B*4601	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.405106	0.191384	-4.213721	25415.919028
HLA B*0801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.409025	0.195249	-4.213776	25646.302423
HLA B*1503	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.455996	0.242192	-4.213804	28575.620090
HLA A*3002	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.362427	0.148535	-4.213892	23037.079611
HLA A*2602	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.437167	0.223225	-4.213942	27363.200365
HLA A*2601	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.393424	0.179347	-4.214078	24741.394764
HLA A*0250	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.509968	0.295880	-4.214088	32356.983900
HLA A*0202	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.596044	0.381799	-4.214245	39449.705491
HLA A*0201	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.390701	0.176401	-4.214300	24586.750020
HLA A*3201	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.623063	0.408739	-4.214324	41981.972797
HLA A*8001	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.431274	0.216943	-4.214332	26994.443711
HLA A*2601	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.362531	0.148101	-4.214430	23042.563898
HLA A*6801	1:113-121	9	KRAIEVIAD	1.166820	-0.708725	-4.672569	0.458095	-4.214474	47050.998181
HLA B*3801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.532034	0.317460	-4.214574	34043.515097
HLA B*5301	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.563092	0.348457	-4.214635	36567.244719
HLA B*4002	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.322000	0.107303	-4.214697	20989.390848
HLA A*0212	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.410150	0.195249	-4.214901	25712.846815
HLA A*6802	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.394298	0.179347	-4.214952	24791.236431
HLA A*6901	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.347203	0.132130	-4.215073	22243.481361
HLA A*2602	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.438440	0.223276	-4.215164	27443.551388
HLA A*2402	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.582910	0.367626	-4.215284	38274.554483
HLA B*7301	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.578087	0.362756	-4.215330	37851.810003
HLA A*3002	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.549463	0.334125	-4.215338	35437.483637
HLA B*4402	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.351336	0.135996	-4.215339	22456.160541
HLA B*1517	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.432285	0.216943	-4.215342	27057.312695
HLA B*5701	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.363912	0.148535	-4.215377	23115.979341
HLA A*0250	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.572011	0.356622	-4.215389	37325.951144
HLA B*5801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.316049	0.100651	-4.215397	20703.729707
HLA B*1502	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.478816	0.263371	-4.215445	30117.312217
HLA B*0702	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.363548	0.148101	-4.215447	23096.603958
HLA A*0301	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.347670	0.132177	-4.215494	22267.440875
HLA B*3801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.568837	0.353175	-4.215662	37054.139230
HLA A*0202	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.566219	0.350532	-4.215687	36831.499699
HLA A*6901	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.355802	0.139887	-4.215915	22688.295787
HLA A*0301	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.364516	0.148535	-4.215981	23148.140799
HLA B*1801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.480989	0.264968	-4.216022	30268.401410
HLA A*0201	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.387628	0.171585	-4.216043	24413.384958
HLA B*0803	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.444908	0.228841	-4.216068	27855.338707
HLA A*1101	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.458293	0.242192	-4.216101	28727.210696
HLA B*4001	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.388676	0.172544	-4.216132	24472.360951
HLA B*4001	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.371405	0.155271	-4.216134	23518.239316
HLA A*1101	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.458803	0.242669	-4.216134	28760.954692
HLA A*0101	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.373475	0.157340	-4.216135	23630.597430
HLA B*3801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.566734	0.350532	-4.216202	36875.162257
HLA B*4501	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.634787	0.418508	-4.216279	43130.726453
HLA A*0203	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.426721	0.210423	-4.216298	26712.902575
HLA B*4403	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.648736	0.432298	-4.216438	44538.508106
HLA B*4402	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.441323	0.224721	-4.216602	27626.325821
HLA B*3901	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.498143	0.281512	-4.216631	31487.854852
HLA A*0250	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.551570	0.334871	-4.216699	35609.867995
HLA A*2301	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.485287	0.268569	-4.216718	30569.384385
HLA A*2501	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.486147	0.269402	-4.216745	30629.972323
HLA A*0250	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.584386	0.367626	-4.216759	38404.809992
HLA A*0206	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.483008	0.266144	-4.216864	30409.388877
HLA B*1509	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.510337	0.293372	-4.216965	32384.478063
HLA B*4403	1:228-236	9	HVREDPIPP	0.388485	0.064198	-4.669667	0.452683	-4.216984	46737.688247
HLA A*2403	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.440306	0.223276	-4.217029	27561.687387
HLA A*0206	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.182774	-0.034337	-4.217111	15232.600511

HLA A*3301	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.433746	0.216497	-4.217249	27148.512583
HLA B*3501	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.459940	0.242669	-4.217271	28836.360661
HLA A*0206	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.513154	0.295880	-4.217274	32595.221339
HLA A*0301	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.359202	0.141914	-4.217288	22866.599232
HLA A*3101	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.359223	0.141914	-4.217309	22867.712611
HLA B*7301	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.510682	0.293372	-4.217310	32410.242182
HLA B*1503	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.357223	0.139887	-4.217336	22762.675848
HLA A*2601	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.393763	0.176401	-4.217361	24760.676415
HLA A*2602	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.624379	0.407006	-4.217373	42109.351628
HLA A*0202	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.386768	0.169330	-4.217438	24365.093806
HLA B*1503	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.242712	0.025261	-4.217450	17486.857232
HLA A*6802	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.412702	0.195249	-4.217453	25864.358018
HLA B*0802	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.458402	0.240938	-4.217464	28734.360493
HLA B*0802	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.482449	0.264968	-4.217481	30370.260354
HLA B*4601	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.389071	0.171585	-4.217486	24494.613046
HLA B*1801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.513401	0.295880	-4.217520	32613.741935
HLA A*0101	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.393927	0.176401	-4.217526	24770.054867
HLA B*1503	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.440841	0.223225	-4.217616	27595.704455
HLA A*0202	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.543223	0.325463	-4.217759	34931.935014
HLA B*4002	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.640498	0.422686	-4.217813	43701.703994
HLA A*2403	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.359159	0.141319	-4.217840	22864.372637
HLA B*3801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.578369	0.360485	-4.217884	37876.390873
HLA B*5801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.353969	0.135996	-4.217973	22592.759388
HLA B*4501	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.621869	0.403854	-4.218015	41866.755339
HLA B*4601	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.391836	0.173777	-4.218059	24651.078627
HLA B*3801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.525992	0.307875	-4.218117	33573.105914
HLA B*7301	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.493338	0.275124	-4.218215	31141.417572
HLA B*5801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.360207	0.141914	-4.218293	22919.606644
HLA B*1501	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.164147	-0.054260	-4.218407	14593.092502
HLA B*4501	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.569046	0.350532	-4.218514	37071.984358
HLA B*1501	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.281159	0.062590	-4.218568	19105.514476
HLA A*6802	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.437075	0.218420	-4.218656	27357.427730
HLA A*0201	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.366772	0.148101	-4.218671	23268.673241
HLA B*3501	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.473546	0.254868	-4.218678	29754.065609
HLA A*0219	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.435659	0.216943	-4.218716	27268.328745
HLA B*2705	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.376014	0.157255	-4.218760	23769.196168
HLA A*8001	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.451184	0.232368	-4.218816	28260.765282
HLA B*1509	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.504571	0.285730	-4.218841	31957.387281
HLA B*5701	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.414125	0.195249	-4.218877	25949.290689
HLA A*0201	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.388215	0.169330	-4.218886	24446.425723
HLA B*1509	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.579426	0.360485	-4.218941	37968.711386
HLA B*4001	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.401325	0.182373	-4.218953	25195.645940
HLA B*4601	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.374227	0.155271	-4.218955	23671.541312
HLA B*4501	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.543279	0.324299	-4.218980	34936.470778
HLA B*3901	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.461651	0.242669	-4.218982	28950.153697
HLA B*0803	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.478140	0.259153	-4.218986	30070.424533
HLA A*0219	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.440343	0.221286	-4.219058	27564.073181
HLA A*2603	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.598943	0.379878	-4.219065	39713.944985
HLA B*1509	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.553946	0.334871	-4.219074	35805.166128
HLA B*5101	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.499680	0.280603	-4.219076	31599.458321
HLA B*1503	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.499705	0.280603	-4.219102	31601.338823
HLA B*5401	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.536651	0.317460	-4.219191	34407.342771
HLA A*1101	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.442514	0.223225	-4.219289	27702.203700
HLA A*2603	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.622356	0.403047	-4.219309	41913.665963
HLA B*4501	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.572638	0.353175	-4.219464	37379.905213
HLA A*3201	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.614565	0.395099	-4.219466	41168.472712
HLA B*4002	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.614577	0.395099	-4.219478	41169.586312
HLA A*6801	1:214-222	9	PPFTGDSPV	0.661651	-0.229353	-4.651856	0.432298	-4.219558	44859.639747
HLA B*3501	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.388941	0.169330	-4.219612	24487.325907
HLA A*3002	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.590997	0.371335	-4.219662	38993.935733
HLA A*0212	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.430111	0.210423	-4.219688	26922.252126
HLA A*6901	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.376992	0.157255	-4.219737	23822.749312
HLA B*0803	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.505504	0.285730	-4.219774	32026.096751
HLA A*0203	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.406673	0.186843	-4.219830	25507.795393
HLA B*0803	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.500669	0.280603	-4.220066	31671.510109

HLA B*1801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.437021	0.216943	-4.220079	27354.023927
HLA A*3002	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.317301	0.096922	-4.220379	20763.514462
HLA A*2902	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.415805	0.195249	-4.220556	26049.858758
HLA A*6901	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.352787	0.132177	-4.220611	22531.364125
HLA A*6801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.389952	0.169330	-4.220622	24544.355913
HLA A*6802	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.445531	0.224721	-4.220810	27895.301333
HLA B*0802	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.437308	0.216497	-4.220810	27372.083719
HLA B*0802	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.480989	0.260101	-4.220888	30268.401410
HLA B*5801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.353046	0.132130	-4.220916	22544.776255
HLA A*0250	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.574208	0.353175	-4.221033	37515.233314
HLA B*4002	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.616783	0.395731	-4.221052	41379.255209
HLA A*0216	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.432632	0.211378	-4.221254	27078.985175
HLA B*7301	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.524601	0.303321	-4.221280	33465.754855
HLA A*2602	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.535155	0.313851	-4.221304	34288.975718
HLA B*1517	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.453679	0.232368	-4.221311	28423.599238
HLA B*3501	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.303425	0.082090	-4.221335	20110.589734
HLA B*4501	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.624489	0.403047	-4.221442	42120.059914
HLA B*0801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.378862	0.157340	-4.221522	23925.557747
HLA B*0803	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.503136	0.281512	-4.221624	31851.928373
HLA B*0702	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.468065	0.246391	-4.221674	29380.891393
HLA A*0212	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.446494	0.224721	-4.221773	27957.243303
HLA B*4601	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.398243	0.176401	-4.221842	25017.446085
HLA A*6801	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.546174	0.324299	-4.221874	35170.099477
HLA B*4001	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.395680	0.173777	-4.221903	24870.223284
HLA B*0702	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.438414	0.216497	-4.221917	27441.918304
HLA B*4002	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.575140	0.353175	-4.221966	37595.892341
HLA B*2705	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.485221	0.263202	-4.222019	30564.754181
HLA A*3001	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.197003	-0.025025	-4.222027	15739.920469
HLA A*3301	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.629103	0.407006	-4.222098	42569.972422
HLA A*0101	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.363482	0.141319	-4.222163	23093.105621
HLA B*5801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.362073	0.139887	-4.222185	23018.268461
HLA B*0802	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.445470	0.223276	-4.222194	27891.377937
HLA B*4403	1:141-149	9	PANIMISAT	0.918739	-0.489656	-4.651313	0.429083	-4.222230	44803.614370
HLA B*5301	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.436981	0.214737	-4.222244	27351.508345
HLA A*2602	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.481438	0.259153	-4.222285	30299.693575
HLA A*2402	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.568390	0.346054	-4.222336	37016.071629
HLA B*5101	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.491623	0.269282	-4.222342	31018.675819
HLA A*0250	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.593708	0.371335	-4.222373	39238.136826
HLA A*0212	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.402016	0.179592	-4.222424	25235.751688
HLA A*0216	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.465156	0.242669	-4.222487	29184.772037
HLA B*0803	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.515872	0.293372	-4.222500	32799.882553
HLA A*2301	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.539962	0.317460	-4.222501	34670.616035
HLA B*0702	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.451919	0.229302	-4.222617	28308.659641
HLA B*1801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.464863	0.242192	-4.222671	29165.042911
HLA B*3901	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.495554	0.272858	-4.222696	31300.692233
HLA A*0250	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.481878	0.259153	-4.222724	30330.361748
HLA A*6901	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.405296	0.182373	-4.222923	25427.058750
HLA B*2705	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.451809	0.228841	-4.222968	28301.462661
HLA B*1503	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.492772	0.269799	-4.222974	31100.842369
HLA B*4601	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.282498	0.059501	-4.222997	19164.519872
HLA A*6801	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.631747	0.408739	-4.223007	42829.848625
HLA B*4601	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.402380	0.179347	-4.223034	25256.921568
HLA A*6901	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.363560	0.140490	-4.223070	23097.228717
HLA B*1509	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.399707	0.176401	-4.223305	25101.906159
HLA A*8001	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.371456	0.148101	-4.223356	23521.038566
HLA B*2705	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.464310	0.240938	-4.223373	29127.988253
HLA A*1101	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.496235	0.272858	-4.223377	31349.837424
HLA B*0801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.410263	0.186843	-4.223420	25719.524657
HLA B*1501	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.383592	0.160089	-4.223503	24187.533510
HLA B*0702	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.418754	0.195249	-4.223505	26227.323712
HLA A*0301	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.363142	0.139599	-4.223543	23074.997709
HLA A*3002	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.492890	0.269282	-4.223608	31109.256112
HLA A*0101	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.363501	0.139887	-4.223614	23094.105092
HLA B*1509	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.195034	-0.028622	-4.223656	15668.725246
HLA B*0802	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.487110	0.263371	-4.223738	30697.986675

HLA B*1517	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.488712	0.264968	-4.223745	30811.457458
HLA A*0250	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.558008	0.334125	-4.223883	36141.648072
HLA A*1101	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.336271	0.112336	-4.223935	21690.552108
HLA B*3901	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.493240	0.269282	-4.223958	31134.342568
HLA B*1801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.493287	0.269282	-4.224005	31137.711417
HLA B*1509	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.479039	0.254868	-4.224171	30132.794671
HLA A*8001	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.419428	0.195249	-4.224179	26268.076885
HLA A*0301	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.367735	0.143550	-4.224185	23320.341708
HLA B*4601	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.403814	0.179592	-4.224222	25340.407905
HLA A*2602	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.128106	-0.096147	-4.224254	13430.934632
HLA A*6901	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.233838	0.009579	-4.224258	17133.171396
HLA A*6802	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.310278	0.086012	-4.224267	20430.465127
HLA B*0802	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.439054	0.214737	-4.224316	27482.328532
HLA A*0206	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.548641	0.324299	-4.224341	35370.447622
HLA B*1517	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.234059	0.009579	-4.224479	17141.886336
HLA A*0301	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.365949	0.141319	-4.224630	23224.656596
HLA A*0201	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.381905	0.157255	-4.224650	24093.764096
HLA B*0801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.262934	0.038251	-4.224683	18320.350649
HLA B*3801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.537051	0.312328	-4.224722	34439.001112
HLA A*0203	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.196138	-0.028622	-4.224760	15708.615990
HLA B*3901	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.435193	0.210423	-4.224770	27239.135693
HLA A*0101	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.373327	0.148535	-4.224792	23622.544950
HLA A*6801	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.559110	0.334125	-4.224985	36233.464466
HLA B*4501	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.620112	0.395099	-4.225013	41697.679770
HLA A*2501	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.485134	0.260101	-4.225033	30558.636771
HLA B*5301	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.596370	0.371335	-4.225035	39479.381824
HLA A*0201	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.307163	0.082090	-4.225073	20284.431333
HLA B*4801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.361215	0.135996	-4.225219	22972.861214
HLA A*0212	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.394627	0.169330	-4.225297	24810.020042
HLA B*1509	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.407679	0.182373	-4.225306	25566.925402
HLA B*1509	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.515771	0.290447	-4.225324	32792.253360
HLA A*6801	1:390-398	9	PDSTIPPDH	0.966917	-0.531726	-4.660537	0.435191	-4.225346	45765.385892
HLA B*4402	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.416799	0.191384	-4.225415	26109.539075
HLA B*4501	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.593067	0.367626	-4.225441	39180.228805
HLA B*1509	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.405049	0.179592	-4.225457	25412.619306
HLA A*2601	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.361476	0.135996	-4.225480	22986.660507
HLA A*0250	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.576026	0.350532	-4.225494	37672.648471
HLA B*3501	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.357642	0.132130	-4.225512	22784.605958
HLA A*0203	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.366992	0.141319	-4.225673	23280.509059
HLA B*1502	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.559906	0.334125	-4.225781	36299.975887
HLA A*2902	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.338181	0.112336	-4.225845	21786.162463
HLA A*0219	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.374414	0.148535	-4.225879	23681.788362
HLA B*5401	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.538249	0.312328	-4.225920	34534.151014
HLA A*8001	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.383274	0.157255	-4.226020	24169.874956
HLA A*2603	1:148-156	9	ATNAVKVMD	1.155503	-0.752849	-4.628704	0.402654	-4.226050	42530.839618
HLA B*4403	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.586559	0.360485	-4.226074	38597.474984
HLA B*0801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.396765	0.170651	-4.226114	24932.460889
HLA A*6802	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.288719	0.062590	-4.226129	19441.034889
HLA B*1509	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.494715	0.268569	-4.226147	31240.298593
HLA A*3101	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.413042	0.186843	-4.226199	25884.654858
HLA A*3201	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.608038	0.381799	-4.226239	40554.391211
HLA A*0203	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.408616	0.182373	-4.226243	25622.172386
HLA B*1801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.450970	0.224721	-4.226249	28246.855934
HLA A*0301	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.338674	0.112336	-4.226338	21810.927280
HLA A*2501	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.474636	0.248296	-4.226341	29828.847744
HLA A*0206	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.495664	0.269282	-4.226383	31308.651909
HLA A*2902	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.451135	0.224721	-4.226413	28257.554825
HLA A*1101	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.386578	0.160089	-4.226489	24354.419336
HLA A*2501	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.458916	0.232368	-4.226548	28768.424153
HLA A*0202	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.358877	0.132130	-4.226747	22849.534207
HLA B*4601	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.409203	0.182373	-4.226831	25656.849108
HLA B*0801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.359068	0.132177	-4.226891	22859.549090
HLA A*3101	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.403301	0.176401	-4.226900	25310.540163
HLA A*2301	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.539367	0.312328	-4.227039	34623.194755
HLA A*0212	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.418434	0.191384	-4.227050	26208.034189

HLA A*3101	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.375737	0.148535	-4.227202	23754.027542
HLA A*0201	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.409586	0.182373	-4.227214	25679.483602
HLA A*3201	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.587767	0.360485	-4.227282	38704.951688
HLA B*3801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.541204	0.313851	-4.227354	34769.979604
HLA A*2602	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.384689	0.157255	-4.227434	24248.718592
HLA B*4601	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.400036	0.172544	-4.227492	25120.925154
HLA A*0206	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.539886	0.312328	-4.227558	34664.614500
HLA A*0301	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.368085	0.140490	-4.227595	23339.147195
HLA A*3001	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.237226	0.009579	-4.227646	17267.350988
HLA A*8001	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.400193	0.172544	-4.227649	25130.032200
HLA A*1101	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.521048	0.293372	-4.227676	33193.129790
HLA B*5101	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.497509	0.269799	-4.227710	31441.895059
HLA B*1501	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.407429	0.179592	-4.227837	25552.268297
HLA B*1503	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.521236	0.293372	-4.227864	33207.498591
HLA A*0301	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.309970	0.082090	-4.227881	20415.991278
HLA B*5701	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.401746	0.173777	-4.227969	25220.056469
HLA A*0211	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.540328	0.312328	-4.228000	34699.888399
HLA B*4501	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.601452	0.373369	-4.228083	39944.066846
HLA A*2902	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.449377	0.221286	-4.228091	28143.438932
HLA A*2501	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.474589	0.246391	-4.228198	29825.620503
HLA A*1101	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.457542	0.229302	-4.228240	28677.522190
HLA A*0301	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.365634	0.137283	-4.228352	23207.826560
HLA A*6901	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.383624	0.155271	-4.228353	24189.365505
HLA B*4402	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.408057	0.179592	-4.228465	25589.203694
HLA B*0802	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.440050	0.211378	-4.228672	27545.439659
HLA B*4601	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.386059	0.157255	-4.228804	24325.318945
HLA A*0301	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.368693	0.139887	-4.228806	23371.872026
HLA A*0202	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.311009	0.082090	-4.228919	20464.867817
HLA A*3301	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.579529	0.350532	-4.228997	37977.750349
HLA A*2402	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.443736	0.214737	-4.228999	27780.243660
HLA B*4403	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.624787	0.395731	-4.229056	42149.008694
HLA A*2403	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.408696	0.179592	-4.229104	25626.885665
HLA B*4001	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.408487	0.179347	-4.229140	25614.549799
HLA B*5101	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.348321	0.119114	-4.229207	22300.834525
HLA A*6801	1:313-321	9	PRQDLDDTD	1.352058	-0.900994	-4.680407	0.451064	-4.229343	47907.854658
HLA A*0101	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.369993	0.140490	-4.229502	23441.897618
HLA B*5701	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.411889	0.182373	-4.229516	25815.989836
HLA B*4001	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.409121	0.179592	-4.229529	25651.991543
HLA B*5801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.366849	0.137283	-4.229567	23272.827683
HLA A*3002	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.492777	0.263202	-4.229575	31101.178875
HLA B*3901	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.447998	0.218420	-4.229578	28054.208245
HLA A*0206	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.475973	0.246391	-4.229582	29920.809172
HLA A*2603	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.239524	0.009850	-4.229674	17358.952436
HLA A*2601	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.390086	0.160089	-4.229997	24551.925668
HLA B*1801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.515818	0.285730	-4.230088	32795.801601
HLA A*3002	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.493637	0.263371	-4.230265	31162.820819
HLA A*6901	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.387642	0.157340	-4.230302	24414.177413
HLA B*3501	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.330956	0.100651	-4.230305	21426.738608
HLA A*3101	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.409673	0.179347	-4.230327	25684.624274
HLA B*0702	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.402009	0.171585	-4.230424	25235.342123
HLA B*4402	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.417405	0.186843	-4.230562	26146.006944
HLA A*2902	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.399932	0.169330	-4.230602	25114.946203
HLA A*6901	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.331254	0.100651	-4.230603	21441.465034
HLA A*2402	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.564737	0.334125	-4.230612	36705.984570
HLA A*3201	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.533942	0.303321	-4.230621	34193.391421
HLA A*3101	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.371952	0.141319	-4.230633	23547.902846
HLA A*0301	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.366675	0.135996	-4.230679	23263.512695
HLA A*1101	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.471622	0.240938	-4.230684	29622.525916
HLA B*5401	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.447286	0.216497	-4.230789	28008.259557
HLA B*5401	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.521250	0.290447	-4.230803	33208.576502
HLA B*4002	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.634690	0.403854	-4.230836	43121.160883
HLA A*0203	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.388199	0.157255	-4.230944	24445.499973
HLA B*0802	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.473138	0.242192	-4.230945	29726.070669
HLA A*0202	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.442329	0.211378	-4.230951	27690.366828
HLA A*1101	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.477369	0.246391	-4.230978	30017.113572

HLA A*0202	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.538909	0.307875	-4.231034	34586.689023
HLA A*6901	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.350156	0.119114	-4.231042	22395.257637
HLA B*0702	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.410498	0.179347	-4.231151	25733.442399
HLA B*1517	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.379701	0.148535	-4.231166	23971.810555
HLA A*3001	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-3.971560	-0.259643	-4.231203	9366.127160
HLA B*4001	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.391361	0.160089	-4.231273	24624.154701
HLA A*0202	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.496315	0.264968	-4.231348	31355.604326
HLA A*3301	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.640278	0.408739	-4.231538	43679.486035
HLA B*4801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.379668	0.148101	-4.231567	23969.995036
HLA B*4601	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.373595	0.141914	-4.231681	23637.118114
HLA B*0802	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.479984	0.248296	-4.231688	30198.398043
HLA B*5801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.353997	0.122274	-4.231724	22594.226128
HLA B*5101	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.517461	0.285730	-4.231730	32920.054118
HLA A*2403	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.443160	0.211378	-4.231782	27743.447481
HLA B*4001	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.427050	0.195249	-4.231801	26733.142176
HLA B*4403	1:603-611	9	VVYQNPPAG	0.805733	-0.379610	-4.657981	0.426123	-4.231857	45496.803896
HLA B*0801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.379962	0.148101	-4.231861	23986.209894
HLA B*4001	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.418796	0.186843	-4.231953	26229.877801
HLA B*4501	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.646245	0.414162	-4.232083	44283.833722
HLA B*4002	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.646283	0.414162	-4.232120	44287.667018
HLA B*1503	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.517855	0.285730	-4.232125	32949.987485
HLA A*2402	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.603536	0.371335	-4.232201	40136.201932
HLA B*1517	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.453625	0.221286	-4.232339	28420.062782
HLA A*2301	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.546244	0.313851	-4.232393	35175.807931
HLA A*2603	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.655124	0.422686	-4.232438	45198.488873
HLA B*1801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.495671	0.263202	-4.232469	31309.160042
HLA A*0216	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.478873	0.246391	-4.232482	30121.222823
HLA B*0801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.368550	0.135996	-4.232554	23364.160505
HLA B*1517	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.166736	-0.065831	-4.232567	14680.351958
HLA A*3201	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.603910	0.371335	-4.232574	40170.740837
HLA A*2403	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.387893	0.155271	-4.232622	24428.313850
HLA B*5101	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.501240	0.268569	-4.232671	31713.172952
HLA A*0250	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.465112	0.232368	-4.232743	29181.772350
HLA A*2501	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.498904	0.266144	-4.232760	31543.095291
HLA B*4001	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.424303	0.191384	-4.232919	26564.610968
HLA A*2403	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.428232	0.195249	-4.232983	26805.986781
HLA B*1501	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.167159	-0.065831	-4.232990	14694.654355
HLA A*3201	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.497969	0.264968	-4.233002	31475.251785
HLA B*3801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.562338	0.329236	-4.233102	36503.798083
HLA B*1801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.499276	0.266144	-4.233131	31570.068672
HLA B*4601	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.381310	0.148101	-4.233209	24060.809471
HLA A*0201	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.388610	0.155271	-4.233339	24468.654235
HLA B*0801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.409779	0.176401	-4.233378	25690.877828
HLA A*0101	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.381583	0.148101	-4.233482	24075.913502
HLA B*1801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.545828	0.312328	-4.233500	35142.141444
HLA B*7301	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.514223	0.280603	-4.233620	32675.553290
HLA A*2501	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.456858	0.223225	-4.233633	28632.411323
HLA A*0206	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.345976	0.112336	-4.233640	22180.755222
HLA B*5301	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.393871	0.160089	-4.233782	24766.838997
HLA B*4501	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.641006	0.407006	-4.234000	43752.800860
HLA A*2601	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.391418	0.157340	-4.234078	24627.352043
HLA A*2603	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.515644	0.281512	-4.234132	32782.675027
HLA A*6802	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.394322	0.160089	-4.234233	24792.577646
HLA B*0801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.394378	0.160089	-4.234289	24795.796857
HLA A*2403	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.416740	0.182373	-4.234368	26106.008070
HLA B*5401	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.560050	0.325463	-4.234586	36311.956973
HLA A*0250	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.595130	0.360485	-4.234645	39366.772976
HLA B*4801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.429921	0.195249	-4.234672	26910.457352
HLA A*2603	1:160-168	9	ARAIADSGN	0.814457	-0.405718	-4.643452	0.408739	-4.234713	43999.898408
HLA B*1517	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.390032	0.155271	-4.234760	24548.870925
HLA B*1509	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.467149	0.232368	-4.234780	29318.967269
HLA A*0202	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.169020	-0.065831	-4.234851	14757.750620
HLA B*3901	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.498242	0.263371	-4.234870	31495.010188
HLA A*0219	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.464247	0.229302	-4.234945	29123.733925
HLA A*1101	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.451919	0.216943	-4.234977	28308.659641

HLA A*0206	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.458338	0.223276	-4.235062	28730.163658
HLA A*1101	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.456412	0.221286	-4.235126	28602.995791
HLA B*0702	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.371158	0.135996	-4.235162	23504.883848
HLA A*3301	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.615519	0.380356	-4.235163	41258.995139
HLA B*4001	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.411593	0.176401	-4.235191	25798.398465
HLA B*5701	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.407812	0.172544	-4.235269	25574.810529
HLA A*0203	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.297864	0.062590	-4.235273	19854.711243
HLA B*5701	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.286184	0.050897	-4.235288	19327.882882
HLA B*0802	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.481680	0.246391	-4.235289	30316.581832
HLA B*1517	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.430588	0.195249	-4.235339	26951.834586
HLA B*1801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.495530	0.260101	-4.235429	31298.998946
HLA B*0802	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.467799	0.232368	-4.235431	29362.935830
HLA A*0201	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.383984	0.148535	-4.235449	24209.395647
HLA B*1503	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.332608	0.096922	-4.235686	21508.382908
HLA B*5801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.317799	0.082090	-4.235709	20787.341725
HLA B*5101	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.499156	0.263371	-4.235784	31561.359554
HLA A*3201	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.586359	0.350532	-4.235827	38579.730379
HLA A*3301	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.570702	0.334871	-4.235831	37213.645837
HLA B*0803	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.460681	0.224721	-4.235959	28885.543032
HLA A*0212	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.412380	0.176401	-4.235979	25845.195627
HLA A*3101	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.406635	0.170651	-4.235984	25505.587579
HLA B*1517	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.482397	0.246391	-4.236006	30366.645975
HLA B*5101	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.501063	0.264968	-4.236096	31700.308206
HLA B*3501	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.460819	0.224721	-4.236098	28894.764291
HLA B*4601	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.377450	0.141319	-4.236131	23847.893867
HLA B*5301	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.596626	0.360485	-4.236141	39502.668808
HLA A*3101	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.287098	0.050897	-4.236202	19368.600214
HLA B*1517	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.465563	0.229302	-4.236261	29212.099167
HLA B*3901	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.477470	0.240938	-4.236532	30024.097123
HLA B*4601	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.274801	0.038251	-4.236550	18827.863042
HLA A*0101	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.365592	0.128996	-4.236597	23205.566738
HLA B*5801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.355764	0.119114	-4.236650	22686.332014
HLA A*0203	1:158-166	9	GIARAIADS	0.697391	-1.036944	-3.897232	-0.339553	-4.236784	7892.811705
HLA B*0702	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.413296	0.176401	-4.236895	25899.782853
HLA B*4501	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.582999	0.346054	-4.236945	38282.423614
HLA A*2601	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.376569	0.139599	-4.236970	23799.562486
HLA B*3801	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.583046	0.346054	-4.236992	38286.565911
HLA B*0803	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.506404	0.269402	-4.237002	32092.523218
HLA A*0101	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.337683	0.100651	-4.237031	21761.190313
HLA A*0219	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.455453	0.218420	-4.237033	28539.931888
HLA B*3801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.532925	0.295880	-4.237045	34113.387757
HLA B*3501	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.410843	0.173777	-4.237066	25753.915154
HLA B*1503	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.454036	0.216943	-4.237094	28446.981666
HLA A*2301	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.545001	0.307875	-4.237126	35075.284610
HLA B*4601	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.397273	0.160089	-4.237184	24961.612398
HLA A*3001	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.247103	0.009850	-4.237253	17664.565189
HLA A*2403	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.409892	0.172544	-4.237348	25697.549965
HLA B*4501	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.622680	0.385288	-4.237392	41944.968910
HLA B*5101	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.492396	0.254868	-4.237528	31073.933679
HLA B*5101	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.496686	0.259153	-4.237533	31382.417378
HLA A*2301	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.528061	0.290447	-4.237614	33733.501035
HLA A*0206	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.500817	0.263202	-4.237615	31682.306328
HLA B*0702	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.411402	0.173777	-4.237626	25787.096057
HLA A*0250	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.502595	0.264968	-4.237628	31812.320477
HLA A*2602	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.605270	0.367626	-4.237644	40296.765958
HLA A*0216	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.478663	0.240938	-4.237726	30106.723543
HLA B*4403	1:99-107	9	TLRDIVHTE	1.055970	-0.637462	-4.656317	0.418508	-4.237810	45322.875273
HLA B*0803	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.506394	0.268569	-4.237826	32091.828757
HLA B*0802	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.466667	0.228841	-4.237826	29286.469758
HLA A*8001	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.456247	0.218420	-4.237827	28592.166109
HLA A*3001	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.302426	0.064589	-4.237837	20064.404523
HLA B*5801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.334776	0.096922	-4.237854	21616.049896
HLA A*0216	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.492892	0.254868	-4.238024	31109.424411
HLA B*7301	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.082315	-0.155719	-4.238034	12086.895650
HLA A*0216	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.467424	0.229302	-4.238122	29337.530790

HLA A*6901	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.324136	0.086012	-4.238124	21092.862257
HLA B*5801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.357263	0.119119	-4.238144	22764.769385
HLA A*0206	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.507670	0.269402	-4.238269	32186.239345
HLA A*0201	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.408954	0.170651	-4.238303	25642.140451
HLA A*0201	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.395675	0.157340	-4.238335	24869.954196
HLA A*0250	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.453075	0.214737	-4.238338	28384.108188
HLA A*0101	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.375636	0.137283	-4.238354	23748.502398
HLA A*1101	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.493341	0.254868	-4.238472	31141.586044
HLA B*4002	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.645505	0.407006	-4.238500	44208.433237
HLA A*0301	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.367514	0.128996	-4.238518	23308.485639
HLA A*2602	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.609934	0.371335	-4.238598	40731.829830
HLA A*1101	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.449025	0.210423	-4.238602	28120.610263
HLA B*5401	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.546611	0.307875	-4.238736	35205.506828
HLA B*0802	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.493747	0.254868	-4.238879	31170.745435
HLA B*1509	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.511758	0.272858	-4.238900	32490.645554
HLA B*1502	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.508857	0.269799	-4.239058	32274.292184
HLA B*1501	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.382619	0.143550	-4.239069	24133.421453
HLA B*0803	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.493949	0.254868	-4.239081	31185.251013
HLA A*0201	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.380443	0.141319	-4.239124	24012.826012
HLA B*1501	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.378735	0.139599	-4.239137	23918.569298
HLA B*5101	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.468471	0.229302	-4.239169	29408.402159
HLA B*1503	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.494123	0.254868	-4.239255	31197.737960
HLA A*2601	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.336210	0.096922	-4.239287	21687.501392
HLA B*4601	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.387877	0.148535	-4.239342	24427.388786
HLA B*4501	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.587799	0.348457	-4.239342	38707.883252
HLA A*6901	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.375380	0.135996	-4.239384	23734.502559
HLA A*6801	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.648423	0.409024	-4.239399	44506.473496
HLA A*0211	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.553267	0.313851	-4.239416	35749.229994
HLA A*0250	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.321539	0.082090	-4.239450	20967.146788
HLA B*5301	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.592632	0.353175	-4.239458	39141.035693
HLA A*0216	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.460760	0.221286	-4.239475	28890.856619
HLA B*4801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.418853	0.179347	-4.239506	26233.283639
HLA B*7301	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.556979	0.317460	-4.239519	36056.110682
HLA B*2705	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.468836	0.229302	-4.239534	29433.072411
HLA B*4001	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.408938	0.169330	-4.239608	25641.169421
HLA A*0216	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.290566	0.050897	-4.239669	19523.877536
HLA B*4403	1:613-621	9	GVNRDGIIT	0.770125	-0.361383	-4.648437	0.408742	-4.239695	44507.918170
HLA A*2301	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.543063	0.303321	-4.239742	34919.086880
HLA A*6801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.509165	0.269402	-4.239763	32297.172936
HLA A*3002	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.480804	0.240938	-4.239866	30255.468027
HLA B*4002	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.643003	0.403047	-4.239956	43954.457285
HLA B*0802	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.464968	0.224721	-4.240247	29172.143859
HLA A*2601	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.395548	0.155271	-4.240277	24862.689897
HLA B*1509	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.503923	0.263371	-4.240551	31909.706373
HLA A*3201	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.482782	0.242067	-4.240715	30393.599881
HLA A*2501	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.482850	0.242067	-4.240783	30398.368609
HLA A*2301	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.536752	0.295880	-4.240872	34415.347719
HLA A*3201	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.608545	0.367626	-4.240919	40601.808178
HLA B*5101	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.457880	0.216943	-4.240937	28699.871373
HLA A*0101	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.398203	0.157255	-4.240948	25015.145384
HLA B*4801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.432543	0.191384	-4.241159	27073.418963
HLA B*1509	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.521894	0.280603	-4.241291	33257.838396
HLA B*4403	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.594505	0.353175	-4.241330	39310.163729
HLA A*2403	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.381259	0.139887	-4.241371	24057.945983
HLA B*1503	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.457988	0.216497	-4.241491	28707.014366
HLA A*2403	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.417920	0.176401	-4.241519	26177.002195
HLA B*3901	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.483602	0.242067	-4.241535	30451.038764
HLA B*4801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.423928	0.182373	-4.241555	26541.627060
HLA A*3002	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.527333	0.285730	-4.241603	33676.975151
HLA B*4001	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.306221	0.064589	-4.241632	20240.474683
HLA B*2705	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.213045	-0.028622	-4.241667	16332.204801
HLA B*4601	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.412476	0.170651	-4.241825	25850.928868
HLA A*0301	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.360992	0.119119	-4.241873	22961.057587
HLA A*3201	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.458402	0.216497	-4.241904	28734.360493
HLA B*5701	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.418387	0.176401	-4.241986	26205.198691

HLA A*2603	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.590501	0.348457	-4.242044	38949.450072
HLA B*0802	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.484168	0.242067	-4.242101	30490.766211
HLA B*0802	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.414781	0.172544	-4.242237	25988.487060
HLA A*2902	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.339160	0.096922	-4.242238	21835.365864
HLA B*5301	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.598924	0.356622	-4.242302	39712.226238
HLA B*1501	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.374499	0.132177	-4.242323	23686.400982
HLA B*1801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.306951	0.064589	-4.242363	20274.557450
HLA A*2402	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.566889	0.324517	-4.242372	36888.330983
HLA A*2301	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.471223	0.228841	-4.242382	29595.295161
HLA A*6801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.339372	0.096922	-4.242450	21845.999874
HLA B*4801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.429298	0.186843	-4.242455	26871.905606
HLA A*3002	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.567949	0.325463	-4.242485	36978.443233
HLA A*2601	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.391037	0.148535	-4.242502	24605.778037
HLA A*3301	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.638271	0.395731	-4.242540	43478.150278
HLA B*2705	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.490881	0.248296	-4.242585	30965.693918
HLA A*2603	1:508-516	9	AQKNLNVYG	0.899800	-0.490776	-4.651616	0.409024	-4.242592	44834.892637
HLA A*6801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.511249	0.268569	-4.242680	32452.525672
HLA A*0250	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.567312	0.324517	-4.242795	36924.269599
HLA A*0203	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.422389	0.179592	-4.242797	26447.743840
HLA B*4601	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.231834	-0.010996	-4.242829	17054.290200
HLA A*2403	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.375011	0.132130	-4.242881	23714.352156
HLA B*3801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.546326	0.303321	-4.243005	35182.468964
HLA B*4601	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.339950	0.096922	-4.243028	21875.092600
HLA B*0803	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.506263	0.263202	-4.243061	32082.107889
HLA B*5301	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.610693	0.367626	-4.243067	40803.066614
HLA B*5101	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.489462	0.246391	-4.243071	30864.676382
HLA B*5801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.372091	0.128996	-4.243095	23555.420147
HLA B*0702	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.466484	0.223276	-4.243207	29274.114314
HLA B*7301	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.516072	0.272858	-4.243214	32814.968738
HLA A*3002	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.512656	0.269402	-4.243254	32557.859423
HLA A*0301	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.365620	0.122274	-4.243346	23207.073261
HLA A*1101	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.461825	0.218420	-4.243405	28961.745684
HLA B*0802	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.461919	0.218420	-4.243499	28968.013556
HLA B*0803	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.513384	0.269799	-4.243586	32612.506902
HLA A*2603	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.589714	0.346054	-4.243660	38878.925408
HLA B*4402	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.417497	0.173777	-4.243720	26151.523959
HLA A*2501	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.454255	0.210423	-4.243832	28461.297503
HLA B*3801	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.578721	0.334871	-4.243850	37907.139408
HLA B*5301	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.590022	0.346054	-4.243968	38906.488493
HLA B*0803	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.476359	0.232368	-4.243990	29947.367347
HLA A*2403	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.423359	0.179347	-4.244012	26506.901680
HLA A*0202	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.404157	0.160089	-4.244068	25360.430776
HLA A*3001	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.196688	-0.047418	-4.244106	15728.514340
HLA B*3901	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.401370	0.157255	-4.244115	25198.235881
HLA A*0301	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.344769	0.100651	-4.244117	22119.163246
HLA B*4403	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.639310	0.395099	-4.244211	43582.238367
HLA B*3901	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.486476	0.242192	-4.244283	30653.179776
HLA A*1101	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.524899	0.280603	-4.244296	33488.755601
HLA A*2301	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.519439	0.275124	-4.244315	33070.351186
HLA A*8001	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.423667	0.179347	-4.244320	26525.693659
HLA A*0212	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.414983	0.170651	-4.244332	26000.581029
HLA B*5301	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.165200	-0.079239	-4.244438	14628.503658
HLA A*2501	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.401835	0.157255	-4.244581	25225.241635
HLA B*1509	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.507908	0.263202	-4.244705	32203.830674
HLA B*4402	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.424059	0.179347	-4.244712	26549.669165
HLA A*6801	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.667400	0.422686	-4.244714	46494.327924
HLA B*5101	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.487458	0.242669	-4.244789	30722.575277
HLA A*2602	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.605310	0.360485	-4.244825	40300.472146
HLA A*0101	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.388387	0.143550	-4.244837	24456.082059
HLA A*2501	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.461804	0.216943	-4.244861	28960.335600
HLA A*2603	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.639979	0.395099	-4.244880	43649.486092
HLA A*2902	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.463338	0.218420	-4.244918	29062.823471
HLA B*0702	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.393537	0.148535	-4.245002	24747.820312
HLA B*4001	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.386933	0.141914	-4.245019	24374.322425
HLA B*4002	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.612685	0.367626	-4.245059	40990.684218

HLA B*5701	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.415751	0.170651	-4.245100	26046.617642
HLA B*3501	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.436596	0.191384	-4.245212	27327.252252
HLA A*0101	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.381268	0.135996	-4.245272	24058.466592
HLA B*5701	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.424639	0.179347	-4.245293	26585.169678
HLA B*1509	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.510313	0.264968	-4.245346	32382.726146
HLA B*0803	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.463812	0.218420	-4.245393	29094.600615
HLA B*5401	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.127528	-0.117875	-4.245403	13413.072194
HLA B*5701	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.417210	0.171585	-4.245625	26134.269479
HLA B*0803	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.493942	0.248296	-4.245646	31184.744891
HLA A*3001	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.303568	0.057919	-4.245649	20117.227389
HLA B*1502	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.606149	0.360485	-4.245664	40378.380883
HLA B*0803	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.518598	0.272858	-4.245739	33006.364486
HLA B*3901	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.419656	0.173777	-4.245879	26281.864919
HLA A*2602	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.494210	0.248296	-4.245914	31203.983308
HLA A*0211	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.417751	0.171585	-4.246166	26166.807923
HLA A*1101	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.475167	0.228841	-4.246327	29865.339839
HLA B*4002	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.619767	0.373369	-4.246397	41664.532718
HLA A*0250	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.592458	0.346054	-4.246404	39125.369428
HLA A*3101	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.378681	0.132177	-4.246505	23915.593357
HLA A*0219	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.471251	0.224721	-4.246529	29597.216510
HLA B*5701	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.387865	0.141319	-4.246546	24426.728047
HLA B*2705	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.501442	0.254868	-4.246574	31727.930954
HLA A*6801	1:135-143	9	IHRDVKPAN	0.926474	-0.531375	-4.641678	0.395099	-4.246579	43820.548828
HLA A*6901	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.384012	0.137283	-4.246730	24210.967340
HLA A*2403	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.395306	0.148535	-4.246771	24848.839804
HLA B*1502	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.564384	0.317460	-4.246924	36676.210356
HLA B*5701	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.402298	0.155271	-4.247027	25252.139721
HLA A*0203	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.426456	0.179347	-4.247109	26696.577501
HLA B*0801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.388432	0.141319	-4.247112	24458.595977
HLA A*3002	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.564664	0.317460	-4.247204	36699.829252
HLA B*3901	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.476540	0.229302	-4.247238	29959.844865
HLA A*3002	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.517172	0.269799	-4.247373	32898.155862
HLA A*3002	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.472144	0.224721	-4.247422	29658.123805
HLA A*0101	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.379619	0.132130	-4.247489	23967.272015
HLA A*2902	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.423899	0.176401	-4.247498	26539.904069
HLA B*4403	1:10-18	9	RYELGEILG	0.929933	-0.507247	-4.670229	0.422686	-4.247543	46798.157456
HLA A*3301	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.541045	0.293372	-4.247673	34757.191038
HLA A*3002	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.507898	0.260101	-4.247797	32203.133805
HLA A*3002	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.420457	0.172544	-4.247914	26330.393721
HLA A*6901	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.391603	0.143550	-4.248053	24637.879561
HLA A*2902	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.427654	0.179592	-4.248062	26770.336224
HLA A*2603	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.651962	0.403854	-4.248107	44870.561932
HLA B*5801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.370568	0.122446	-4.248122	23472.988645
HLA B*5101	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.496433	0.248296	-4.248137	31364.086990
HLA A*2601	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.390083	0.141914	-4.248169	24551.792845
HLA B*0803	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.367307	0.119119	-4.248188	23297.391804
HLA A*8001	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.430621	0.182373	-4.248248	26953.875953
HLA B*5801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.355558	0.107303	-4.248254	22675.534296
HLA A*0216	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.473062	0.224721	-4.248341	29720.925043
HLA A*2601	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.360722	0.112336	-4.248386	22946.777100
HLA A*8001	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.439937	0.191384	-4.248553	27538.287735
HLA B*0801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.390490	0.141914	-4.248576	24574.781890
HLA A*2403	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.389071	0.140490	-4.248580	24494.613046
HLA A*0216	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.397317	0.148535	-4.248782	24964.178281
HLA A*0250	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.574278	0.325463	-4.248815	37521.322406
HLA B*4501	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.630675	0.381799	-4.248877	42724.321483
HLA B*1503	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.481307	0.232368	-4.248938	30290.515558
HLA A*2501	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.472245	0.223276	-4.248968	29665.023836
HLA A*0206	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.513967	0.264968	-4.248999	32656.290918
HLA B*3501	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.381205	0.132177	-4.249028	24054.952700
HLA B*3901	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.477926	0.228841	-4.249085	30055.624509
HLA A*0216	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.418488	0.169330	-4.249159	26211.295390
HLA B*5101	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.463909	0.214737	-4.249171	29101.054672
HLA A*0212	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.371635	0.122446	-4.249189	23530.711267
HLA A*0301	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.368334	0.119114	-4.249220	23352.534827

HLA A*0212	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.436316	0.186843	-4.249473	27309.665262
HLA A*0211	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.312080	0.062590	-4.249490	20515.415115
HLA A*2501	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.422104	0.172544	-4.249561	26430.436902
HLA A*0201	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.389456	0.139887	-4.249569	24516.354844
HLA A*6801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.409690	0.160089	-4.249601	25685.596949
HLA B*2705	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.409692	0.160089	-4.249603	25685.735905
HLA A*0206	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.419022	0.169330	-4.249692	26243.503809
HLA A*2501	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.490653	0.240938	-4.249715	30949.448646
HLA A*0201	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.390278	0.140490	-4.249788	24562.819587
HLA A*6901	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.372084	0.122274	-4.249810	23555.037854
HLA A*6901	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.391740	0.141914	-4.249826	24645.611489
HLA A*6801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.423646	0.173777	-4.249869	26524.402181
HLA B*1801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.490815	0.240938	-4.249877	30961.003686
HLA A*3002	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.574483	0.324517	-4.249966	37538.986361
HLA A*0101	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.391911	0.141914	-4.249997	24655.346503
HLA A*0219	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.445444	0.195249	-4.250195	27889.718204
HLA B*0702	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.392191	0.141914	-4.250277	24671.224154
HLA A*0216	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.445536	0.195249	-4.250287	27895.603156
HLA B*3901	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.466784	0.216497	-4.250287	29294.392658
HLA A*0216	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.441762	0.191384	-4.250378	27654.288115
HLA A*0201	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.394115	0.143550	-4.250565	24780.777447
HLA B*1503	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.519152	0.268569	-4.250584	33048.531741
HLA A*2601	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.394148	0.143550	-4.250598	24782.654375
HLA B*1509	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.509785	0.259153	-4.250631	32343.333060
HLA A*1101	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.467172	0.216497	-4.250675	29320.553436
HLA A*6802	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.392616	0.141914	-4.250702	24695.393800
HLA B*0702	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.421383	0.170651	-4.250732	26386.576714
HLA A*0201	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.382924	0.132177	-4.250748	24150.400111
HLA A*3301	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.584954	0.334125	-4.250829	38455.122234
HLA A*6801	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.554246	0.303321	-4.250926	35829.968567
HLA B*1502	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.607718	0.356622	-4.251096	40524.564497
HLA B*1503	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.499405	0.248296	-4.251109	31579.463551
HLA B*0702	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.423688	0.172544	-4.251144	26526.985200
HLA B*5101	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.480097	0.228841	-4.251256	30206.240821
HLA B*4403	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.599718	0.348457	-4.251261	39784.908163
HLA A*3201	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.604448	0.353175	-4.251273	40220.537785
HLA B*1509	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.391418	0.139887	-4.251530	24627.352043
HLA B*3501	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.446793	0.195249	-4.251544	27976.458093
HLA A*2902	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.399655	0.148101	-4.251554	25098.918769
HLA A*0206	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.314192	0.062590	-4.251602	20615.434663
HLA A*2602	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.575989	0.324299	-4.251689	37669.387734
HLA B*5301	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.576021	0.324299	-4.251722	37672.240863
HLA A*0212	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.393044	0.141319	-4.251724	24719.720854
HLA B*4501	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.623150	0.371335	-4.251814	41990.376997
HLA A*3301	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.555177	0.303321	-4.251856	35906.809966
HLA A*3002	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.470339	0.218420	-4.251920	29535.156015
HLA A*3001	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.121147	-0.130925	-4.252072	13217.431272
HLA B*5401	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.481015	0.228841	-4.252175	30270.202699
HLA A*2501	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.481483	0.229302	-4.252181	30302.808176
HLA A*2601	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.384386	0.132177	-4.252209	24231.801904
HLA A*3101	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.364650	0.112336	-4.252314	23155.279946
HLA A*0212	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.434707	0.182373	-4.252334	27208.649100
HLA A*0250	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.519974	0.267585	-4.252389	33111.167134
HLA A*3101	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.388410	0.135996	-4.252414	24457.405141
HLA B*4801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.426230	0.173777	-4.252453	26682.716251
HLA B*5701	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.384684	0.132177	-4.252508	24248.456228
HLA A*0206	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.538258	0.285730	-4.252528	34534.898325
HLA B*5401	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.525418	0.272858	-4.252560	33528.818216
HLA A*0250	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.521866	0.269282	-4.252584	33255.679412
HLA B*4001	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.423300	0.170651	-4.252649	26503.316937
HLA A*2601	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.204803	-0.047884	-4.252686	16025.176586
HLA A*0202	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.577248	0.324517	-4.252731	37778.776200
HLA A*2603	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.659771	0.407006	-4.252766	45684.744098
HLA B*4801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.412932	0.160089	-4.252843	25878.074138
HLA A*8001	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.349891	0.096922	-4.252968	22381.571209

HLA B*1509	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.534685	0.281512	-4.253173	34251.895870
HLA B*1501	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.390548	0.137283	-4.253266	24578.105786
HLA A*3002	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.187497	-0.065831	-4.253327	15399.141771
HLA B*4403	1:6-14	9	HLSDRYELG	1.029020	-0.614858	-4.667496	0.414162	-4.253334	46504.641763
HLA A*0212	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.413468	0.160089	-4.253379	25910.013265
HLA A*8001	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.463925	0.210423	-4.253502	29102.156727
HLA B*0702	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.464097	0.210423	-4.253674	29113.652076
HLA B*4001	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.375951	0.122274	-4.253677	23765.724526
HLA B*3901	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.500154	0.246391	-4.253763	31634.009009
HLA B*0801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.245564	-0.008210	-4.253774	17602.081971
HLA B*7301	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.579311	0.325463	-4.253847	37958.647801
HLA A*3101	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.445273	0.191384	-4.253888	27878.706118
HLA A*0250	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.561788	0.307875	-4.253913	36457.616649
HLA A*0216	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.436798	0.182373	-4.254425	27339.969227
HLA B*1503	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.523778	0.269282	-4.254497	33402.448699
HLA A*0219	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.414626	0.160089	-4.254537	25979.209457
HLA A*0211	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.535187	0.280603	-4.254584	34291.572810
HLA B*4801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.434188	0.179592	-4.254596	27176.138272
HLA A*2301	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.477879	0.223276	-4.254602	30052.372733
HLA A*2603	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.635008	0.380356	-4.254652	43152.665281
HLA B*0802	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.477973	0.223225	-4.254748	30058.876637
HLA A*0203	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.414948	0.160089	-4.254859	25998.471210
HLA A*3001	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.293378	0.038504	-4.254875	19650.717326
HLA A*2902	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.387160	0.132177	-4.254984	24387.116433
HLA B*4001	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.403553	0.148535	-4.255018	25325.195617
HLA B*0803	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.515128	0.260101	-4.255026	32743.681096
HLA B*2705	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.487411	0.232368	-4.255042	30719.251342
HLA A*0201	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.391211	0.135996	-4.255215	24615.630484
HLA A*6901	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.374541	0.119119	-4.255422	23688.707629
HLA A*2301	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.537053	0.281512	-4.255541	34439.187423
HLA B*5401	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.558873	0.303321	-4.255552	36213.671952
HLA B*0802	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.450801	0.195249	-4.255552	28235.855587
HLA A*3201	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.487951	0.232368	-4.255583	30757.498314
HLA A*3101	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.392921	0.137283	-4.255639	24712.767823
HLA B*1503	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.438050	0.182373	-4.255678	27418.917000
HLA A*2402	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.518992	0.263202	-4.255790	33036.376332
HLA A*3101	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.374938	0.119119	-4.255819	23710.375437
HLA A*2301	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.541580	0.285730	-4.255850	34800.088911
HLA A*0250	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.428396	0.172544	-4.255853	26816.139922
HLA B*5101	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.466301	0.210423	-4.255877	29261.764083
HLA A*2403	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.363236	0.107303	-4.255933	23079.991577
HLA A*0250	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.525752	0.269799	-4.255953	33554.585092
HLA B*4601	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.413367	0.157340	-4.256026	25903.986643
HLA B*1501	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.245127	-0.010996	-4.256123	17584.378972
HLA B*7301	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.537760	0.281512	-4.256248	34495.313076
HLA B*1502	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.473206	0.216943	-4.256263	29730.734663
HLA A*0201	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.388401	0.132130	-4.256271	24456.875900
HLA A*2601	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.396175	0.139887	-4.256288	24898.628520
HLA A*6801	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.585748	0.329236	-4.256512	38525.503389
HLA A*0211	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.549930	0.293372	-4.256559	35475.655039
HLA A*3001	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.281887	0.025261	-4.256626	19137.582560
HLA B*5301	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.585908	0.329236	-4.256672	38539.678468
HLA B*4403	1:586-594	9	MLDKGADVD	1.256082	-0.849076	-4.663737	0.407006	-4.256732	46103.842957
HLA A*0101	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.379203	0.122274	-4.256929	23944.333129
HLA A*3201	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.412302	0.155271	-4.257031	25840.581991
HLA A*3201	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.429670	0.172544	-4.257126	26894.884522
HLA B*0702	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.397099	0.139887	-4.257211	24951.621470
HLA B*7301	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.607747	0.350532	-4.257215	40527.195383
HLA B*0801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.448607	0.191384	-4.257222	28093.544267
HLA A*3201	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.582835	0.325463	-4.257372	38267.929101
HLA A*6802	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.414732	0.157340	-4.257391	25985.534736
HLA B*4801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.429113	0.171585	-4.257528	26860.423511
HLA A*2601	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.394815	0.137283	-4.257532	24820.759922
HLA A*2403	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.444422	0.186843	-4.257579	27824.162447
HLA A*2402	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.569917	0.312328	-4.257589	37146.465103

HLA B*1801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.516751	0.259153	-4.257598	32866.313690
HLA A*3301	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.582168	0.324517	-4.257651	38209.179073
HLA A*6901	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.320259	0.062590	-4.257668	20905.418516
HLA B*0801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.354629	0.096922	-4.257707	22627.130542
HLA A*0212	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.437064	0.179347	-4.257717	27356.687737
HLA A*2601	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.398351	0.140490	-4.257861	25023.672574
HLA A*2602	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.587189	0.329236	-4.257953	38653.476132
HLA B*5301	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.539475	0.281512	-4.257963	34631.811979
HLA B*5701	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.399937	0.141914	-4.258023	25115.217943
HLA A*2602	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.233001	-0.025025	-4.258026	17100.206024
HLA A*2402	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.543772	0.285730	-4.258042	34976.183843
HLA A*3301	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.354975	0.096922	-4.258053	22645.132008
HLA B*5701	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.415326	0.157255	-4.258071	26021.125539
HLA B*5301	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.608736	0.350532	-4.258204	40619.603830
HLA A*2603	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.614849	0.356622	-4.258227	41195.430276
HLA A*2301	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.521546	0.263202	-4.258344	33231.220713
HLA B*1801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.476798	0.218420	-4.258378	29977.678909
HLA B*3501	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.430010	0.171585	-4.258425	26915.990059
HLA A*0211	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.527942	0.269402	-4.258540	33724.195099
HLA B*0801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.395856	0.137283	-4.258573	24880.316218
HLA B*5401	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.528435	0.269799	-4.258636	33762.530144
HLA B*1801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.469129	0.210423	-4.258706	29452.982850
HLA B*4002	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.639319	0.380356	-4.258963	43583.181477
HLA B*5701	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.416355	0.157340	-4.259015	26082.856522
HLA A*1101	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.355962	0.096922	-4.259039	22696.643722
HLA B*4501	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.619680	0.360485	-4.259195	41656.193734
HLA B*4002	1:503-511	9	QTVDVAQKN	0.937761	-0.552473	-4.644504	0.385288	-4.259216	44106.667228
HLA A*0101	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.381686	0.122446	-4.259240	24081.645097
HLA B*1517	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.514192	0.254868	-4.259324	32673.255347
HLA A*6901	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.388389	0.128996	-4.259394	24456.214364
HLA A*3201	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.552783	0.293372	-4.259411	35709.411915
HLA A*3301	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.641234	0.381799	-4.259435	43775.766572
HLA A*0101	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.399129	0.139599	-4.259530	25068.521940
HLA B*4402	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.432115	0.172544	-4.259572	27046.775599
HLA A*2603	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.567495	0.307875	-4.259620	36939.853871
HLA B*1502	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.627275	0.367626	-4.259649	42391.176461
HLA B*1801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.523024	0.263371	-4.259653	33344.493198
HLA B*4402	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.442120	0.182373	-4.259747	27677.037675
HLA B*1502	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.529152	0.269402	-4.259750	33818.284850
HLA B*4403	1:70-78	9	AIVAVYDTG	0.896659	-0.516303	-4.640144	0.380356	-4.259788	43666.018944
HLA B*0802	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.481130	0.221286	-4.259845	30278.227926
HLA B*3901	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.514745	0.254868	-4.259876	32714.820054
HLA A*0219	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.439568	0.179592	-4.259976	27514.907949
HLA B*1517	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.342109	0.082090	-4.260019	21984.119538
HLA B*3801	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.541547	0.281512	-4.260036	34797.453306
HLA B*4403	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.584339	0.324299	-4.260039	38400.654902
HLA A*0301	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.367357	0.107303	-4.260054	23300.038717
HLA B*3501	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.415519	0.155271	-4.260248	26032.671355
HLA A*0201	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.372603	0.112336	-4.260267	23583.216757
HLA A*0216	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.436688	0.176401	-4.260286	27333.018519
HLA A*3002	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.540897	0.280603	-4.260293	34745.347006
HLA A*0250	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.476817	0.216497	-4.260319	29978.976344
HLA B*5401	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.528888	0.268569	-4.260320	33797.800302
HLA B*2705	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.429717	0.169330	-4.260387	26897.794646
HLA B*4403	1:91-99	9	VMEYVDGVT	0.689957	-0.286103	-4.664266	0.403854	-4.260411	46159.995878
HLA B*3801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.520534	0.260101	-4.260433	33153.826994
HLA B*4002	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.631801	0.371335	-4.260465	42835.178165
HLA A*8001	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.437190	0.176401	-4.260789	27364.680724
HLA A*2501	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.373226	0.112336	-4.260890	23617.050390
HLA A*0212	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.409041	0.148101	-4.260940	25647.273647
HLA B*0802	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.477883	0.216943	-4.260941	30052.697895
HLA B*3501	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.443320	0.182373	-4.260947	27753.655409
HLA A*3101	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.400858	0.139887	-4.260971	25168.535711
HLA A*0202	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.521133	0.260101	-4.261032	33199.594981
HLA A*2301	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.527239	0.266144	-4.261095	33669.688392

HLA B*4403	1:223-231	9	SVAYQHVRE	0.970768	-0.567721	-4.664155	0.403047	-4.261108	46148.260509
HLA B*4001	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.393307	0.132130	-4.261177	24734.703259
HLA B*5101	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.484446	0.223225	-4.261221	30510.236722
HLA B*3901	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.509594	0.248296	-4.261299	32329.163283
HLA A*0250	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.585671	0.324299	-4.261371	38518.626185
HLA B*4403	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.629009	0.367626	-4.261383	42560.761465
HLA B*5401	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.542036	0.280603	-4.261433	34836.631420
HLA B*1509	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.456832	0.195249	-4.261583	28630.707494
HLA A*3301	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.632926	0.371335	-4.261590	42946.322487
HLA A*2402	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.590875	0.329236	-4.261639	38982.967726
HLA A*3002	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.527888	0.266144	-4.261743	33719.999144
HLA A*2602	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.614955	0.353175	-4.261780	41205.460319
HLA B*4402	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.409889	0.148101	-4.261789	25697.410945
HLA B*1801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.485071	0.223276	-4.261794	30554.173489
HLA A*0216	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.384311	0.122446	-4.261864	24227.607344
HLA A*2501	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.516859	0.254868	-4.261991	32874.493651
HLA A*6901	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.401720	0.139599	-4.262122	25218.555699
HLA B*1801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.417457	0.155271	-4.262186	26149.118963
HLA B*2705	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.485428	0.223225	-4.262203	30579.308615
HLA A*2301	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.525576	0.263371	-4.262204	33540.973360
HLA B*4001	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.394390	0.132177	-4.262213	24796.467579
HLA A*2902	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.404140	0.141914	-4.262226	25359.470414
HLA A*1101	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.457488	0.195249	-4.262239	28673.954141
HLA B*3901	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.485538	0.223225	-4.262313	30587.084845
HLA A*2402	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.558194	0.295880	-4.262313	36157.097636
HLA B*5401	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.240607	-0.021825	-4.262432	17402.298980
HLA A*6801	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.588018	0.325463	-4.262554	38727.362850
HLA A*0250	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.580027	0.317460	-4.262567	38021.331885
HLA B*5401	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.431963	0.169330	-4.262633	27037.266467
HLA A*0219	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.454024	0.191384	-4.262640	28446.212201
HLA A*0219	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.432141	0.169330	-4.262812	27048.385167
HLA A*0203	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.439286	0.176401	-4.262885	27497.051433
HLA A*0201	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.402714	0.139599	-4.263115	25276.331497
HLA B*2705	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.486523	0.223276	-4.263246	30656.496562
HLA B*7301	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.481687	0.218420	-4.263268	30317.073864
HLA A*0212	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.434864	0.171585	-4.263279	27218.513005
HLA B*0803	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.528289	0.264968	-4.263322	33751.207647
HLA A*0203	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.420671	0.157340	-4.263331	26343.359363
HLA B*0702	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.406922	0.143550	-4.263372	25522.426988
HLA B*1501	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.403299	0.139887	-4.263412	25310.403236
HLA B*1502	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.577293	0.313851	-4.263442	37782.659600
HLA A*2402	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.545161	0.281512	-4.263649	35088.190215
HLA B*3801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.554202	0.290447	-4.263755	35826.285870
HLA B*1502	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.588067	0.324299	-4.263768	38731.762825
HLA A*2402	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.539005	0.275124	-4.263882	34594.361390
HLA A*0201	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.401271	0.137283	-4.263989	25192.511105
HLA B*0802	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.493320	0.229302	-4.264018	31140.069829
HLA A*0202	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.485308	0.221286	-4.264022	30570.872814
HLA B*1509	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.524138	0.260101	-4.264037	33430.107787
HLA A*2301	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.533930	0.269799	-4.264132	34192.466521
HLA A*2403	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.424249	0.160089	-4.264161	26561.305807
HLA B*4801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.433506	0.169330	-4.264177	27133.535930
HLA B*1801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.433513	0.169330	-4.264184	27133.976302
HLA B*4002	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.644072	0.379878	-4.264194	44062.784431
HLA A*0211	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.421479	0.157255	-4.264225	26392.430050
HLA B*1501	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.404716	0.140490	-4.264225	25393.104721
HLA A*6802	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.400249	0.135996	-4.264253	25133.295228
HLA B*1801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.496656	0.232368	-4.264288	31380.210375
HLA B*1501	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.371619	0.107303	-4.264316	23529.820194
HLA A*8001	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.443926	0.179592	-4.264334	27792.419659
HLA A*6802	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.235715	-0.028622	-4.264337	17207.389843
HLA B*4002	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.646170	0.381799	-4.264371	44276.168126
HLA A*6802	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.446866	0.182373	-4.264493	27981.150322
HLA A*0216	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.474963	0.210423	-4.264540	29851.286715
HLA B*0803	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.475938	0.211378	-4.264560	29918.381247

HLA A*3002	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.567902	0.303321	-4.264581	36974.442464
HLA A*2902	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.276735	0.012088	-4.264647	18911.877959
HLA B*3901	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.489441	0.224721	-4.264719	30863.173648
HLA A*2403	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.400773	0.135996	-4.264777	25163.634465
HLA A*2501	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.400820	0.135996	-4.264824	25166.357262
HLA A*2301	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.537720	0.272858	-4.264862	34492.140753
HLA A*6901	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.372187	0.107303	-4.264884	23560.645447
HLA A*1101	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.436509	0.171585	-4.264924	27321.782815
HLA B*0802	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.397141	0.132130	-4.265011	24954.051328
HLA A*3201	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.438790	0.173777	-4.265014	27465.681825
HLA A*0219	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.436716	0.171585	-4.265131	27334.793000
HLA B*4002	1:1-9	9	MTTPSHLSD	1.144018	-0.795561	-4.613592	0.348457	-4.265135	41076.371105
HLA A*0219	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.447620	0.182373	-4.265247	28029.783888
HLA A*3002	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.579170	0.313851	-4.265319	37946.328675
HLA A*3002	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.387856	0.122446	-4.265410	24426.199470
HLA A*2403	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.377812	0.112336	-4.265476	23867.770373
HLA B*1503	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.029545	-0.236114	-4.265660	10703.981248
HLA B*4402	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.384787	0.119119	-4.265668	24254.228899
HLA A*2501	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.487115	0.221286	-4.265829	30698.318822
HLA B*5101	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.507924	0.242067	-4.265857	32205.050231
HLA A*0211	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.506801	0.240938	-4.265863	32121.877907
HLA B*1502	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.590400	0.324517	-4.265884	38940.390501
HLA A*2501	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.490658	0.224721	-4.265936	30949.783514
HLA A*6802	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.254971	-0.010996	-4.265967	17987.523614
HLA A*2301	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.526097	0.260101	-4.265996	33581.280114
HLA A*0216	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.437618	0.171585	-4.266033	27391.637252
HLA B*4601	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.388488	0.122446	-4.266042	24461.771822
HLA A*3201	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.556502	0.290447	-4.266055	36016.535326
HLA B*7301	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.579912	0.313851	-4.266061	38011.254352
HLA A*8001	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.452930	0.186843	-4.266087	28374.589382
HLA A*2501	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.398241	0.132130	-4.266111	25017.310744
HLA B*1501	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.385260	0.119119	-4.266141	24280.616994
HLA B*4402	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.426275	0.160089	-4.266186	26685.459052
HLA B*5801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.352228	0.086012	-4.266217	22502.372454
HLA A*0219	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.414396	0.148101	-4.266295	25965.439733
HLA A*0211	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.414844	0.148535	-4.266309	25992.283398
HLA B*4601	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.378665	0.112336	-4.266329	23914.687709
HLA A*2402	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.583791	0.317460	-4.266331	38352.281210
HLA B*4601	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.406328	0.139887	-4.266440	25487.518288
HLA A*0219	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.442869	0.176401	-4.266468	27724.842689
HLA B*4002	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.626954	0.360485	-4.266469	42359.769677
HLA A*2301	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.547085	0.280603	-4.266482	35244.000350
HLA B*1517	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.477949	0.211378	-4.266571	30057.250529
HLA B*4501	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.646461	0.379878	-4.266584	44305.879706
HLA A*6802	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.443052	0.176401	-4.266651	27736.544248
HLA A*1101	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.421970	0.155271	-4.266699	26422.287972
HLA A*0219	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.317644	0.050897	-4.266747	20779.920874
HLA A*0212	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.398882	0.132130	-4.266752	25054.286101
HLA B*4402	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.436110	0.169330	-4.266780	27296.667037
HLA A*6901	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.340211	0.073404	-4.266806	21888.232488
HLA B*2705	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.443212	0.176401	-4.266811	27746.749635
HLA B*1801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.495777	0.228841	-4.266936	31316.783029
HLA A*2601	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.395940	0.128996	-4.266945	24885.162281
HLA B*4801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.424301	0.157340	-4.266961	26564.467257
HLA A*2902	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.317879	0.050897	-4.266982	20791.165622
HLA B*3901	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.427095	0.160089	-4.267006	26735.890161
HLA B*0801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.353088	0.086012	-4.267076	22546.971728
HLA B*4001	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.406992	0.139887	-4.267105	25526.569530
HLA B*0802	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.477594	0.210423	-4.267171	30032.706990
HLA A*0219	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.424538	0.157255	-4.267284	26578.986016
HLA A*0211	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.515633	0.248296	-4.267337	32781.788286
HLA B*0702	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.458775	0.191384	-4.267391	28759.087629
HLA A*2301	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.536823	0.269402	-4.267421	34420.933668
HLA A*6801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-3.878878	-0.388552	-4.267430	7566.195617
HLA A*0216	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.485853	0.218420	-4.267433	30609.266231

HLA B*5101	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.484133	0.216497	-4.267636	30488.292037
HLA B*1517	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.447249	0.179592	-4.267656	28005.835316
HLA B*5701	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.407991	0.139887	-4.268104	25585.327815
HLA B*3801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.534278	0.266144	-4.268134	34219.854147
HLA A*3201	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.535869	0.267585	-4.268283	34345.413980
HLA A*0211	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.485360	0.216943	-4.268417	30574.511502
HLA B*4601	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.404490	0.135996	-4.268494	25379.920252
HLA B*0702	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.115941	-0.152648	-4.268588	13059.922570
HLA B*1801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.404674	0.135996	-4.268677	25390.632111
HLA A*3101	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.387896	0.119114	-4.268781	24428.446004
HLA B*0802	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.387924	0.119119	-4.268805	24430.031918
HLA B*3801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.536524	0.267585	-4.268939	34397.292684
HLA B*0801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.397989	0.128996	-4.268994	25002.833461
HLA B*4801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.439780	0.170651	-4.269129	27528.307945
HLA A*1101	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.448524	0.179347	-4.269178	28088.225367
HLA A*2402	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.583140	0.313851	-4.269290	38294.851851
HLA A*3301	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.636984	0.367626	-4.269357	43349.444992
HLA A*0211	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.492678	0.223276	-4.269402	31094.113013
HLA A*3201	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.626075	0.356622	-4.269453	42274.149863
HLA A*0206	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.492685	0.223225	-4.269460	31094.617664
HLA B*4001	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.410836	0.141319	-4.269517	25753.497180
HLA A*0219	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.456578	0.186843	-4.269735	28613.984373
HLA B*7301	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.538397	0.268569	-4.269828	34545.923053
HLA A*0219	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.440503	0.170651	-4.269852	27574.215110
HLA A*2902	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.456712	0.186843	-4.269869	28622.809247
HLA B*4002	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.615930	0.346054	-4.269875	41298.074788
HLA A*2902	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.440604	0.170651	-4.269953	27580.630314
HLA B*1801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.516410	0.246391	-4.270019	32840.542348
HLA B*1501	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-3.893726	-0.376448	-4.270174	7829.360863
HLA A*0203	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.406182	0.135996	-4.270186	25478.970873
HLA A*3101	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.377532	0.107303	-4.270229	23852.409801
HLA B*4601	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.389418	0.119119	-4.270299	24514.232844
HLA B*1801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.525249	0.254868	-4.270381	33515.760881
HLA A*0101	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.377774	0.107303	-4.270471	23865.704511
HLA B*1801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.491785	0.221286	-4.270500	31030.256704
HLA A*1101	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.418615	0.148101	-4.270515	26218.953720
HLA A*3002	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.480987	0.210423	-4.270564	30268.237661
HLA B*1503	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.491877	0.221286	-4.270591	31036.804335
HLA A*3201	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.551230	0.280603	-4.270626	35581.945359
HLA A*2402	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.530742	0.260101	-4.270641	33942.371242
HLA B*4801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.419269	0.148535	-4.270733	26258.415361
HLA A*2601	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.393185	0.122446	-4.270738	24727.746014
HLA A*1101	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.453228	0.182373	-4.270855	28394.091010
HLA A*0301	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.356960	0.086012	-4.270948	22748.887948
HLA A*0201	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.393415	0.122446	-4.270969	24740.859377
HLA B*7301	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.595515	0.324517	-4.270999	39401.715534
HLA A*8001	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.442766	0.171585	-4.271181	27718.243989
HLA A*2602	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.541019	0.269799	-4.271220	34755.122742
HLA B*1502	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.567169	0.295880	-4.271288	36912.086481
HLA A*8001	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.431643	0.160089	-4.271555	27017.381251
HLA A*6801	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.653463	0.381799	-4.271664	45025.944255
HLA A*0212	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.407857	0.135996	-4.271861	25577.439445
HLA A*0211	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.514542	0.242669	-4.271873	32699.603009
HLA B*4001	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.411518	0.139599	-4.271919	25793.932724
HLA B*4402	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.442629	0.170651	-4.271979	27709.548100
HLA A*2601	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.394434	0.122274	-4.272161	24799.016487
HLA A*2602	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.622727	0.350532	-4.272195	41949.507508
HLA B*1801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.451600	0.179347	-4.272253	28287.839349
HLA A*0201	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.401363	0.128996	-4.272367	25197.826925
HLA B*4801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.444951	0.172544	-4.272407	27858.051336
HLA A*3101	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.412951	0.140490	-4.272460	25879.194143
HLA A*2301	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.540180	0.267585	-4.272595	34688.063893
HLA B*3901	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.493905	0.221286	-4.272619	31182.045711
HLA A*2301	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.537636	0.264968	-4.272668	34485.423855
HLA A*1101	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.497422	0.224721	-4.272700	31435.602093

HLA A*6901	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.282578	0.009850	-4.272728	19168.045246
HLA A*0250	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.532850	0.260101	-4.272749	34107.482679
HLA A*2403	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.414682	0.141914	-4.272768	25982.582748
HLA B*1502	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.607641	0.334871	-4.272769	40517.330440
HLA B*0702	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.459656	0.186843	-4.272813	28817.490654
HLA B*2705	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.452587	0.179592	-4.272994	28352.186736
HLA A*3001	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.238760	-0.034337	-4.273097	17328.458499
HLA B*1509	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.521497	0.248296	-4.273201	33227.445606
HLA B*4601	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.410484	0.137283	-4.273201	25732.607122
HLA B*1509	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.494506	0.221286	-4.273220	31225.260630
HLA A*3101	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.311476	0.038251	-4.273225	20486.911501
HLA A*1101	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.496505	0.223276	-4.273229	31369.347394
HLA B*4501	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.539416	0.266144	-4.273272	34627.128439
HLA B*5701	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.416851	0.143550	-4.273301	26112.646753
HLA A*6802	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.428582	0.155271	-4.273311	26827.603087
HLA A*0211	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.536529	0.263202	-4.273327	34397.664857
HLA B*7301	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.533656	0.260101	-4.273554	34170.831007
HLA A*0212	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.405801	0.132177	-4.273625	25456.650833
HLA A*0211	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.177600	-0.096147	-4.273748	15052.217547
HLA B*5101	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.506141	0.232368	-4.273772	32073.084004
HLA A*8001	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.414391	0.140490	-4.273901	25965.158794
HLA B*3801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.567295	0.293372	-4.273924	36922.871332
HLA B*2705	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.520362	0.246391	-4.273971	33140.736407
HLA B*4002	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.598351	0.324299	-4.274052	39659.840168
HLA A*3301	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.598363	0.324299	-4.274063	39660.912959
HLA B*4601	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.374720	0.100651	-4.274069	23698.449281
HLA A*0201	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.396514	0.122274	-4.274240	24918.032708
HLA B*5401	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.560181	0.285730	-4.274451	36322.959485
HLA B*4403	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.625006	0.350532	-4.274474	42170.220026
HLA A*3301	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.556037	0.281512	-4.274525	35977.976579
HLA A*6801	1:365-373	9	VRGQSSADA	0.641608	-0.245877	-4.670273	0.395731	-4.274542	46802.967987
HLA A*0101	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.393690	0.119114	-4.274575	24756.524235
HLA B*1517	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.416498	0.141914	-4.274585	26091.465370
HLA A*3002	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.556100	0.281512	-4.274588	35983.232159
HLA A*3301	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.631251	0.356622	-4.274629	42780.986819
HLA B*4601	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.418204	0.143550	-4.274654	26194.143180
HLA B*5101	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.466129	0.191384	-4.274745	29250.210252
HLA A*2402	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.540890	0.266144	-4.274745	34744.783105
HLA B*5701	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.412037	0.137283	-4.274754	25824.790019
HLA B*4601	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.407011	0.132177	-4.274835	25527.674321
HLA B*0801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.414452	0.139599	-4.274854	25968.811235
HLA A*0211	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.521492	0.246391	-4.275101	33227.086094
HLA A*2402	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.565557	0.290447	-4.275110	36775.352817
HLA B*4402	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.407298	0.132130	-4.275168	25544.528312
HLA B*0802	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.457600	0.182373	-4.275228	28681.401008
HLA B*0801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.423768	0.148535	-4.275233	26531.864923
HLA B*1509	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.493853	0.218420	-4.275433	31178.334721
HLA B*2705	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.432776	0.157340	-4.275436	27087.922802
HLA A*0250	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.587870	0.312328	-4.275541	38714.165922
HLA B*4002	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.626155	0.350532	-4.275623	42281.926326
HLA B*0702	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.444988	0.169330	-4.275658	27860.462784
HLA B*5701	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.407824	0.132130	-4.275694	25575.502323
HLA A*0101	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.372643	0.096922	-4.275721	23585.385761
HLA A*3301	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.628925	0.353175	-4.275750	42552.473308
HLA A*2601	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.394947	0.119114	-4.275832	24828.280605
HLA B*1503	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.417762	0.141914	-4.275849	26167.515730
HLA A*0206	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.569267	0.293372	-4.275895	37090.841353
HLA A*3301	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.446609	0.170651	-4.275959	27964.655320
HLA A*0212	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.415862	0.139887	-4.275974	26053.241222
HLA A*0212	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.383314	0.107303	-4.276011	24172.097916
HLA B*4402	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.262863	-0.013165	-4.276028	18317.377559
HLA B*0801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.419595	0.143550	-4.276045	26278.168448
HLA A*6802	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.433375	0.157255	-4.276120	27125.316968
HLA A*0202	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.588453	0.312328	-4.276124	38766.141739
HLA A*2602	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.569516	0.293372	-4.276144	37112.117131

HLA B*0702	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.388483	0.112336	-4.276147	24461.507153
HLA B*3901	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.167084	-0.109105	-4.276190	14692.110689
HLA B*0702	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.431479	0.155271	-4.276208	27007.151916
HLA A*8001	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.419851	0.143550	-4.276301	26293.668673
HLA B*0802	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.455949	0.179592	-4.276357	28572.528439
HLA B*3901	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.499694	0.223276	-4.276417	31600.484035
HLA B*4002	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.633128	0.356622	-4.276506	42966.307932
HLA B*7301	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.519185	0.242669	-4.276516	33051.034880
HLA A*2603	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.658350	0.381799	-4.276551	45535.463140
HLA B*4501	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.549479	0.272858	-4.276621	35438.825653
HLA B*1801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.505986	0.229302	-4.276684	32061.634268
HLA B*4601	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.416362	0.139599	-4.276764	26083.279842
HLA A*2301	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.546096	0.269282	-4.276815	35163.821249
HLA B*5401	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.531898	0.254868	-4.277030	34032.834818
HLA A*2603	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.648393	0.371335	-4.277057	44503.343530
HLA A*8001	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.418975	0.141914	-4.277061	26240.664474
HLA B*5101	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.495481	0.218420	-4.277061	31295.443342
HLA B*5701	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.399516	0.122446	-4.277070	25090.908887
HLA B*5701	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.416729	0.139599	-4.277130	26105.301927
HLA A*3101	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.399451	0.122274	-4.277177	25087.108482
HLA B*4501	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.633852	0.356622	-4.277230	43037.960043
HLA A*2301	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.492025	0.214737	-4.277288	31047.384195
HLA B*4402	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.449011	0.171585	-4.277426	28119.697502
HLA B*5701	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.417922	0.140490	-4.277432	26177.143810
HLA A*2601	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.396577	0.119119	-4.277458	24921.672676
HLA A*3001	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.167042	-0.110482	-4.277523	14690.680070
HLA B*0803	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.492300	0.214737	-4.277563	31067.042075
HLA A*0301	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.340237	0.062590	-4.277646	21889.535068
HLA B*7301	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.607023	0.329236	-4.277787	40459.723340
HLA A*2603	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.603292	0.325463	-4.277828	40113.626513
HLA A*0212	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.400163	0.122274	-4.277889	25128.264903
HLA A*2403	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.448543	0.170651	-4.277892	28089.441026
HLA A*0101	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.397031	0.119119	-4.277912	24947.707198
HLA B*4801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.418420	0.140490	-4.277930	26207.183507
HLA B*4403	1:250-258	9	VVLKALAKN	0.787148	-0.407270	-4.657906	0.379878	-4.278028	45488.928333
HLA A*2402	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.506871	0.228841	-4.278031	32127.091604
HLA B*3801	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.553175	0.275124	-4.278051	35741.688214
HLA B*5401	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.538178	0.260101	-4.278077	34528.546691
HLA B*4601	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.407223	0.128996	-4.278227	25540.106517
HLA A*0250	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.520468	0.242192	-4.278276	33148.805336
HLA A*0202	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.564025	0.285730	-4.278295	36645.865539
HLA A*0201	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.397442	0.119119	-4.278323	24971.337139
HLA B*4601	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.400684	0.122274	-4.278410	25158.461963
HLA B*5401	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.544771	0.266144	-4.278627	35056.693705
HLA A*3201	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.607876	0.329236	-4.278640	40539.255797
HLA A*3201	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.603158	0.324517	-4.278641	40101.258835
HLA A*6901	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.401088	0.122446	-4.278642	25181.882830
HLA B*0803	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.502069	0.223276	-4.278793	31773.793173
HLA A*2501	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.474124	0.195249	-4.278875	29793.689654
HLA B*4002	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.641659	0.362756	-4.278903	43818.652355
HLA B*4501	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.343523	0.064589	-4.278935	22055.833104
HLA B*7301	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.341550	0.062590	-4.278959	21955.832020
HLA A*2501	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.470412	0.191384	-4.279028	29540.109670
HLA B*3901	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.458533	0.179347	-4.279186	28743.066995
HLA B*4403	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.635858	0.356622	-4.279236	43237.257396
HLA B*0803	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.521384	0.242067	-4.279317	33218.818400
HLA A*0212	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.436688	0.157340	-4.279347	27333.018519
HLA A*0206	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.527662	0.248296	-4.279366	33702.491231
HLA B*0803	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.461757	0.182373	-4.279384	28957.202326
HLA B*0803	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.490026	0.210423	-4.279602	30904.776283
HLA B*4402	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.420923	0.141319	-4.279603	26358.612845
HLA B*4601	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.420096	0.140490	-4.279605	26308.466402
HLA B*5401	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.549162	0.269402	-4.279760	35412.952886
HLA B*2705	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.471204	0.191384	-4.279820	29594.014330
HLA B*1509	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.549211	0.269282	-4.279930	35416.976297

HLA A*3002	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.592296	0.312328	-4.279968	39110.767343
HLA B*2705	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.491388	0.211378	-4.280010	31001.899597
HLA A*0203	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.423575	0.143550	-4.280025	26520.097708
HLA B*4402	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.417356	0.137283	-4.280073	26143.036726
HLA B*0803	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.526532	0.246391	-4.280141	33614.906073
HLA A*2601	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.362291	0.082090	-4.280202	23029.852318
HLA A*2902	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.459647	0.179347	-4.280300	28816.867063
HLA B*5301	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.605796	0.325463	-4.280333	40345.627790
HLA B*1501	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.251720	-0.028622	-4.280342	17853.348799
HLA A*2501	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.498836	0.218420	-4.280417	31538.146984
HLA A*2403	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.423991	0.143550	-4.280441	26545.504200
HLA A*3301	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.640938	0.360485	-4.280453	43745.937162
HLA B*4403	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.588565	0.307875	-4.280690	38776.209632
HLA A*2603	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.641189	0.360485	-4.280704	43771.267184
HLA B*5801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.354122	0.073404	-4.280718	22600.705366
HLA B*0702	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.413017	0.132177	-4.280840	25883.114540
HLA A*3301	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.440971	0.160089	-4.280882	27603.916611
HLA A*0216	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.467802	0.186843	-4.280959	29363.094680
HLA B*0803	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.497943	0.216943	-4.281001	31473.378787
HLA B*4402	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.429559	0.148535	-4.281024	26888.046969
HLA B*7301	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.522063	0.240938	-4.281126	33270.795247
HLA A*0201	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.400242	0.119114	-4.281128	25132.887326
HLA B*1501	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.273062	-0.008210	-4.281272	18752.639792
HLA B*1503	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.492704	0.211378	-4.281326	31095.963441
HLA A*3002	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.247042	-0.034337	-4.281379	17662.080717
HLA B*1501	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.410413	0.128996	-4.281418	25728.431145
HLA A*0219	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.460885	0.179347	-4.281538	28899.141512
HLA A*2601	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.273356	-0.008210	-4.281566	18765.325293
HLA B*1801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.504841	0.223225	-4.281616	31977.275348
HLA A*3002	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.502920	0.221286	-4.281634	31836.079300
HLA A*3002	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.554542	0.272858	-4.281684	35854.400249
HLA A*1101	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.458174	0.176401	-4.281772	28719.285827
HLA B*5301	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.599413	0.317460	-4.281953	39756.937848
HLA A*3101	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.234554	-0.047418	-4.281973	17161.464742
HLA A*3002	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.382682	0.100651	-4.282031	24136.946807
HLA B*4403	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.616209	0.334125	-4.282084	41324.670091
HLA A*0202	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.575481	0.293372	-4.282109	37625.395405
HLA B*4001	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.394472	0.112336	-4.282136	24801.163139
HLA A*0203	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.422090	0.139887	-4.282203	26429.579002
HLA B*5801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.320470	0.038251	-4.282219	20915.599634
HLA B*1517	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.414419	0.132130	-4.282289	25966.844472
HLA B*7301	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.461933	0.179592	-4.282341	28968.953854
HLA A*3101	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.294459	0.012088	-4.282371	19699.679997
HLA A*2402	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.585739	0.303321	-4.282418	38524.669723
HLA A*3101	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-3.905972	-0.376448	-4.282420	8053.261963
HLA A*6802	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.422924	0.140490	-4.282434	26480.386062
HLA A*2601	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.383096	0.100651	-4.282444	24159.939516
HLA B*1503	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.492934	0.210423	-4.282511	31112.453932
HLA B*4801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.437787	0.155271	-4.282516	27402.308702
HLA B*4402	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.422898	0.139887	-4.283011	26478.810293
HLA B*5101	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.452366	0.169330	-4.283036	28337.772476
HLA A*3101	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.426691	0.143550	-4.283141	26711.023961
HLA B*4002	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.512456	0.229302	-4.283154	32542.891440
HLA B*1503	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.512470	0.229302	-4.283168	32543.947778
HLA A*6802	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.321490	0.038251	-4.283239	20964.764895
HLA A*0206	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.563903	0.280603	-4.283300	36635.557985
HLA B*3501	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.293160	0.009850	-4.283310	19640.833150
HLA A*6801	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.607831	0.324517	-4.283315	40535.089067
HLA A*2601	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.356824	0.073404	-4.283419	22741.751067
HLA A*0216	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.463112	0.179592	-4.283520	29047.733631
HLA A*2402	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.551129	0.267585	-4.283543	35573.669064
HLA A*0201	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.390901	0.107303	-4.283598	24598.058605
HLA B*2705	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.415735	0.132130	-4.283605	26045.631296
HLA B*5101	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.508333	0.224721	-4.283611	32235.379784
HLA A*0219	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.396150	0.112336	-4.283814	24897.146877

HLA B*5701	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.396152	0.112336	-4.283816	24897.281569
HLA A*0206	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.443926	0.160089	-4.283838	27792.419659
HLA B*3801	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.553255	0.269402	-4.283853	35748.263010
HLA A*2603	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.618744	0.334871	-4.283873	41566.598778
HLA B*4403	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.655246	0.371335	-4.283911	45211.205640
HLA A*3002	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.526586	0.242669	-4.283917	33619.088951
HLA B*3801	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.547135	0.263202	-4.283932	35248.004566
HLA A*3201	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.601398	0.317460	-4.283938	39939.097017
HLA B*4801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.416249	0.132130	-4.284119	26076.507554
HLA B*5401	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.543284	0.259153	-4.284130	34936.848785
HLA B*3501	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.460551	0.176401	-4.284150	28876.949593
HLA A*2501	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.381125	0.096922	-4.284202	24050.528530
HLA B*3501	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.381162	0.096922	-4.284240	24052.610391
HLA A*0250	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.550431	0.266144	-4.284287	35516.557425
HLA A*2501	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.439582	0.155271	-4.284311	27515.801079
HLA A*0212	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.424844	0.140490	-4.284354	26597.685208
HLA B*4001	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.385037	0.100651	-4.284385	24268.141433
HLA B*3901	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.457069	0.172544	-4.284526	28646.355553
HLA A*0212	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.403771	0.119119	-4.284652	25337.940427
HLA B*4403	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.347435	0.062590	-4.284845	22255.397694
HLA B*7301	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.580887	0.295880	-4.285007	38096.689440
HLA A*0206	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.506308	0.221286	-4.285022	32085.405711
HLA A*6901	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.342985	0.057919	-4.285066	22028.525831
HLA A*2602	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.513976	0.228841	-4.285136	32656.997593
HLA A*6802	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.425048	0.139887	-4.285161	26610.206631
HLA A*0212	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.397613	0.112336	-4.285277	24981.200815
HLA B*5101	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.506611	0.221286	-4.285325	32107.805151
HLA A*1101	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.417518	0.132177	-4.285342	26152.797282
HLA A*0202	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.599234	0.313851	-4.285384	39740.595080
HLA A*2301	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.540314	0.254868	-4.285446	34698.762082
HLA A*6801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.514378	0.228841	-4.285537	32687.222268
HLA A*2603	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.653179	0.367626	-4.285552	44996.480070
HLA A*0212	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.429108	0.143550	-4.285558	26860.132889
HLA B*5801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.348274	0.062590	-4.285684	22298.421754
HLA B*5301	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.579109	0.293372	-4.285737	37940.991630
HLA B*4001	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.404859	0.119119	-4.285740	25401.485910
HLA A*0202	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.555207	0.269402	-4.285806	35909.335329
HLA B*5401	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.496235	0.210423	-4.285812	31349.837424
HLA B*5401	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.549059	0.263202	-4.285857	35404.524362
HLA B*5701	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.408259	0.122274	-4.285985	25601.111853
HLA B*0803	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.507280	0.221286	-4.285994	32157.347739
HLA A*2301	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.532446	0.246391	-4.286055	34075.760396
HLA A*0206	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.477482	0.191384	-4.286097	30024.909269
HLA B*2705	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.468749	0.182373	-4.286376	29427.181504
HLA B*4403	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.501150	0.214737	-4.286413	31706.654162
HLA A*0216	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.426340	0.139887	-4.286453	26689.501588
HLA B*7301	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.443722	0.157255	-4.286467	27779.341947
HLA A*2902	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.477926	0.191384	-4.286541	30055.624509
HLA A*0203	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.457286	0.170651	-4.286635	28660.616673
HLA A*6901	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.325160	0.038504	-4.286656	21142.672958
HLA B*5101	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.498115	0.211378	-4.286737	31485.810768
HLA A*2403	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.276918	-0.009859	-4.286777	18919.859914
HLA B*1502	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.551850	0.264968	-4.286882	35632.800183
HLA B*4403	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.556288	0.269402	-4.286886	35998.808753
HLA A*2301	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.529152	0.242192	-4.286960	33818.284850
HLA A*6801	1:494-502	9	TKDIPDVAG	0.974040	-0.602705	-4.658300	0.371335	-4.286965	45530.290256
HLA A*0250	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.600851	0.313851	-4.287000	39888.785334
HLA B*4002	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.621176	0.334125	-4.287051	41799.992748
HLA B*4403	1:457-465	9	SPSTPELVG	1.036935	-0.655136	-4.668897	0.381799	-4.287098	46654.828390
HLA A*2902	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.419257	0.132130	-4.287127	26257.705095
HLA B*5301	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.590473	0.303321	-4.287152	38946.921608
HLA A*6801	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.640458	0.353175	-4.287284	43697.685016
HLA B*7301	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.529478	0.242192	-4.287286	33843.724905
HLA A*3002	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.458883	0.171585	-4.287298	28766.245360
HLA B*2705	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.457957	0.170651	-4.287307	28704.995514

HLA A*0202	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.577774	0.290447	-4.287327	37824.584844
HLA A*8001	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.399730	0.112336	-4.287394	25103.264181
HLA A*3201	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.528411	0.240938	-4.287474	33760.703678
HLA B*5101	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.482747	0.195249	-4.287498	30391.133591
HLA A*2402	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.595388	0.307875	-4.287513	39390.206634
HLA B*5301	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.562683	0.275124	-4.287560	36532.839410
HLA A*2301	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.546714	0.259153	-4.287561	35213.887972
HLA B*3901	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.258961	-0.028622	-4.287583	18153.518102
HLA B*4402	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.325844	0.038251	-4.287592	21175.983611
HLA A*6801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.568271	0.280603	-4.287667	37005.860143
HLA A*3201	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.516514	0.228841	-4.287673	32848.360481
HLA B*4501	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.650510	0.362756	-4.287753	44720.796163
HLA A*2902	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.427461	0.139599	-4.287863	26758.463244
HLA A*3201	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.583801	0.295880	-4.287920	38353.111145
HLA A*3201	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.600266	0.312328	-4.287937	39835.088826
HLA A*2501	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.461865	0.173777	-4.288088	28964.409364
HLA B*1801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.536466	0.248296	-4.288170	34392.640860
HLA B*0801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.407324	0.119114	-4.288209	25546.048481
HLA B*1503	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.534750	0.246391	-4.288359	34257.084634
HLA A*2602	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.460147	0.171585	-4.288562	28850.092062
HLA B*7301	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.511796	0.223225	-4.288571	32493.458008
HLA B*4402	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.400926	0.112336	-4.288590	25172.484632
HLA B*3801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.521011	0.232368	-4.288642	33190.256776
HLA A*2602	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.614175	0.325463	-4.288711	41131.518307
HLA A*0203	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.420941	0.132177	-4.288765	26359.753647
HLA A*3001	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.278960	-0.009859	-4.288818	19009.015244
HLA B*4001	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.385997	0.096922	-4.289075	24321.897656
HLA B*4801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.260474	-0.028622	-4.289096	18216.874692
HLA B*4402	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.351794	0.062590	-4.289203	22479.862682
HLA A*3002	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.579816	0.290447	-4.289369	38002.824183
HLA B*5301	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.601720	0.312328	-4.289392	39968.709043
HLA A*0206	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.518739	0.229302	-4.289437	33017.079872
HLA A*2402	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.531661	0.242192	-4.289469	34014.244397
HLA A*8001	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.446913	0.157340	-4.289572	27984.177984
HLA B*1509	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.512851	0.223225	-4.289626	32572.481862
HLA A*3301	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.472026	0.182373	-4.289653	29650.102532
HLA A*3002	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.513046	0.223276	-4.289769	32587.110868
HLA B*5701	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.425838	0.135996	-4.289841	26658.620597
HLA A*2501	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.431775	0.141914	-4.289861	27025.567509
HLA B*5401	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.519244	0.229302	-4.289942	33055.505244
HLA A*0216	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.450054	0.160089	-4.289965	28187.321940
HLA B*1501	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.255009	-0.035208	-4.290217	17989.080649
HLA A*3001	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.282087	-0.008210	-4.290297	19146.384821
HLA B*1517	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-3.879357	-0.410971	-4.290328	7574.550411
HLA A*2602	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.422480	0.132130	-4.290350	26453.324524
HLA A*0250	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.553584	0.263202	-4.290382	35775.348445
HLA A*6801	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.604269	0.313851	-4.290419	40204.004447
HLA B*5801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.349945	0.059501	-4.290444	22384.356264
HLA A*3101	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.419447	0.128996	-4.290451	26269.213769
HLA B*1517	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.412908	0.122274	-4.290635	25876.674201
HLA B*4801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.434207	0.143550	-4.290657	27177.314457
HLA B*4402	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.447925	0.157255	-4.290670	28049.503764
HLA A*8001	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.409805	0.119119	-4.290686	25692.406707
HLA A*8001	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.439270	0.148535	-4.290735	27496.010161
HLA A*2902	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.439321	0.148535	-4.290786	27499.282864
HLA A*2403	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.428131	0.137283	-4.290848	26799.751757
HLA B*5401	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.560165	0.269282	-4.290883	36321.583988
HLA B*3801	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.507416	0.216497	-4.290919	32167.439448
HLA A*2501	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.470530	0.179592	-4.290938	29548.101186
HLA B*1517	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.473321	0.182373	-4.290948	29738.616866
HLA B*1501	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.350454	0.059501	-4.290954	22410.649719
HLA A*0216	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.403409	0.112336	-4.291073	25316.839599
HLA B*3801	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.560898	0.269799	-4.291099	36382.942429
HLA A*2602	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.533811	0.242669	-4.291142	34183.033972
HLA B*5801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.355771	0.064589	-4.291182	22686.700208

HLA A*0216	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.461853	0.170651	-4.291202	28963.625903
HLA B*4002	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.615725	0.324517	-4.291209	41278.641995
HLA B*0803	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.507792	0.216497	-4.291295	32195.295066
HLA A*3201	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.560590	0.269282	-4.291309	36357.167136
HLA A*0203	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.373465	0.082090	-4.291376	23630.086080
HLA A*0211	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.512752	0.221286	-4.291466	32565.081735
HLA B*4501	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.616021	0.324517	-4.291505	41306.789010
HLA A*0206	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.546387	0.254868	-4.291519	35187.417977
HLA A*2301	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.539903	0.248296	-4.291607	34665.927247
HLA B*0803	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.521152	0.229302	-4.291850	33201.031861
HLA A*0219	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.427856	0.135996	-4.291860	26782.794033
HLA A*3002	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.508361	0.216497	-4.291864	32237.472530
HLA A*2402	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.533963	0.242067	-4.291896	34195.056303
HLA B*4403	1:294-302	9	TSLLSSAAG	0.878021	-0.531967	-4.637952	0.346054	-4.291897	43446.173214
HLA A*6802	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.435478	0.143550	-4.291928	27256.972175
HLA A*0219	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.414473	0.122446	-4.292027	25970.075661
HLA B*4403	1:485-493	9	IIIVGSGPA	0.488811	-0.115442	-4.665443	0.373369	-4.292074	46285.275528
HLA B*3801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.546961	0.254868	-4.292092	35233.896494
HLA A*0202	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.343065	0.050897	-4.292169	22032.578048
HLA B*4801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.434394	0.141914	-4.292481	27189.079103
HLA A*2301	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.508979	0.216497	-4.292482	32283.372679
HLA B*3901	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.432388	0.139887	-4.292501	27063.754052
HLA A*0301	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.343451	0.050897	-4.292554	22052.134506
HLA B*4403	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.617140	0.324517	-4.292623	41413.295495
HLA B*5801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.350586	0.057919	-4.292667	22417.440138
HLA B*3801	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.565658	0.272858	-4.292799	36783.908687
HLA A*2602	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.588695	0.295880	-4.292814	38787.748973
HLA A*0201	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.343841	0.050897	-4.292944	22071.947135
HLA B*4402	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.448233	0.155271	-4.292962	28069.389366
HLA B*5401	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.525374	0.232368	-4.293005	33525.372036
HLA B*4501	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.556450	0.263371	-4.293079	36012.248981
HLA B*1503	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.469517	0.176401	-4.293116	29479.285254
HLA B*3501	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.352698	0.059501	-4.293198	22526.732698
HLA A*2301	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.535326	0.242067	-4.293259	34302.519860
HLA A*6802	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.425478	0.132177	-4.293302	26636.564039
HLA B*7301	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.548274	0.254868	-4.293406	35340.609583
HLA A*2501	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.475781	0.182373	-4.293408	29907.538919
HLA A*3101	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.394106	0.100651	-4.293454	24780.241208
HLA A*3002	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.522867	0.229302	-4.293565	33332.409258
HLA B*0802	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.425755	0.132177	-4.293579	26653.573369
HLA B*5401	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.558612	0.264968	-4.293644	36191.932254
HLA B*1509	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.536332	0.242669	-4.293662	34382.037054
HLA B*0803	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.467459	0.173777	-4.293682	29339.911578
HLA B*4001	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.416134	0.122446	-4.293688	26069.595990
HLA A*0101	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.379738	0.086012	-4.293727	23973.885602
HLA B*4402	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.435750	0.141914	-4.293836	27274.082578
HLA A*0219	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.431133	0.137283	-4.293851	26985.682916
HLA B*3901	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.470269	0.176401	-4.293867	29530.362946
HLA B*0802	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.464592	0.170651	-4.293942	29146.903894
HLA B*2705	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.465551	0.171585	-4.293966	29211.309007
HLA A*2603	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.562604	0.268569	-4.294035	36526.120315
HLA A*3101	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.245447	-0.048602	-4.294048	17597.321350
HLA A*3201	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.601943	0.307875	-4.294068	39989.255820
HLA B*4501	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.629031	0.334871	-4.294159	42562.833757
HLA A*2403	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.413355	0.119119	-4.294236	25903.285964
HLA A*3002	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.436180	0.141914	-4.294266	27301.097555
HLA B*4801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.433885	0.139599	-4.294286	27157.179322
HLA A*0101	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.345196	0.050897	-4.294300	22140.952496
HLA A*6801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.535239	0.240938	-4.294301	34295.654353
HLA B*4801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.435816	0.141319	-4.294497	27278.214285
HLA A*2501	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.380690	0.086012	-4.294678	24026.470093
HLA A*0301	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.368125	0.073404	-4.294720	23341.293752
HLA A*0250	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.575333	0.280603	-4.294730	37612.573989
HLA B*0803	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.517970	0.223225	-4.294745	32958.723176
HLA B*1509	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.395449	0.100651	-4.294798	24857.041354

HLA B*1503	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.283814	-0.010996	-4.294809	19222.667548
HLA A*2601	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.402113	0.107303	-4.294810	25241.349736
HLA A*2403	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.426994	0.132177	-4.294817	26729.671442
HLA A*2403	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.434439	0.139599	-4.294841	27191.873955
HLA B*1501	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.417163	0.122274	-4.294889	26131.441962
HLA B*0702	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.377053	0.082090	-4.294963	23826.100387
HLA A*2602	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.619510	0.324517	-4.294994	41639.971306
HLA B*5701	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.424059	0.128996	-4.295064	26549.669165
HLA A*6901	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.354608	0.059501	-4.295108	22626.028876
HLA A*0219	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.247225	-0.047884	-4.295109	17669.535182
HLA B*1509	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.537248	0.242067	-4.295181	34454.654807
HLA B*1509	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.511737	0.216497	-4.295240	32489.063655
HLA A*2602	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.612737	0.317460	-4.295277	40995.563119
HLA A*2902	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.438891	0.143550	-4.295341	27472.071779
HLA A*0219	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.377443	0.082090	-4.295353	23847.506827
HLA B*4402	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.427600	0.132177	-4.295423	26767.005466
HLA A*8001	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.435083	0.139599	-4.295484	27232.210620
HLA B*1502	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.568393	0.272858	-4.295534	37016.271882
HLA B*1502	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.307684	0.012088	-4.295596	20308.807477
HLA B*3801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.560576	0.264968	-4.295608	36355.987026
HLA B*4002	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.565033	0.269402	-4.295631	36731.013588
HLA B*4601	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.402980	0.107303	-4.295676	25291.788084
HLA B*4801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.435583	0.139887	-4.295696	27263.608557
HLA A*0250	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.581458	0.285730	-4.295728	38146.804398
HLA B*4601	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.414863	0.119114	-4.295749	25993.408345
HLA B*1501	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.369166	0.073404	-4.295761	23397.300135
HLA B*4001	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.414882	0.119114	-4.295768	25994.533341
HLA A*8001	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.381902	0.086012	-4.295891	24093.633751
HLA B*4801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.241659	-0.054260	-4.295919	17444.526872
HLA A*3001	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.304896	0.008974	-4.295922	20178.811523
HLA B*0802	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.467764	0.171585	-4.296179	29360.553173
HLA A*2602	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.565592	0.269282	-4.296311	36778.337197
HLA B*5701	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.415636	0.119119	-4.296517	26039.714001
HLA A*1101	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.428739	0.132130	-4.296609	26837.328851
HLA B*7301	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.560000	0.263371	-4.296629	36307.831890
HLA B*4801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.428918	0.132177	-4.296741	26848.365330
HLA A*2403	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.378855	0.082090	-4.296765	23925.169446
HLA A*8001	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.419290	0.122446	-4.296844	26259.693888
HLA B*1517	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.467506	0.170651	-4.296855	29343.086264
HLA B*1509	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.526205	0.229302	-4.296903	33589.638020
HLA B*2705	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.409283	0.112336	-4.296947	25661.568767
HLA B*1517	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.393875	0.096922	-4.296953	24767.106970
HLA A*0202	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.560231	0.263202	-4.297028	36327.086286
HLA B*0802	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.470903	0.173777	-4.297126	29573.528581
HLA B*4501	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.631349	0.334125	-4.297225	42790.708420
HLA A*3301	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.626479	0.329236	-4.297243	42313.504306
HLA A*0203	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.437778	0.140490	-4.297287	27401.715735
HLA B*1502	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.539440	0.242067	-4.297373	34629.001779
HLA A*2403	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.426369	0.128996	-4.297373	26691.234292
HLA A*8001	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.468201	0.170651	-4.297550	29390.111787
HLA B*1502	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.609957	0.312328	-4.297629	40734.033436
HLA A*2402	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.520957	0.223276	-4.297680	33186.127254
HLA A*2902	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.287890	-0.009859	-4.297749	19403.943949
HLA A*0201	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.250392	-0.047418	-4.297810	17798.861793
HLA A*3001	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.276006	-0.021825	-4.297832	18880.188079
HLA A*2603	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.567744	0.269799	-4.297946	36961.043041
HLA B*7301	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.455397	0.157340	-4.298056	28536.226580
HLA B*3801	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.578674	0.280603	-4.298071	37903.038162
HLA A*0211	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.522935	0.224721	-4.298213	33337.639082
HLA B*3901	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.446332	0.148101	-4.298231	27946.809305
HLA B*2705	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.485101	0.186843	-4.298258	30556.322395
HLA B*4501	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.441826	0.143550	-4.298276	27658.327789
HLA B*5701	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.398974	0.100651	-4.298322	25059.572754
HLA B*0702	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.455801	0.157340	-4.298460	28562.791923
HLA A*8001	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.439916	0.141319	-4.298597	27536.946956

HLA B*1509	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.539557	0.240938	-4.298620	34638.369999
HLA B*5301	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.606513	0.307875	-4.298638	40412.253681
HLA B*4403	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.545043	0.246391	-4.298652	35078.700337
HLA B*0803	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.493926	0.195249	-4.298677	31183.563971
HLA B*2705	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.454067	0.155271	-4.298796	28448.982371
HLA A*0216	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.384891	0.086012	-4.298879	24260.002945
HLA B*2705	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.471502	0.172544	-4.298959	29614.354060
HLA A*6901	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.290806	-0.008210	-4.299015	19534.653954
HLA B*2705	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.441022	0.141914	-4.299109	27607.202157
HLA A*2301	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.528414	0.229302	-4.299112	33760.886320
HLA A*2301	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.541822	0.242669	-4.299153	34819.485570
HLA B*0802	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.454555	0.155271	-4.299284	28481.012804
HLA B*5401	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.562742	0.263371	-4.299371	36537.780709
HLA A*2602	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.611893	0.312328	-4.299565	40916.020844
HLA A*3002	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.431733	0.132130	-4.299603	27022.935942
HLA A*2603	1:593-601	9	VDAGGSQHN	1.082067	-0.728892	-4.652875	0.353175	-4.299701	44965.089075
HLA A*8001	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.431859	0.132130	-4.299729	27030.831414
HLA A*2603	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.650385	0.350532	-4.299853	44707.975470
HLA B*1502	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.563275	0.263202	-4.300073	36582.678305
HLA A*0219	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.441452	0.141319	-4.300133	27634.547089
HLA A*1101	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.448790	0.148535	-4.300255	28105.401439
HLA A*1101	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.479848	0.179592	-4.300256	30188.924070
HLA A*3201	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.581773	0.281512	-4.300261	38174.468002
HLA B*0801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.382351	0.082090	-4.300261	24118.542301
HLA B*1502	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.412758	0.112336	-4.300422	25867.716396
HLA A*3201	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.614278	0.313851	-4.300427	41141.310219
HLA A*2902	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.458181	0.157340	-4.300841	28719.751936
HLA B*4801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.420199	0.119119	-4.301080	26314.729486
HLA B*4001	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.430231	0.128996	-4.301236	26929.681117
HLA A*2501	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.383345	0.082090	-4.301255	24173.797964
HLA A*2501	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.480621	0.179347	-4.301274	30242.703779
HLA A*8001	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.437273	0.135996	-4.301276	27369.862610
HLA A*0206	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.496592	0.195249	-4.301344	31375.627096
HLA B*0802	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.492760	0.191384	-4.301376	31100.001120
HLA A*2402	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.566360	0.264968	-4.301393	36843.456899
HLA A*0206	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.519817	0.218420	-4.301397	33099.167750
HLA B*1501	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.387447	0.086012	-4.301435	24403.217401
HLA A*0203	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.441081	0.139599	-4.301483	27610.936207
HLA A*0250	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.594867	0.293372	-4.301495	39342.927574
HLA A*2902	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.441452	0.139887	-4.301565	27634.547089
HLA A*0101	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.375152	0.073404	-4.301748	23722.050926
HLA A*2603	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.619236	0.317460	-4.301775	41613.623332
HLA B*4002	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.561889	0.260101	-4.301788	36466.098597
HLA A*0216	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.443111	0.141319	-4.301792	27740.295792
HLA A*0250	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.473417	0.171585	-4.301832	29745.213785
HLA A*0301	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.361356	0.059501	-4.301855	22980.319262
HLA B*4403	1:71-79	9	IVAVYDTGE	0.896683	-0.533927	-4.664684	0.362756	-4.301928	46204.467529
HLA A*0216	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.441577	0.139599	-4.301978	27642.471716
HLA B*5701	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.290989	-0.010996	-4.301985	19542.898758
HLA A*0201	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.364718	0.062590	-4.302128	23158.912988
HLA A*6802	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.439415	0.137283	-4.302133	27505.234231
HLA B*1801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.472797	0.170651	-4.302146	29702.761674
HLA A*0202	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.582767	0.280603	-4.302164	38261.925840
HLA B*4402	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.441795	0.139599	-4.302197	27656.382687
HLA A*0250	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.592684	0.290447	-4.302237	39145.694441
HLA B*1502	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.545133	0.242669	-4.302464	35085.912410
HLA B*0802	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.489321	0.186843	-4.302478	30854.659539
HLA A*0206	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.434618	0.132130	-4.302488	27203.056236
HLA B*1509	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.531480	0.228841	-4.302639	34000.078324
HLA A*2501	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.473408	0.170651	-4.302757	29744.570119
HLA B*5701	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.421921	0.119114	-4.302807	26419.286368
HLA A*2301	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.543758	0.240938	-4.302821	34975.048558
HLA A*0219	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.435106	0.132177	-4.302930	27233.683892
HLA B*4001	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.385126	0.082090	-4.303036	24273.130888
HLA B*3501	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.440456	0.137283	-4.303174	27571.231802

HLA B*5301	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.544146	0.240938	-4.303208	35006.282333
HLA B*1501	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.385342	0.082090	-4.303252	24285.214870
HLA A*0211	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.558198	0.254868	-4.303330	36157.488850
HLA A*6801	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.599251	0.295880	-4.303371	39742.100054
HLA B*4501	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.632621	0.329236	-4.303385	42916.129576
HLA B*0702	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.400388	0.096922	-4.303466	25141.318641
HLA A*0212	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.385575	0.082090	-4.303485	24298.225006
HLA B*3901	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.498850	0.195249	-4.303601	31539.170708
HLA A*2402	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.566974	0.263371	-4.303602	36895.515907
HLA B*5401	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.551993	0.248296	-4.303697	35644.561063
HLA B*4001	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.389782	0.086012	-4.303771	24534.797453
HLA B*5101	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.463930	0.160089	-4.303841	29102.471607
HLA A*3101	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.389855	0.086012	-4.303844	24538.912445
HLA A*3101	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.443492	0.139599	-4.303893	27764.618100
HLA A*0301	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.368628	0.064589	-4.304039	23368.331996
HLA A*3002	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.268878	-0.035208	-4.304086	18572.825519
HLA A*0216	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.436347	0.132177	-4.304170	27311.585979
HLA A*2602	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.536708	0.232368	-4.304339	34411.810419
HLA B*5101	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.423758	0.119119	-4.304639	26531.290791
HLA B*4002	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.639540	0.334871	-4.304668	43605.350450
HLA A*0101	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.367300	0.062590	-4.304710	23297.013698
HLA A*2402	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.563903	0.259153	-4.304750	36635.557985
HLA A*2402	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.577708	0.272858	-4.304850	37818.855727
HLA B*7301	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.533728	0.228841	-4.304888	34176.562160
HLA B*3901	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.427177	0.122274	-4.304903	26740.952977
HLA A*8001	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.444869	0.139887	-4.304981	27852.777021
HLA A*6802	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.363031	0.057919	-4.305112	23069.131296
HLA A*3301	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.630720	0.325463	-4.305256	42728.713252
HLA B*0801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.364883	0.059501	-4.305382	23167.684750
HLA A*2403	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.427731	0.122274	-4.305457	26775.115861
HLA B*4801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.442756	0.137283	-4.305474	27717.644185
HLA B*5301	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.574795	0.269282	-4.305513	37566.005954
HLA A*6802	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.434634	0.128996	-4.305639	27204.086414
HLA A*6802	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.428239	0.122446	-4.305793	26806.421836
HLA A*0203	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.413103	0.107303	-4.305800	25888.295975
HLA B*3801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.575124	0.269282	-4.305842	37594.468641
HLA B*1517	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.242077	-0.063767	-4.305844	17461.333349
HLA A*3101	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.365397	0.059501	-4.305896	23195.149295
HLA A*2402	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.575735	0.269799	-4.305936	37647.385144
HLA B*4801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.425053	0.119114	-4.305938	26610.494549
HLA B*1509	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.522904	0.216943	-4.305962	33335.294577
HLA A*0203	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.425145	0.119119	-4.306025	26616.109574
HLA B*5101	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.492906	0.186843	-4.306063	31110.434218
HLA B*0802	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.485512	0.179347	-4.306166	30585.264699
HLA A*0202	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.454400	0.148101	-4.306300	28470.845397
HLA A*3002	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.493181	0.186843	-4.306338	31130.132019
HLA B*0802	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.466456	0.160089	-4.306367	29272.213939
HLA A*2902	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.392397	0.086012	-4.306386	24682.972186
HLA A*0301	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.364328	0.057919	-4.306409	23138.124657
HLA B*0802	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.463787	0.157255	-4.306532	29092.869282
HLA B*5701	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.403468	0.096922	-4.306546	25320.263863
HLA B*2705	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.501886	0.195249	-4.306637	31760.388371
HLA B*1509	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.518050	0.211378	-4.306672	32964.786037
HLA A*6801	1:448-456	9	GFGRFKQAN	0.928520	-0.577988	-4.657267	0.350532	-4.306735	45422.041061
HLA A*0212	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.444065	0.137283	-4.306782	27801.291955
HLA B*5301	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.576646	0.269799	-4.306848	37726.491392
HLA B*5101	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.448181	0.141319	-4.306862	28066.048815
HLA A*0203	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.429341	0.122274	-4.307067	26874.522466
HLA B*0802	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.464430	0.157340	-4.307090	29136.025900
HLA B*4002	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.632569	0.325463	-4.307105	42911.022106
HLA B*4402	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.429399	0.122274	-4.307126	26878.157416
HLA A*0301	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.345389	0.038251	-4.307138	22150.776643
HLA B*1502	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.567350	0.260101	-4.307248	36927.465837
HLA B*2705	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.407911	0.100651	-4.307260	25580.622179
HLA A*6802	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.446889	0.139599	-4.307291	27982.664112

HLA B*0801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.447803	0.140490	-4.307313	28041.614149
HLA A*1101	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.464658	0.157340	-4.307318	29151.319311
HLA B*1517	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.483776	0.176401	-4.307375	30463.231723
HLA A*2603	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.550069	0.242669	-4.307400	35486.980089
HLA A*2301	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.530634	0.223225	-4.307409	33933.925567
HLA B*4402	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.436488	0.128996	-4.307492	27320.452577
HLA B*2705	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.486849	0.179347	-4.307502	30679.558138
HLA A*2403	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.047862	-0.259643	-4.307505	11165.082196
HLA A*0211	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.467626	0.160089	-4.307537	29351.183266
HLA B*5401	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.525992	0.218420	-4.307572	33573.105914
HLA B*5401	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.519105	0.211378	-4.307727	33044.956157
HLA B*3801	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.576303	0.268569	-4.307735	37696.705121
HLA B*3501	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.358790	0.050897	-4.307894	22844.960967
HLA A*6901	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.346145	0.038251	-4.307894	22189.396576
HLA A*2402	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.577330	0.269282	-4.308049	37785.930142
HLA B*1502	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.540464	0.232368	-4.308096	34710.778015
HLA B*4501	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.415495	0.107303	-4.308192	26031.263055
HLA A*6802	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.427334	0.119114	-4.308220	26750.647329
HLA B*7301	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.554622	0.246391	-4.308231	35860.995779
HLA A*6802	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.381672	0.073404	-4.308268	24080.863436
HLA B*3501	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.448787	0.140490	-4.308297	28105.249392
HLA A*0216	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.273976	-0.034337	-4.308314	18792.145280
HLA B*1517	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.477721	0.169330	-4.308392	30041.481847
HLA A*1101	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.499849	0.191384	-4.308464	31611.769088
HLA B*4601	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.390581	0.082090	-4.308492	24579.967364
HLA A*0212	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.274237	-0.034337	-4.308574	18803.433309
HLA B*1509	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.523433	0.214737	-4.308696	33375.895838
HLA A*2403	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.431173	0.122446	-4.308727	26988.164853
HLA B*3801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.567970	0.259153	-4.308816	36980.243720
HLA B*1503	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.504148	0.195249	-4.308899	31926.282962
HLA A*6802	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.428098	0.119119	-4.308979	26797.722062
HLA A*0211	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.519441	0.210423	-4.309018	33070.530093
HLA B*1509	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.371656	0.062590	-4.309066	23531.856981
HLA A*2501	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.485775	0.176401	-4.309374	30603.802158
HLA B*5401	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.532626	0.223225	-4.309401	34089.958001
HLA A*0202	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.541811	0.232368	-4.309442	34818.543735
HLA A*2603	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.524182	0.214737	-4.309445	33433.544174
HLA B*4801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.431777	0.122274	-4.309503	27025.713715
HLA B*1502	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.578084	0.268569	-4.309516	37851.605230
HLA B*4501	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.584708	0.275124	-4.309584	38433.284453
HLA A*0212	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.438638	0.128996	-4.309642	27456.025414
HLA A*3201	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.579139	0.269402	-4.309738	37943.660059
HLA B*5401	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.556194	0.246391	-4.309803	35991.019613
HLA B*0802	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.457965	0.148101	-4.309864	28705.461390
HLA A*2603	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.613261	0.303321	-4.309940	41045.050228
HLA B*5301	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.600454	0.290447	-4.310007	39852.332830
HLA B*3801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.528484	0.218420	-4.310065	33766.366044
HLA B*7301	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.524810	0.214737	-4.310072	33481.871831
HLA A*0219	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.442221	0.132130	-4.310091	27683.476802
HLA B*0702	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.410836	0.100651	-4.310185	25753.497180
HLA B*1509	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.467456	0.157255	-4.310202	29339.752853
HLA B*0702	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.470330	0.160089	-4.310241	29534.516894
HLA B*4001	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.447568	0.137283	-4.310285	28026.448050
HLA A*6801	1:442-450	9	KKLTAAGFG	0.869978	-0.509493	-4.670908	0.360485	-4.310423	46871.381634
HLA A*2402	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.591068	0.280603	-4.310464	39000.264832
HLA A*0219	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.450430	0.139887	-4.310542	28211.730948
HLA B*0803	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.467973	0.157255	-4.310719	29374.693100
HLA A*8001	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.433112	0.122274	-4.310838	27108.886511
HLA A*3301	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.553194	0.242192	-4.311002	35743.235116
HLA A*2501	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.459125	0.148101	-4.311024	28782.278913
HLA B*4002	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.640280	0.329236	-4.311044	43679.722337
HLA A*0216	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.468650	0.157340	-4.311310	29420.495956
HLA B*3801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.574722	0.263371	-4.311351	37559.706416
HLA B*1501	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.430711	0.119114	-4.311596	26959.417587
HLA B*4403	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.581472	0.269799	-4.311674	38148.042638

HLA B*0702	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.451323	0.139599	-4.311724	28269.787091
HLA A*3001	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.264423	-0.047362	-4.311786	18383.294949
HLA A*2902	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.434249	0.122446	-4.311803	27179.961059
HLA B*7301	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.575009	0.263202	-4.311807	37584.504248
HLA B*4501	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.593330	0.281512	-4.311818	39203.975596
HLA B*1502	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.581172	0.269282	-4.311890	38121.635567
HLA A*0212	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.264007	-0.047884	-4.311891	18365.700443
HLA B*3801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.554698	0.242669	-4.312028	35867.204445
HLA A*2602	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.615389	0.303321	-4.312069	41246.720603
HLA A*6801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.560414	0.248296	-4.312118	36342.418510
HLA B*5401	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.554204	0.242067	-4.312137	35826.479686
HLA B*1503	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.503530	0.191384	-4.312146	31880.890520
HLA B*1501	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.324354	0.012088	-4.312266	21103.477161
HLA B*5301	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.592952	0.280603	-4.312349	39169.844108
HLA A*0219	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.455902	0.143550	-4.312352	28569.437122
HLA B*1502	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.454309	0.141914	-4.312395	28464.839090
HLA B*5301	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.598142	0.285730	-4.312412	39640.749339
HLA A*0206	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.537243	0.224721	-4.312522	34454.282017
HLA B*5301	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.554773	0.242192	-4.312581	35873.414186
HLA B*1509	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.523019	0.210423	-4.312596	33344.132420
HLA A*3001	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.277421	-0.035208	-4.312629	18941.776428
HLA B*0802	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.482171	0.169330	-4.312841	30350.879171
HLA B*1801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.409849	0.096922	-4.312927	25695.047711
HLA A*0211	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.542262	0.229302	-4.312960	34854.728501
HLA B*2705	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.445200	0.132177	-4.313023	27874.031068
HLA A*0211	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.524408	0.211378	-4.313030	33450.912373
HLA A*2301	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.531459	0.218420	-4.313039	33998.422934
HLA B*3801	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.561450	0.248296	-4.313154	36429.226349
HLA B*3501	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.278036	-0.035208	-4.313245	18968.643367
HLA B*1509	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.453792	0.140490	-4.313302	28430.981086
HLA B*1509	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.559737	0.246391	-4.313346	36285.839363
HLA A*2402	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.582910	0.269402	-4.313508	38274.554483
HLA B*7301	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.546004	0.232368	-4.313636	35156.402969
HLA A*3001	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.312339	-0.001305	-4.313644	20527.627221
HLA B*4801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.426113	0.112336	-4.313777	26675.499700
HLA B*0801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.387266	0.073404	-4.313862	24393.054078
HLA B*1517	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.471206	0.157340	-4.313866	29594.174431
HLA A*0211	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.532293	0.218420	-4.313873	34063.780007
HLA A*0216	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.451252	0.137283	-4.313969	28265.199370
HLA A*2603	1:224-232	9	VAYQHVRED	0.968608	-0.634483	-4.648226	0.334125	-4.314101	44486.252984
HLA A*2403	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.411055	0.096922	-4.314132	25766.457531
HLA A*2501	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.415046	0.100651	-4.314395	26004.379133
HLA B*5701	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.421853	0.107303	-4.314550	26415.141856
HLA A*0206	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.437000	0.122446	-4.314554	27352.692120
HLA B*4403	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.589754	0.275124	-4.314631	38882.501194
HLA B*5301	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.577920	0.263202	-4.314718	37837.273834
HLA A*3001	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.286135	-0.028622	-4.314757	19325.687211
HLA B*1801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.488614	0.173777	-4.314837	30804.457418
HLA A*0216	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.462976	0.148101	-4.314875	29038.620650
HLA B*7301	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.574076	0.259153	-4.314923	37503.869653
HLA A*0216	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.422379	0.107303	-4.315076	26447.171529
HLA A*0101	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.353342	0.038251	-4.315091	22560.149051
HLA B*1801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.491499	0.176401	-4.315097	31009.783291
HLA A*2602	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.578484	0.263371	-4.315112	37886.432650
HLA B*4403	1:204-212	9	CVLYEVLTG	0.903330	-0.568459	-4.649990	0.334871	-4.315119	44667.360578
HLA A*2402	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.538467	0.223225	-4.315242	34551.530197
HLA B*5801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.353753	0.038504	-4.315250	22581.517548
HLA B*5401	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.557923	0.242669	-4.315254	36134.609954
HLA A*2902	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.456583	0.141319	-4.315264	28614.293971
HLA B*5301	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.584677	0.269402	-4.315275	38430.581590
HLA A*2301	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.547705	0.232368	-4.315337	35294.372172
HLA A*0202	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.558144	0.242669	-4.315475	36152.990145
HLA A*1101	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.484885	0.169330	-4.315555	30541.117998
HLA A*2403	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.378155	0.062590	-4.315564	23886.629631
HLA A*6802	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.375070	0.059501	-4.315569	23717.559673

HLA A*2601	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.375079	0.059501	-4.315579	23718.072916
HLA B*5401	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.249753	-0.065831	-4.315584	17772.690209
HLA B*1503	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.475687	0.160089	-4.315598	29901.067760
HLA A*3301	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.611494	0.295880	-4.315614	40878.408450
HLA A*3001	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.272329	-0.043361	-4.315690	18721.014182
HLA A*3001	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.298641	-0.017067	-4.315708	19890.296395
HLA A*0206	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.527204	0.211378	-4.315826	33666.956263
HLA A*2603	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.580883	0.264968	-4.315915	38096.277245
HLA A*0216	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.495300	0.179347	-4.315954	31282.409581
HLA A*2501	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.438363	0.122274	-4.316089	27438.652428
HLA A*0211	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.507736	0.191384	-4.316352	32191.115186
HLA A*1101	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.503209	0.186843	-4.316366	31857.270598
HLA A*0202	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.545699	0.229302	-4.316397	35131.686669
HLA B*4601	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.367307	0.050897	-4.316411	23297.391804
HLA A*2603	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.630386	0.313851	-4.316535	42695.901477
HLA A*2602	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.585123	0.268569	-4.316555	38470.103884
HLA B*2705	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.465180	0.148535	-4.316645	29186.350944
HLA A*0212	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.435870	0.119114	-4.316755	27281.608654
HLA B*1509	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.558992	0.242192	-4.316800	36223.664840
HLA B*7301	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.541665	0.224721	-4.316944	34806.867097
HLA B*7301	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.381696	0.064589	-4.317107	24082.166219
HLA A*1101	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.459135	0.141914	-4.317221	28782.901755
HLA B*3901	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.488959	0.171585	-4.317374	30828.964520
HLA B*7301	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.538754	0.221286	-4.317468	34574.341957
HLA B*4801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.414391	0.096922	-4.317469	25965.158794
HLA A*0250	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.560172	0.242669	-4.317503	36322.173480
HLA A*2402	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.565834	0.248296	-4.317538	36798.836480
HLA A*0216	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.439892	0.122274	-4.317618	27535.457278
HLA A*6802	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.439958	0.122274	-4.317684	27539.628579
HLA A*3301	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.631589	0.313851	-4.317738	42814.327221
HLA B*5701	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.399850	0.082090	-4.317760	25110.191236
HLA A*0203	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.455101	0.137283	-4.317818	28516.781602
HLA B*5401	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.542593	0.224721	-4.317872	34881.325635
HLA B*1517	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.453961	0.135996	-4.317965	28442.057451
HLA A*6802	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.282768	-0.035208	-4.317976	19176.446543
HLA B*3901	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.504865	0.186843	-4.318022	31979.005330
HLA A*6801	1:28-36	9	ARDLRLHRD	1.059591	-0.691965	-4.685735	0.367626	-4.318109	48499.287150
HLA A*2902	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.455401	0.137283	-4.318119	28536.535337
HLA B*4402	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.437242	0.119114	-4.318128	27367.937795
HLA B*1801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.509522	0.191384	-4.318137	32323.741925
HLA B*1517	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.489885	0.171585	-4.318300	30894.746426
HLA B*1501	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.383086	0.064589	-4.318498	24159.416711
HLA B*3501	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.310297	-0.008210	-4.318507	20431.349358
HLA A*0203	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.369422	0.050897	-4.318525	23411.101075
HLA A*3201	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.541839	0.223276	-4.318562	34820.804182
HLA B*4001	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.392141	0.073404	-4.318737	24668.421473
HLA B*3501	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.458782	0.139887	-4.318895	28759.554384
HLA A*2501	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.451170	0.132177	-4.318993	28259.847971
HLA A*2301	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.536033	0.216943	-4.319091	34358.422785
HLA B*2705	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.401196	0.082090	-4.319107	25188.150245
HLA A*3301	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.460441	0.141319	-4.319122	28869.608135
HLA B*1503	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.476500	0.157340	-4.319159	29957.089641
HLA A*3101	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.290620	-0.028622	-4.319242	19526.306993
HLA B*4002	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.534074	0.214737	-4.319337	34203.752007
HLA A*2603	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.605106	0.285730	-4.319375	40281.508774
HLA B*1801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.491936	0.172544	-4.319392	31041.002260
HLA A*3101	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.392853	0.073404	-4.319449	24708.891020
HLA B*5101	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.495946	0.176401	-4.319545	31328.983668
HLA A*0206	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.370648	0.050897	-4.319752	23477.306575
HLA A*3001	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.306599	-0.013165	-4.319764	20258.111657
HLA B*1503	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.499419	0.179592	-4.319827	31580.488616
HLA B*3501	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.254013	-0.065831	-4.319843	17947.864711
HLA A*2301	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.530279	0.210423	-4.319856	33906.216492
HLA A*2501	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.468401	0.148535	-4.319866	29403.629661
HLA A*2603	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.615784	0.295880	-4.319904	41284.225195

HLA A*6901	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.308967	-0.010996	-4.319963	20368.884305
HLA A*0101	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.379717	0.059501	-4.320217	23972.718366
HLA A*2601	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.330124	0.009850	-4.320275	21385.743512
HLA A*0219	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.442578	0.122274	-4.320304	27706.250374
HLA A*2301	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.541677	0.221286	-4.320391	34807.808616
HLA A*1101	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.460298	0.139887	-4.320410	28860.082643
HLA B*0702	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.442864	0.122446	-4.320418	27724.542714
HLA B*3501	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.211593	-0.108943	-4.320536	16277.692330
HLA B*0802	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.496968	0.176401	-4.320567	31402.797040
HLA B*3801	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.561582	0.240938	-4.320644	36440.264393
HLA B*3901	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.402815	0.082090	-4.320725	25282.212094
HLA B*1502	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.569069	0.248296	-4.320774	37073.989965
HLA B*4801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.385372	0.064589	-4.320784	24286.922874
HLA B*5301	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.589369	0.268569	-4.320800	38848.019090
HLA B*4801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.449875	0.128996	-4.320880	28175.735060
HLA B*5101	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.492636	0.171585	-4.321051	31091.085278
HLA B*1502	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.224938	-0.096147	-4.321085	16785.640220
HLA A*0250	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.590506	0.269402	-4.321104	38949.871499
HLA A*3001	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.266850	-0.054260	-4.321110	18486.316033
HLA A*2301	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.545894	0.224721	-4.321173	35147.465070
HLA A*2902	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.461705	0.140490	-4.321215	28953.756115
HLA B*4801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.443687	0.122446	-4.321241	27777.087791
HLA B*4002	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.635095	0.313851	-4.321244	43161.303837
HLA A*6802	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.428551	0.107303	-4.321248	26825.716406
HLA B*7301	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.606981	0.285730	-4.321250	40455.783645
HLA B*1517	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.464968	0.143550	-4.321418	29172.143859
HLA A*2902	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.443745	0.122274	-4.321471	27780.844819
HLA B*7301	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.563640	0.242067	-4.321573	36613.366946
HLA A*0101	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.386181	0.064589	-4.321592	24332.162966
HLA A*2902	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.450789	0.128996	-4.321794	28235.091833
HLA A*0250	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.570188	0.248296	-4.321892	37169.582493
HLA A*2603	1:599-607	9	QHNRVVYQN	0.902423	-0.578124	-4.646196	0.324299	-4.321897	44278.803025
HLA A*0219	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.479274	0.157340	-4.321934	30149.100589
HLA B*4002	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.568364	0.246391	-4.321973	37013.868913
HLA B*0702	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.462523	0.140490	-4.322032	29008.316999
HLA A*0203	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.441170	0.119114	-4.322056	27616.612930
HLA A*2602	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.532493	0.210423	-4.322069	34079.447517
HLA A*2501	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.479530	0.157340	-4.322190	30166.884091
HLA B*0803	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.502013	0.179592	-4.322421	31769.668017
HLA A*2603	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.634928	0.312328	-4.322599	43144.728672
HLA B*1801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.479873	0.157255	-4.322619	30190.720630
HLA A*0202	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.569072	0.246391	-4.322681	37074.190532
HLA B*5701	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.382243	0.059501	-4.322742	24112.541030
HLA B*4601	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.408917	0.086012	-4.322905	25639.921009
HLA A*2602	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.592329	0.269402	-4.322928	39113.729644
HLA B*5301	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.590520	0.267585	-4.322935	38951.135806
HLA A*0212	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.462562	0.139599	-4.322964	29010.984962
HLA B*5701	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.385579	0.062590	-4.322989	24298.487908
HLA A*3301	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.640480	0.317460	-4.323019	43699.812664
HLA B*3901	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.514418	0.191384	-4.323034	32690.228588
HLA A*6901	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.288741	-0.034337	-4.323078	19441.981477
HLA B*1502	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.564145	0.240938	-4.323207	36655.977687
HLA B*4403	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.589362	0.266144	-4.323218	38847.388604
HLA B*4501	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.648693	0.325463	-4.323230	44534.171247
HLA A*0219	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.442355	0.119114	-4.323240	27692.014697
HLA B*1801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.518577	0.195249	-4.323328	33004.757478
HLA B*1509	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.510210	0.186843	-4.323367	32375.018837
HLA A*3301	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.586585	0.263202	-4.323383	38599.771941
HLA A*2403	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.442521	0.119114	-4.323407	27702.653302
HLA B*1502	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.604937	0.281512	-4.323425	40265.821698
HLA A*0219	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.463960	0.140490	-4.323470	29104.518414
HLA B*3801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.565646	0.242067	-4.323579	36782.913716
HLA B*4501	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.619463	0.295880	-4.323583	41635.466197
HLA A*2501	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.483698	0.160089	-4.323610	30457.793719
HLA B*1517	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.464999	0.141319	-4.323680	29174.195566

HLA A*0219	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.386282	0.062590	-4.323691	24337.823900
HLA B*0802	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.424350	0.100651	-4.323699	26567.485355
HLA A*3301	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.493063	0.169330	-4.323734	31121.712630
HLA A*0203	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.452758	0.128996	-4.323762	28363.385847
HLA B*4403	1:470-478	9	TNPPANQTS	1.396729	-1.071266	-4.649448	0.325463	-4.323984	44611.575338
HLA B*0803	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.496625	0.172544	-4.324082	31378.003528
HLA A*0201	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.397595	0.073404	-4.324190	24980.119674
HLA A*0301	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.313260	-0.010996	-4.324255	20571.205871
HLA B*7301	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.589343	0.264968	-4.324375	38845.707360
HLA B*3901	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.479735	0.155271	-4.324464	30181.085789
HLA A*8001	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.461750	0.137283	-4.324467	28956.732364
HLA B*4501	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.545758	0.221286	-4.324472	35136.438454
HLA A*6901	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.389214	0.064589	-4.324625	24502.697681
HLA B*1517	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.464607	0.139887	-4.324719	29147.849999
HLA A*3101	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.389329	0.064589	-4.324740	24509.193829
HLA B*5101	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.507130	0.182373	-4.324757	32146.215734
HLA B*4001	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.432113	0.107303	-4.324810	27046.629279
HLA A*3301	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.589895	0.264968	-4.324928	38895.124244
HLA A*3301	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.588330	0.263371	-4.324959	38755.237805
HLA B*5101	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.498752	0.173777	-4.324975	31532.005339
HLA A*0250	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.277092	-0.047884	-4.324975	18927.435652
HLA A*2902	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.461033	0.135996	-4.325037	28908.992683
HLA A*0250	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.482293	0.157255	-4.325039	30359.418506
HLA B*5801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.334013	0.008974	-4.325039	21578.077646
HLA B*3901	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.507473	0.182373	-4.325100	32171.616253
HLA B*1509	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.548399	0.223276	-4.325122	35350.744042
HLA A*6801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.512014	0.186843	-4.325171	32509.810220
HLA B*2705	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.461437	0.135996	-4.325441	28935.905047
HLA B*5101	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.473626	0.148101	-4.325525	29759.538963
HLA A*0301	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.364037	0.038504	-4.325533	23122.608200
HLA B*1509	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.504919	0.179347	-4.325572	31982.984644
HLA B*3501	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.465302	0.139599	-4.325703	29194.562635
HLA A*0219	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.433215	0.107303	-4.325912	27115.340146
HLA B*5301	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.598814	0.272858	-4.325955	39702.130101
HLA B*1801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.497666	0.171585	-4.326081	31453.293635
HLA B*1509	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.551096	0.224721	-4.326374	35570.974871
HLA A*2402	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.537760	0.211378	-4.326382	34495.313076
HLA B*0702	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.433744	0.107303	-4.326441	27148.365713
HLA B*1517	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.433753	0.107303	-4.326450	27148.953198
HLA A*2301	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.537983	0.211378	-4.326605	34513.046135
HLA B*5101	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.499198	0.172544	-4.326654	31564.433086
HLA A*3301	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.634542	0.307875	-4.326668	43106.466703
HLA B*7301	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.574967	0.248296	-4.326671	37580.844523
HLA A*0216	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.470243	0.143550	-4.326693	29528.605682
HLA B*0802	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.462708	0.135996	-4.326712	29020.717259
HLA A*2601	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.389303	0.062590	-4.326713	24507.735360
HLA B*4501	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.462718	0.135996	-4.326721	29021.345261
HLA B*0802	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.475402	0.148535	-4.326867	29881.501028
HLA A*2501	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.468189	0.141319	-4.326870	29389.316811
HLA B*3501	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.470537	0.143550	-4.326987	29548.580746
HLA A*6801	1:576-584	9	PRLRALGWT	0.847303	-0.490681	-4.683696	0.356622	-4.327074	48272.078862
HLA A*0206	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.463263	0.135996	-4.327266	29057.792653
HLA A*0101	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.385382	0.057919	-4.327463	24287.448438
HLA B*1503	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.446802	0.119119	-4.327683	27977.063498
HLA A*0211	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.510273	0.182373	-4.327901	32379.748104
HLA A*0202	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.551201	0.223225	-4.327976	35579.635502
HLA A*0250	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.551300	0.223225	-4.328075	35587.720659
HLA B*3501	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.485421	0.157340	-4.328080	30578.812327
HLA B*3901	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.497490	0.169330	-4.328160	31440.534311
HLA B*1503	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.497546	0.169330	-4.328216	31444.616731
HLA A*2402	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.569196	0.240938	-4.328259	37084.822121
HLA B*3801	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.570460	0.242192	-4.328268	37192.915479
HLA B*5301	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.593370	0.264968	-4.328403	39207.581278
HLA A*2501	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.468056	0.139599	-4.328457	29380.255611
HLA A*0211	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.476634	0.148101	-4.328533	29966.328744

HLA A*2402	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.497899	0.169330	-4.328569	31470.143871
HLA A*0219	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.457582	0.128996	-4.328586	28680.159729
HLA B*1801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.460845	0.132130	-4.328715	28896.483834
HLA B*4501	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.642643	0.313851	-4.328793	43918.090660
HLA A*2603	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.379713	0.050897	-4.328816	23972.458987
HLA A*3101	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.411052	0.082090	-4.328963	25766.318138
HLA A*3301	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.619419	0.290447	-4.328972	41631.186795
HLA A*0201	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.415009	0.086012	-4.328997	26002.128338
HLA B*7301	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.598358	0.269282	-4.329076	39660.483839
HLA B*1502	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.614875	0.285730	-4.329145	41197.881839
HLA B*1501	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.338728	0.009579	-4.329149	21813.641327
HLA B*5701	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.415180	0.086012	-4.329169	26012.399176
HLA A*0202	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.500805	0.171585	-4.329220	31681.449351
HLA B*3901	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.499940	0.170651	-4.329290	31618.439422
HLA B*1509	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.472867	0.143550	-4.329317	29707.582725
HLA B*0801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.380244	0.050897	-4.329347	24001.786478
HLA B*5101	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.500037	0.170651	-4.329386	31625.453342
HLA B*3501	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.367986	0.038504	-4.329483	23333.844786
HLA A*0203	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.415509	0.086012	-4.329498	26032.108026
HLA B*0802	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.470898	0.141319	-4.329579	29573.208604
HLA B*1517	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.508944	0.179347	-4.329597	32280.753043
HLA A*0202	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.516554	0.186843	-4.329711	32851.381621
HLA B*5101	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.485244	0.155271	-4.329973	30566.407745
HLA A*2902	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.449138	0.119114	-4.330023	28127.913422
HLA A*0202	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.584893	0.254868	-4.330025	38449.713628
HLA A*0101	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.281431	-0.048602	-4.330033	19117.507849
HLA B*5401	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.551542	0.221286	-4.330256	35607.556325
HLA B*0803	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.500986	0.170651	-4.330335	31694.649371
HLA A*2902	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.449654	0.119119	-4.330535	28161.410508
HLA B*3501	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.459778	0.128996	-4.330783	28825.598565
HLA A*8001	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.431634	0.100651	-4.330983	27016.796614
HLA B*5401	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.522463	0.191384	-4.331078	33301.407845
HLA A*0211	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.507600	0.176401	-4.331198	32181.016050
HLA A*6802	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.222180	-0.109105	-4.331285	16679.368929
HLA B*3801	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.542689	0.211378	-4.331311	34889.063361
HLA B*0802	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.473255	0.141914	-4.331341	29734.112494
HLA B*1502	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.624797	0.293372	-4.331425	42149.920790
HLA A*2402	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.541865	0.210423	-4.331441	34822.876388
HLA A*0250	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.554773	0.223276	-4.331496	35873.414186
HLA A*3201	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.296367	-0.035208	-4.331575	19786.407693
HLA A*3201	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.579938	0.248296	-4.331642	38013.516423
HLA A*3301	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.644018	0.312328	-4.331689	44057.302153
HLA B*5301	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.597876	0.266144	-4.331732	39616.523662
HLA B*7301	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.548774	0.216943	-4.331832	35381.356265
HLA B*1501	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.306991	-0.025025	-4.332016	20276.422148
HLA A*2301	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.514514	0.182373	-4.332142	32697.480263
HLA B*3801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.555473	0.223276	-4.332196	35931.294044
HLA B*3901	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.473605	0.141319	-4.332286	29758.090036
HLA A*0206	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.511963	0.179592	-4.332371	32505.941212
HLA A*1101	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.503131	0.170651	-4.332480	31851.583744
HLA A*0201	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.397233	0.064589	-4.332644	24959.316831
HLA B*3801	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.561523	0.228841	-4.332682	36435.336282
HLA A*3002	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.527939	0.195249	-4.332690	33724.012655
HLA B*5301	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.561579	0.228841	-4.332739	36440.067256
HLA B*3501	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.395358	0.062590	-4.332767	24851.797428
HLA B*0801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.395395	0.062590	-4.332805	24853.948648
HLA B*5101	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.512231	0.179347	-4.332884	32525.994699
HLA A*0216	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.465100	0.132130	-4.332970	29180.983010
HLA A*0201	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.392571	0.059501	-4.333071	24692.855543
HLA B*3801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.579527	0.246391	-4.333136	37977.544894
HLA A*0206	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.473058	0.139887	-4.333170	29720.603471
HLA A*2402	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.588149	0.254868	-4.333281	38739.097229
HLA A*0216	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.469381	0.135996	-4.333384	29470.036884
HLA A*0250	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.574586	0.240938	-4.333648	37547.923022
HLA B*1517	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.474164	0.140490	-4.333674	29796.429850

HLA A*0211	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.528971	0.195249	-4.333722	33804.200390
HLA A*2601	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.391754	0.057919	-4.333835	24646.411482
HLA A*0212	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.419931	0.086012	-4.333919	26298.505476
HLA A*0219	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.473542	0.139599	-4.333943	29753.743679
HLA B*7301	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.550473	0.216497	-4.333976	35520.016125
HLA A*2603	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.557472	0.223225	-4.334247	36097.096467
HLA B*1801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.456555	0.122274	-4.334281	28612.436430
HLA A*0202	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.559021	0.224721	-4.334299	36226.016509
HLA B*7301	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.557609	0.223276	-4.334332	36108.424559
HLA B*3801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.555619	0.221286	-4.334333	35943.347893
HLA A*2603	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.597538	0.263202	-4.334336	39585.673456
HLA A*2602	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.594479	0.260101	-4.334378	39307.824499
HLA B*5801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.359768	0.025261	-4.334507	22896.431765
HLA A*2603	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.625011	0.290447	-4.334563	42170.676301
HLA A*2601	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.372824	0.038251	-4.334573	23595.212570
HLA B*0802	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.474472	0.139887	-4.334585	29817.553929
HLA B*4801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.435283	0.100651	-4.334631	27244.735975
HLA B*1503	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.466839	0.132177	-4.334662	29298.037911
HLA A*0202	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.583049	0.248296	-4.334753	38286.773038
HLA A*0203	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.287413	-0.047418	-4.334831	19382.646090
HLA B*2705	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.442185	0.107303	-4.334882	27681.230425
HLA A*6801	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.558215	0.223276	-4.334938	36158.858132
HLA B*1801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.517439	0.182373	-4.335067	32918.451313
HLA A*0250	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.504409	0.169330	-4.335079	31945.460379
HLA A*2601	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.399693	0.064589	-4.335104	25101.091381
HLA A*0101	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.344999	0.009850	-4.335149	22130.893253
HLA A*0212	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.306702	-0.028622	-4.335325	20262.934373
HLA A*3301	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.564460	0.228841	-4.335619	36682.560161
HLA B*5301	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.595821	0.260101	-4.335719	39429.435939
HLA A*3301	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.621552	0.285730	-4.335822	41836.189744
HLA A*2301	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.522705	0.186843	-4.335862	33319.969179
HLA B*0803	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.527256	0.191384	-4.335871	33670.963461
HLA A*2501	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.476392	0.140490	-4.335901	29949.635600
HLA B*4501	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.554406	0.218420	-4.335987	35843.151851
HLA B*4002	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.609036	0.272858	-4.336178	40647.741258
HLA B*4402	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.458625	0.122446	-4.336179	28749.132010
HLA B*3801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.559411	0.223225	-4.336186	36258.563591
HLA A*2601	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.374696	0.038504	-4.336193	23697.167255
HLA B*0801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.400839	0.064589	-4.336250	25167.446463
HLA B*4001	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.394228	0.057919	-4.336309	24787.213223
HLA B*0803	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.493757	0.157340	-4.336416	31171.419963
HLA B*0802	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.458728	0.122274	-4.336454	28755.976128
HLA A*0206	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.523332	0.186843	-4.336489	33368.132665
HLA B*1801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.496693	0.160089	-4.336605	31382.926708
HLA B*5301	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.595762	0.259153	-4.336609	39424.103578
HLA B*0802	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.480165	0.143550	-4.336615	30210.980152
HLA A*1101	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.478170	0.141319	-4.336851	30072.539417
HLA A*0202	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.516509	0.179592	-4.336917	32848.005071
HLA A*8001	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.465969	0.128996	-4.336974	29239.451885
HLA B*4601	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.375486	0.038504	-4.336982	23740.281308
HLA B*4801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.444298	0.107303	-4.336995	27816.185732
HLA B*3901	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.477524	0.140490	-4.337034	30027.833177
HLA B*4402	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.349475	0.012088	-4.337387	22360.149984
HLA A*2603	1:85-93	9	GPLPYIVME	1.137893	-0.813376	-4.661907	0.324517	-4.337390	45909.956200
HLA B*3901	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.494781	0.157340	-4.337441	31245.031135
HLA A*6801	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.596626	0.259153	-4.337473	39502.668808
HLA B*4002	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.649840	0.312328	-4.337511	44651.897945
HLA A*6901	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.302407	-0.035208	-4.337616	20063.536172
HLA B*5801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.349707	0.012088	-4.337619	22372.128819
HLA A*0212	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.375911	0.038251	-4.337660	23763.538938
HLA A*2403	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.388627	0.050897	-4.337730	24469.580861
HLA A*2501	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.481304	0.143550	-4.337754	30290.351690
HLA B*1801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.423946	0.086012	-4.337935	26542.775783
HLA B*1502	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.580168	0.242192	-4.337976	38033.675359
HLA A*0211	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.424033	0.086012	-4.338022	26548.089274

HLA A*0216	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.467069	0.128996	-4.338073	29313.574945
HLA A*3201	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.580789	0.242669	-4.338119	38088.034271
HLA B*2705	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.182436	-0.155719	-4.338155	15220.738570
HLA A*1101	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.481739	0.143550	-4.338189	30320.682343
HLA A*2501	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.457347	0.119119	-4.338227	28664.648277
HLA B*0702	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.475520	0.137283	-4.338237	29889.584902
HLA B*0702	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.424353	0.086012	-4.338341	26567.629083
HLA B*0803	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.493865	0.155271	-4.338593	31179.178089
HLA B*1502	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.597808	0.259153	-4.338655	39610.308840
HLA B*3901	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.457838	0.119114	-4.338723	28697.076773
HLA B*0802	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.451151	0.112336	-4.338815	28258.624937
HLA B*4002	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.632409	0.293372	-4.339037	42895.239226
HLA B*0803	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.461517	0.122446	-4.339071	28941.227898
HLA B*5301	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.549524	0.210423	-4.339101	35442.468522
HLA A*0201	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.397031	0.057919	-4.339111	24947.707198
HLA B*4402	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.439857	0.100651	-4.339206	27533.222912
HLA B*4403	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.560515	0.221286	-4.339229	36350.873657
HLA B*4403	1:535-543	9	TGTNPPAGT	0.756723	-0.427487	-4.668481	0.329236	-4.339245	46610.175424
HLA A*3001	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.291489	-0.047884	-4.339373	19565.431145
HLA B*3801	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.554120	0.214737	-4.339382	35819.502944
HLA A*0211	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.526231	0.186843	-4.339388	33591.636958
HLA A*2301	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.534837	0.195249	-4.339588	34263.942420
HLA A*3101	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.397517	0.057919	-4.339598	24975.660463
HLA B*5801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.273777	-0.065831	-4.339607	18783.505876
HLA B*0803	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.440327	0.100651	-4.339676	27563.029370
HLA B*3801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.535079	0.195249	-4.339830	34283.040246
HLA A*0206	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.550259	0.210423	-4.339836	35502.533927
HLA A*2902	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.402557	0.062590	-4.339966	25267.171433
HLA A*0203	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.274136	-0.065831	-4.339967	18799.059664
HLA A*2603	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.556652	0.216497	-4.340155	36029.007595
HLA A*0219	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.459346	0.119119	-4.340227	28796.919275
HLA A*2301	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.516641	0.176401	-4.340239	32857.958006
HLA B*4403	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.607883	0.267585	-4.340298	40539.913741
HLA B*1502	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.497593	0.157255	-4.340339	31448.019153
HLA B*4601	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.413778	0.073404	-4.340373	25928.522352
HLA B*7301	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.516779	0.176401	-4.340378	32868.447397
HLA B*1801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.497739	0.157340	-4.340399	31458.569001
HLA B*1801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.482340	0.141914	-4.340427	30362.703506
HLA A*3301	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.609769	0.269282	-4.340488	40716.407922
HLA B*5101	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.480393	0.139887	-4.340505	30226.837804
HLA A*2602	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.630992	0.290447	-4.340545	42755.535949
HLA B*5701	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.414006	0.073404	-4.340601	25942.132155
HLA A*0219	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.426709	0.086012	-4.340698	26712.180015
HLA B*5301	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.557268	0.216497	-4.340770	36080.110993
HLA A*0211	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.480731	0.139887	-4.340844	30250.394411
HLA B*4402	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.437834	0.096922	-4.340912	27405.273732
HLA A*0206	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.473133	0.132177	-4.340956	29725.749042
HLA A*2602	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.626719	0.285730	-4.340988	42336.859709
HLA A*0211	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.520623	0.179592	-4.341031	33160.643319
HLA A*3301	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.582008	0.240938	-4.341070	38195.125553
HLA A*3002	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.570054	0.228841	-4.341213	37158.122511
HLA B*1502	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.570131	0.228841	-4.341291	37164.756806
HLA B*3801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.566088	0.224721	-4.341366	36820.343146
HLA A*2602	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.608975	0.267585	-4.341390	40642.024266
HLA B*4002	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.637282	0.295880	-4.341402	43379.238719
HLA B*1503	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.185791	-0.155719	-4.341510	15338.779035
HLA B*4002	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.644890	0.303321	-4.341569	44145.816990
HLA B*4501	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.583676	0.242067	-4.341609	38342.115960
HLA B*5301	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.596511	0.254868	-4.341643	39492.198648
HLA B*1503	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.514204	0.172544	-4.341660	32674.139152
HLA A*3001	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-3.940241	-0.401420	-4.341661	8714.478738
HLA B*2705	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.464012	0.122274	-4.341738	29107.982569
HLA B*3501	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.464188	0.122446	-4.341742	29119.795287
HLA B*4402	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.401405	0.059501	-4.341905	25200.280759
HLA A*0201	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.313431	-0.028622	-4.342053	20579.331495

HLA B*4601	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.404676	0.062590	-4.342085	25390.769472
HLA B*5301	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.559032	0.216943	-4.342090	36226.996416
HLA B*1509	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.464390	0.122274	-4.342116	29133.346438
HLA A*1101	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.424238	0.082090	-4.342148	26560.587348
HLA B*5101	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.479474	0.137283	-4.342191	30162.967557
HLA A*1101	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.464581	0.122274	-4.342307	29146.115497
HLA B*1801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.483691	0.141319	-4.342372	30457.299403
HLA B*1517	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.479796	0.137283	-4.342513	30185.331272
HLA A*2601	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.246370	-0.096147	-4.342517	17634.774576
HLA B*0802	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.461663	0.119114	-4.342548	28950.936793
HLA B*1509	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.454903	0.112336	-4.342567	28503.825646
HLA A*0216	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.483059	0.140490	-4.342569	30413.008344
HLA B*0803	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.514169	0.171585	-4.342584	32671.487808
HLA B*5301	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.590917	0.248296	-4.342621	38986.763995
HLA A*0301	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.367935	0.025261	-4.342673	23331.067813
HLA B*0702	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.471709	0.128996	-4.342713	29628.455929
HLA A*2602	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.490867	0.148101	-4.342766	30964.688808
HLA A*2602	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.513671	0.170651	-4.343020	32634.038472
HLA A*2501	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.405679	0.062590	-4.343089	25449.490522
HLA A*0301	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.352686	0.009579	-4.343107	22526.123371
HLA A*3201	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.603339	0.260101	-4.343238	40117.966954
HLA B*1509	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.517113	0.173777	-4.343336	32893.706779
HLA A*3002	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.479436	0.135996	-4.343440	30160.356817
HLA B*5801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.353314	0.009850	-4.343464	22558.684524
HLA A*6801	1:78-86	9	GEAETPAGP	0.399025	-0.081565	-4.661063	0.317460	-4.343603	45820.878698
HLA B*2705	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.487199	0.143550	-4.343649	30704.298086
HLA B*5801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.332697	-0.010996	-4.343693	21512.804965
HLA B*4501	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.647046	0.303321	-4.343726	44365.602707
HLA A*8001	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.462903	0.119114	-4.343789	29033.751091
HLA B*1517	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.483433	0.139599	-4.343834	30439.180028
HLA B*2705	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.466503	0.122446	-4.344057	29275.381299
HLA B*3901	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.492598	0.148535	-4.344063	31088.394205
HLA B*1801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.354122	0.009850	-4.344272	22600.705366
HLA B*4501	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.611898	0.267585	-4.344313	40916.463549
HLA A*2402	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.587012	0.242669	-4.344343	38637.795986
HLA A*8001	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.451673	0.107303	-4.344370	28292.583803
HLA A*0250	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.599455	0.254868	-4.344587	39760.809487
HLA B*3501	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.430953	0.086012	-4.344941	26974.444061
HLA A*0206	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.524429	0.179347	-4.345082	33452.541105
HLA B*4403	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.409697	0.064589	-4.345108	25686.013821
HLA B*4801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.383425	0.038251	-4.345174	24178.244811
HLA B*5401	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.524565	0.179347	-4.345219	33463.039275
HLA B*1502	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.611402	0.266144	-4.345258	40869.784601
HLA A*6801	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.577708	0.232368	-4.345340	37818.855727
HLA A*2403	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.409939	0.064589	-4.345350	25700.330533
HLA B*5301	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.608874	0.263371	-4.345503	40632.571005
HLA A*2602	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.291377	-0.054260	-4.345636	19560.351157
HLA B*0803	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.467931	0.122274	-4.345657	29371.832790
HLA A*2403	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.384151	0.038251	-4.345900	24218.696314
HLA B*1501	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.403823	0.057919	-4.345904	25340.956266
HLA B*1502	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.560696	0.214737	-4.345959	36366.019185
HLA B*1502	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.564401	0.218420	-4.345981	36677.599282
HLA B*1509	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.518647	0.172544	-4.346103	33010.114476
HLA B*1801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.335159	-0.010996	-4.346155	21635.119593
HLA A*0203	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.355807	0.009579	-4.346227	22688.541271
HLA B*4501	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.658721	0.312328	-4.346393	45574.401785
HLA A*2402	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.562911	0.216497	-4.346414	36552.015386
HLA A*3001	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.282733	-0.063767	-4.346500	19174.890470
HLA B*4002	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.257727	-0.088805	-4.346532	18102.031779
HLA A*0250	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.592931	0.246391	-4.346540	39167.937013
HLA B*2705	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.443492	0.096922	-4.346569	27764.618100
HLA A*0206	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.504144	0.157340	-4.346803	31925.937529
HLA A*1101	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.487303	0.140490	-4.346812	30711.607657
HLA B*4601	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.411412	0.064589	-4.346823	25787.654084
HLA A*3002	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.479108	0.132177	-4.346931	30137.522479

HLA A*0211	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.479225	0.132130	-4.347095	30145.675614
HLA B*0803	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.523501	0.176401	-4.347100	33381.132486
HLA B*1501	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.299271	-0.047884	-4.347154	19919.155263
HLA A*0101	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.385661	0.038504	-4.347158	24303.089168
HLA B*4801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.429350	0.082090	-4.347261	26875.104025
HLA B*4002	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.628803	0.281512	-4.347291	42540.504375
HLA B*3901	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.447963	0.100651	-4.347311	28051.931785
HLA B*0702	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.336332	-0.010996	-4.347327	21693.603253
HLA A*2602	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.299489	-0.047884	-4.347373	19929.179504
HLA B*5101	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.398389	0.050897	-4.347492	25025.838672
HLA A*3201	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.516857	0.169330	-4.347527	32874.315804
HLA A*0201	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.385847	0.038251	-4.347596	24313.478073
HLA B*3501	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.359857	0.012088	-4.347769	22901.139201
HLA B*1503	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.360123	0.012088	-4.348035	22915.143348
HLA A*2902	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.251950	-0.096147	-4.348097	17862.816603
HLA A*0202	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.566525	0.218420	-4.348105	36857.411872
HLA A*2402	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.577410	0.229302	-4.348108	37792.880983
HLA B*1801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.496952	0.148535	-4.348417	31401.607863
HLA A*2603	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.616092	0.267585	-4.348507	41313.493508
HLA B*1503	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.470851	0.122274	-4.348578	29570.009021
HLA B*5101	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.490528	0.141914	-4.348615	30940.575965
HLA A*2403	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.387179	0.038504	-4.348676	24388.171909
HLA B*5301	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.471063	0.122274	-4.348789	29584.409869
HLA B*1517	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.467926	0.119119	-4.348807	29371.514995
HLA B*7301	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.560195	0.211378	-4.348817	36324.138523
HLA B*2705	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.490143	0.141319	-4.348824	30913.136985
HLA B*0803	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.518407	0.169330	-4.349078	32991.904232
HLA A*0301	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.361208	0.012088	-4.349120	22972.488375
HLA A*1101	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.456585	0.107303	-4.349282	28614.448772
HLA B*5401	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.486572	0.137283	-4.349289	30659.979573
HLA B*3801	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.559930	0.210423	-4.349507	36301.939728
HLA B*2705	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.489997	0.140490	-4.349507	30902.770051
HLA B*0702	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.490984	0.141319	-4.349665	30973.065718
HLA A*0202	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.388016	0.038251	-4.349764	24435.186849
HLA A*3301	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.598093	0.248296	-4.349797	39636.246102
HLA A*3201	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.615942	0.266144	-4.349797	41299.191893
HLA A*2601	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.400743	0.050897	-4.349846	25161.864805
HLA B*2705	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.489567	0.139599	-4.349969	30872.191148
HLA B*1503	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.487274	0.137283	-4.349992	30709.613965
HLA A*0203	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.409643	0.059501	-4.350142	25682.817975
HLA B*0803	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.537029	0.186843	-4.350186	34437.324352
HLA B*5301	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.596608	0.246391	-4.350217	39500.959205
HLA B*0803	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.490113	0.139887	-4.350225	30910.962985
HLA B*0802	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.490759	0.140490	-4.350268	30956.984052
HLA B*5101	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.507635	0.157340	-4.350295	32183.627592
HLA A*2402	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.568874	0.218420	-4.350455	37057.346710
HLA A*2602	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.575178	0.224721	-4.350457	37599.146716
HLA A*3201	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.596850	0.246391	-4.350459	39522.976007
HLA B*5101	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.494031	0.143550	-4.350481	31191.156378
HLA B*1801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.410026	0.059501	-4.350525	25705.475378
HLA B*4501	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.620199	0.269402	-4.350797	41706.027059
HLA B*4801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.410350	0.059501	-4.350849	25724.673344
HLA B*0702	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.415507	0.064589	-4.350918	26031.967195
HLA B*3901	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.470078	0.119119	-4.350959	29517.425546
HLA A*2301	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.523532	0.172544	-4.350988	33383.480215
HLA B*3901	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.488280	0.137283	-4.350997	30780.802389
HLA B*4002	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.618646	0.267585	-4.351061	41557.155282
HLA B*3801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.568050	0.216943	-4.351107	36987.046352
HLA B*1801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.470231	0.119119	-4.351112	29527.806961
HLA B*1801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.242030	-0.109105	-4.351136	17459.444173
HLA B*7301	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.448132	0.096922	-4.351210	28062.860477
HLA B*0801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.334149	-0.017067	-4.351216	21584.849339
HLA B*7301	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.580692	0.229302	-4.351390	38079.587074
HLA A*0301	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.360383	0.008974	-4.351410	22928.907971
HLA A*0216	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.414060	0.062590	-4.351469	25945.360269

HLA A*0211	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.304104	-0.047418	-4.351522	20142.056388
HLA B*4002	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.621357	0.269799	-4.351559	41817.408641
HLA B*1509	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.520893	0.169330	-4.351563	33181.280209
HLA A*3301	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.617856	0.266144	-4.351712	41481.684509
HLA B*5101	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.509047	0.157255	-4.351792	32288.437911
HLA A*2601	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.341270	-0.010996	-4.352266	21941.701913
HLA A*1101	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.390581	0.038251	-4.352330	24579.967364
HLA A*0212	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.425748	0.073404	-4.352344	26653.140793
HLA B*4002	1:513-521	9	NVYGFTKFS	1.072928	-0.797804	-4.627499	0.275124	-4.352375	42412.968559
HLA A*2501	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.492298	0.139887	-4.352410	31066.874007
HLA A*2603	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.594615	0.242192	-4.352423	39320.160190
HLA B*1801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.492319	0.139887	-4.352431	31068.386659
HLA A*3301	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.621935	0.269402	-4.352533	41873.097666
HLA A*0101	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.335484	-0.017067	-4.352550	21651.277641
HLA A*2402	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.598971	0.246391	-4.352580	39716.523245
HLA B*5101	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.501251	0.148535	-4.352716	31714.030788
HLA B*4501	1:351-359	9	NTFGGITRD	0.998912	-0.729113	-4.622515	0.269799	-4.352717	41929.087683
HLA B*4002	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.638452	0.285730	-4.352722	43496.265372
HLA B*3801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.535117	0.182373	-4.352744	34286.007854
HLA B*1503	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.524345	0.171585	-4.352760	33446.026656
HLA A*6801	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.617772	0.264968	-4.352804	41473.606488
HLA B*5301	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.582236	0.229302	-4.352934	38215.174058
HLA B*4402	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.426601	0.073404	-4.353197	26705.533386
HLA A*0250	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.577983	0.224721	-4.353262	37842.801015
HLA B*3501	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.324683	-0.028622	-4.353305	21119.466661
HLA B*1503	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.475877	0.122446	-4.353431	29914.173310
HLA B*3901	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.495406	0.141914	-4.353492	31290.026055
HLA A*2603	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.601861	0.248296	-4.353565	39981.684726
HLA B*0801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.305182	-0.048602	-4.353784	20192.134065
HLA B*3801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.583096	0.229302	-4.353794	38290.915806
HLA A*2403	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.439869	0.086012	-4.353857	27533.967680
HLA A*2603	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.647335	0.293372	-4.353964	44395.134129
HLA A*3002	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.600381	0.246391	-4.353990	39845.649893
HLA B*0803	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.514286	0.160089	-4.354198	32680.326459
HLA B*1502	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.575568	0.221286	-4.354282	37632.927480
HLA A*1101	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.473546	0.119119	-4.354427	29754.065609
HLA A*3301	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.622055	0.267585	-4.354470	41884.652229
HLA B*5801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.353199	-0.001305	-4.354504	22552.705357
HLA B*4501	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.647906	0.293372	-4.354534	44453.534487
HLA B*4601	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.412464	0.057919	-4.354545	25850.229624
HLA A*6801	1:605-613	9	YQNPPAGTG	0.869461	-0.601876	-4.622154	0.267585	-4.354568	41894.170146
HLA B*4801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.440661	0.086012	-4.354649	27584.211542
HLA B*0801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.366758	0.012088	-4.354670	23267.917968
HLA B*5401	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.405595	0.050897	-4.354698	25444.534564
HLA B*3801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.511996	0.157255	-4.354741	32508.403255
HLA B*0802	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.494407	0.139599	-4.354809	31218.166578
HLA A*0301	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.364683	0.009850	-4.354833	23157.033757
HLA B*4002	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.621002	0.266144	-4.354858	41783.262231
HLA B*5701	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.393401	0.038504	-4.354897	24740.056318
HLA A*6801	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.512155	0.157255	-4.354901	32520.364401
HLA A*0202	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.494807	0.139887	-4.354919	31246.890544
HLA A*1101	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.492215	0.137283	-4.354933	31060.992171
HLA B*3501	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.329915	-0.025025	-4.354940	21375.449180
HLA B*4002	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.623528	0.268569	-4.354959	42026.966218
HLA B*2705	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.474265	0.119114	-4.355151	29803.362057
HLA B*4501	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.614309	0.259153	-4.355155	41144.203729
HLA B*4403	1:473-481	9	PANQTSAIT	0.892340	-0.596460	-4.651111	0.295880	-4.355231	44782.774316
HLA B*5301	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.566635	0.211378	-4.355257	36866.784606
HLA A*2902	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.320933	-0.034337	-4.355270	20937.902278
HLA A*1101	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.474458	0.119114	-4.355343	29816.586087
HLA B*2705	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.492629	0.137283	-4.355346	31090.580684
HLA A*1101	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.406259	0.050897	-4.355363	25483.519947
HLA A*2902	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.462722	0.107303	-4.355419	29021.659268
HLA A*0101	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.308072	-0.047362	-4.355434	20326.943855
HLA B*5301	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.587917	0.232368	-4.355549	38718.354936

HLA B*0803	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.504123	0.148535	-4.355587	31924.383125
HLA B*5801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.365207	0.009579	-4.355627	23184.987383
HLA A*2301	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.525007	0.169330	-4.355677	33497.090479
HLA B*1501	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.394369	0.038504	-4.355865	24795.260293
HLA A*2402	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.528437	0.172544	-4.355894	33762.712796
HLA A*2402	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.580723	0.224721	-4.356001	38082.265251
HLA B*4403	1:213-221	9	EPPFTGDSP	0.510174	-0.196323	-4.669853	0.313851	-4.356002	46757.667327
HLA B*5401	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.504287	0.148101	-4.356186	31936.474930
HLA B*3901	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.488444	0.132130	-4.356314	30792.461048
HLA A*1101	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.478898	0.122446	-4.356452	30123.015353
HLA B*5301	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.475619	0.119119	-4.356499	29896.377046
HLA A*1101	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.492829	0.135996	-4.356832	31104.880682
HLA B*4402	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.407803	0.050897	-4.356906	25574.257108
HLA B*1503	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.500711	0.143550	-4.357161	31674.594368
HLA B*0802	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.486241	0.128996	-4.357245	30636.601231
HLA B*5101	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.454351	0.096922	-4.357429	28467.611075
HLA B*1517	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.486443	0.128996	-4.357447	30650.858240
HLA B*4402	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.443492	0.086012	-4.357480	27764.618100
HLA A*2602	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.623631	0.266144	-4.357487	42036.971303
HLA B*3901	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.501106	0.143550	-4.357556	31703.395269
HLA B*7301	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.498066	0.140490	-4.357575	31482.233942
HLA A*2601	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.332674	-0.025025	-4.357698	21511.641177
HLA A*0219	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.310288	-0.047418	-4.357706	20430.907238
HLA B*4402	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.439998	0.082090	-4.357908	27542.161463
HLA B*4001	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.417450	0.059501	-4.357949	26148.694575
HLA B*4002	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.621355	0.263371	-4.357983	41817.182414
HLA B*5101	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.490256	0.132177	-4.358079	30921.165386
HLA A*2501	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.480621	0.122446	-4.358175	30242.703779
HLA A*2301	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.549580	0.191384	-4.358196	35447.070577
HLA B*4002	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.420876	0.062590	-4.358285	26355.761056
HLA B*0801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-3.956923	-0.401420	-4.358342	9055.715253
HLA B*1502	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.604767	0.246391	-4.358376	40250.140731
HLA B*1517	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.367437	0.008974	-4.358463	23304.324832
HLA B*0803	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.537835	0.179347	-4.358489	34501.285299
HLA B*5701	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.423427	0.064589	-4.358838	26511.060588
HLA A*6901	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.341825	-0.017067	-4.358891	21969.733517
HLA B*0801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.368783	0.009850	-4.358933	23376.677211
HLA A*2601	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.371177	0.012088	-4.359089	23505.901140
HLA A*3201	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.535490	0.176401	-4.359089	34315.512418
HLA B*1502	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.583937	0.224721	-4.359215	38365.147226
HLA B*5301	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.601908	0.242669	-4.359239	39986.010890
HLA A*6801	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.625403	0.266144	-4.359259	42208.792677
HLA B*1502	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.614139	0.254868	-4.359271	41128.180688
HLA B*4501	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.569762	0.210423	-4.359339	37133.204225
HLA A*3002	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.614219	0.254868	-4.359351	41135.746347
HLA B*1503	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.538803	0.179347	-4.359457	34578.270091
HLA A*0250	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.576400	0.216943	-4.359457	37705.067383
HLA B*1509	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.519570	0.160089	-4.359482	33080.371492
HLA A*0212	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.424170	0.064589	-4.359581	26556.420670
HLA A*6801	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.652958	0.293372	-4.359586	44973.603846
HLA A*1101	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.460446	0.100651	-4.359794	28869.920500
HLA A*2403	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.417727	0.057919	-4.359808	26165.392366
HLA B*3501	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.433239	0.073404	-4.359834	27116.807095
HLA B*1503	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.501254	0.141319	-4.359935	31714.202357
HLA B*1502	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.576466	0.216497	-4.359968	37710.779262
HLA B*5101	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.499621	0.139599	-4.360022	31595.184871
HLA B*4501	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.628598	0.268569	-4.360030	42520.486957
HLA B*1501	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.123966	-0.236114	-4.360081	13303.516201
HLA B*3901	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.398363	0.038251	-4.360112	25024.349460
HLA A*3201	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.615037	0.254868	-4.360169	41213.263152
HLA A*0211	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.501627	0.141319	-4.360308	31741.493774
HLA A*2501	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.335425	-0.025025	-4.360449	21648.349563
HLA A*2301	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.540110	0.179592	-4.360518	34682.434593
HLA B*0803	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.457591	0.096922	-4.360669	28680.780362
HLA A*3002	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.540037	0.179347	-4.360690	34676.618608

HLA B*1503	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.509289	0.148535	-4.360754	32306.434642
HLA B*0802	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.498096	0.137283	-4.360813	31484.448120
HLA A*2402	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.516107	0.155271	-4.360836	32817.631727
HLA B*0802	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.483287	0.122446	-4.360841	30428.972039
HLA A*2301	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.534734	0.173777	-4.360957	34255.787369
HLA A*6901	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.251858	-0.109105	-4.360964	17859.048202
HLA B*0801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.325794	-0.035208	-4.361003	21173.577993
HLA B*5801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.351204	-0.009859	-4.361063	22449.358392
HLA B*1502	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.537577	0.176401	-4.361176	34480.760113
HLA B*5101	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.490251	0.128996	-4.361256	30920.830828
HLA B*5401	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.534013	0.172544	-4.361469	34198.941345
HLA A*8001	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.421012	0.059501	-4.361511	26364.032095
HLA B*7301	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.572034	0.210423	-4.361611	37327.970491
HLA A*2501	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.498923	0.137283	-4.361640	31544.460478
HLA A*2402	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.594080	0.232368	-4.361711	39271.690452
HLA A*2301	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.517101	0.155271	-4.361830	32892.817034
HLA A*8001	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.424466	0.062590	-4.361875	26574.528919
HLA B*4001	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.400402	0.038504	-4.361899	25142.134724
HLA A*6901	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.370881	0.008974	-4.361907	23489.883896
HLA A*2403	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.435315	0.073404	-4.361911	27246.799527
HLA A*0212	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.421632	0.059501	-4.362131	26401.712390
HLA B*0802	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.459062	0.096922	-4.362139	28778.075079
HLA A*8001	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.413195	0.050897	-4.362298	25893.758611
HLA B*5301	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.604415	0.242067	-4.362348	40217.491660
HLA B*5401	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.491471	0.128996	-4.362475	31007.770242
HLA B*0802	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.444568	0.082090	-4.362478	27833.496602
HLA B*4403	1:88-96	9	PYIVMEYVD	1.124863	-0.831491	-4.655873	0.293372	-4.362502	45276.557719
HLA B*4002	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.643125	0.280603	-4.362522	43966.824039
HLA B*3901	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.494710	0.132177	-4.362534	31239.960582
HLA B*1517	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.481762	0.119114	-4.362648	30322.322702
HLA A*0201	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.401166	0.038504	-4.362662	25186.378861
HLA A*2602	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.536597	0.173777	-4.362820	34403.061820
HLA A*0202	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.436260	0.073404	-4.362856	27306.119678
HLA B*4501	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.425502	0.062590	-4.362911	26638.005086
HLA B*1503	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.470217	0.107303	-4.362914	29526.848523
HLA A*0212	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.327714	-0.035208	-4.362922	21267.369777
HLA A*1101	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.491976	0.128996	-4.362980	31043.857174
HLA A*0206	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.485327	0.122274	-4.363053	30572.195923
HLA B*0801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.253973	-0.109105	-4.363078	17946.214155
HLA B*0803	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.505034	0.141914	-4.363120	31991.463963
HLA B*4403	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.675452	0.312328	-4.363123	47364.358483
HLA A*0211	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.475574	0.112336	-4.363238	29893.304218
HLA A*0211	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.533926	0.170651	-4.363275	34192.096568
HLA B*7301	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.542633	0.179347	-4.363286	34884.533752
HLA A*6901	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.388619	0.025261	-4.363358	24469.183731
HLA B*4403	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.649170	0.285730	-4.363440	44583.105873
HLA A*0202	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.573930	0.210423	-4.363507	37491.292472
HLA A*3001	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.254652	-0.108943	-4.363595	17974.294252
HLA B*5401	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.558945	0.195249	-4.363696	36219.745732
HLA A*3301	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.596084	0.232368	-4.363715	39453.333773
HLA A*2301	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.543305	0.179347	-4.363958	34938.549867
HLA B*5101	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.471288	0.107303	-4.363985	29599.778504
HLA B*7301	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.555388	0.191384	-4.364004	35924.296890
HLA A*0219	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.428671	0.064589	-4.364082	26833.118759
HLA A*0301	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.316685	-0.047418	-4.364104	20734.105292
HLA B*1801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.446273	0.082090	-4.364184	27943.029833
HLA B*4002	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.507774	0.143550	-4.364224	32193.901713
HLA A*0206	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.316342	-0.047884	-4.364226	20717.735053
HLA B*4402	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.335695	-0.028622	-4.364317	21661.821998
HLA A*3002	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.543946	0.179592	-4.364354	34990.188725
HLA A*3001	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.249751	-0.114630	-4.364380	17772.594061
HLA B*1501	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.374440	0.009850	-4.364591	23683.197678
HLA A*6801	1:551-559	9	IELQVSKGN	0.880588	-0.590141	-4.655178	0.290447	-4.364731	45204.113155
HLA B*5401	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.551608	0.186843	-4.364765	35612.950455
HLA B*5801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.330451	-0.034337	-4.364788	21401.831096

HLA A*2603	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.581754	0.216943	-4.364812	38172.815881
HLA B*4501	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.611224	0.246391	-4.364833	40852.984378
HLA B*1517	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.427548	0.062590	-4.364958	26763.819912
HLA B*0702	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.403229	0.038251	-4.364977	25306.295775
HLA A*0101	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.390276	0.025261	-4.365015	24562.686705
HLA B*1502	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.575474	0.210423	-4.365051	37624.784762
HLA A*1101	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.329939	-0.035208	-4.365147	21376.605599
HLA A*0101	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.317855	-0.047418	-4.365274	20790.040874
HLA B*0803	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.513424	0.148101	-4.365323	32615.506350
HLA B*4601	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.377459	0.012088	-4.365371	23848.409931
HLA A*3201	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.583892	0.218420	-4.365473	38361.203956
HLA B*1801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.502833	0.137283	-4.365550	31829.707441
HLA A*3301	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.624773	0.259153	-4.365620	42147.640588
HLA B*4001	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.416583	0.050897	-4.365686	26096.547334
HLA A*2403	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.425274	0.059501	-4.365773	26624.030214
HLA A*3201	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.587104	0.221286	-4.365818	38645.948868
HLA A*0211	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.404084	0.038251	-4.365833	25356.178022
HLA A*0101	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.375422	0.009579	-4.365843	23736.813890
HLA B*1509	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.521161	0.155271	-4.365890	33201.750324
HLA B*0802	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.473260	0.107303	-4.365957	29734.434212
HLA B*5701	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.404267	0.038251	-4.366016	25366.879861
HLA A*0250	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.595341	0.229302	-4.366039	39385.944931
HLA A*0250	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.577422	0.211378	-4.366044	37793.903273
HLA A*6801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.355182	-0.010996	-4.366177	22655.915248
HLA A*2602	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.612744	0.246391	-4.366353	40996.228469
HLA A*2403	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.300648	-0.065831	-4.366478	19982.403071
HLA A*6801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.270459	-0.096147	-4.366606	18640.569740
HLA B*4501	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.652485	0.285730	-4.366755	44924.726681
HLA A*0202	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.549169	0.182373	-4.366796	35413.527631
HLA B*0702	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.429404	0.062590	-4.366814	26878.448234
HLA A*0211	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.546199	0.179347	-4.366853	35172.192469
HLA A*6801	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.583888	0.216943	-4.366945	38360.788899
HLA B*1502	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.489485	0.122446	-4.367039	30866.346172
HLA B*1517	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.426559	0.059501	-4.367058	26702.932981
HLA A*3301	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.546735	0.179592	-4.367143	35215.602543
HLA B*1502	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.467807	0.100651	-4.367155	29363.412384
HLA A*2602	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.585582	0.218420	-4.367162	38510.708502
HLA B*4403	1:283-291	9	EAPKVLTDA	0.648269	-0.366757	-4.648717	0.281512	-4.367205	44536.580561
HLA A*3001	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-3.934316	-0.432915	-4.367231	8596.388084
HLA A*6801	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.636706	0.269282	-4.367425	43321.780971
HLA A*0250	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.588791	0.221286	-4.367505	38796.353261
HLA B*3801	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.547120	0.179592	-4.367528	35246.860458
HLA A*2402	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.584489	0.216943	-4.367546	38413.952774
HLA A*0250	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.577990	0.210423	-4.367567	37843.415196
HLA B*5701	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.425600	0.057919	-4.367681	26644.058337
HLA A*2602	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.608639	0.240938	-4.367702	40610.595180
HLA A*2301	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.538460	0.170651	-4.367809	34550.969441
HLA A*3301	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.591187	0.223276	-4.367911	39011.026660
HLA A*0216	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.320536	-0.047418	-4.367954	20918.768104
HLA B*3901	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.497006	0.128996	-4.368010	31405.515328
HLA A*0211	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.500192	0.132177	-4.368015	31636.747311
HLA A*2402	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.550405	0.182373	-4.368032	35514.443941
HLA B*1801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.441499	0.073404	-4.368095	27637.537247
HLA B*5801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.355048	-0.013165	-4.368213	22648.930064
HLA B*1503	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.507832	0.139599	-4.368234	32198.256143
HLA A*6801	1:238-246	9	ARHEGLSAD	0.908272	-0.600397	-4.676121	0.307875	-4.368246	47437.442049
HLA A*2402	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.589747	0.221286	-4.368461	38881.870149
HLA B*5101	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.504494	0.135996	-4.368498	31951.682555
HLA B*1801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.480942	0.112336	-4.368606	30265.126613
HLA A*0216	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.487895	0.119114	-4.368780	30753.505101
HLA A*6801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.539682	0.170651	-4.369031	34648.303079
HLA A*0206	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.545462	0.176401	-4.369060	35112.496001
HLA B*0803	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.509674	0.140490	-4.369184	32335.110335
HLA A*0203	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.442601	0.073404	-4.369197	27707.749292
HLA B*1502	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.598607	0.229302	-4.369305	39683.233596

HLA A*3301	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.611419	0.242067	-4.369352	40871.332337
HLA A*0101	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.381583	0.012088	-4.369495	24075.913502
HLA A*6801	1:308-316	9	RTDPLPRQD	1.117145	-0.831415	-4.655448	0.285730	-4.369718	45232.245068
HLA B*5301	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.592947	0.223225	-4.369722	39169.420301
HLA B*5401	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.546183	0.176401	-4.369782	35170.860551
HLA B*5101	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.510360	0.140490	-4.369870	32386.230074
HLA B*3901	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.509472	0.139599	-4.369874	32320.069909
HLA A*0206	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.552271	0.182373	-4.369898	35667.322636
HLA B*0802	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.455956	0.086012	-4.369944	28572.992165
HLA B*5801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.361758	-0.008210	-4.369968	23001.587986
HLA A*2402	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.557031	0.186843	-4.370188	36060.402248
HLA B*4801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.443649	0.073404	-4.370245	27774.683559
HLA A*0301	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.368985	-0.001305	-4.370290	23387.555751
HLA B*4403	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.612401	0.242067	-4.370334	40963.860636
HLA B*5301	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.518466	0.148101	-4.370365	32996.366598
HLA A*6802	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.316190	-0.054260	-4.370449	20710.451091
HLA B*1502	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.543251	0.172544	-4.370707	34934.202822
HLA B*0803	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.506775	0.135996	-4.370779	32119.966430
HLA A*2301	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.542433	0.171585	-4.370848	34868.496116
HLA A*3001	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.250482	-0.120427	-4.370908	17802.521185
HLA B*0803	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.503110	0.132177	-4.370933	31850.032960
HLA A*0202	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.327592	-0.043361	-4.370953	21261.387804
HLA B*4501	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.625823	0.254868	-4.370955	42249.686209
HLA A*2501	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.478290	0.107303	-4.370987	30080.837706
HLA B*1503	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.541733	0.170651	-4.371082	34812.328263
HLA A*6801	1:528-536	9	PRPAGEVTG	1.019782	-0.707454	-4.683475	0.312328	-4.371147	48247.537323
HLA A*0202	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.566450	0.195249	-4.371201	36851.031800
HLA A*6901	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.383401	0.012088	-4.371313	24176.936830
HLA A*3201	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.519472	0.148101	-4.371371	33072.855978
HLA A*6801	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.634780	0.263371	-4.371408	43130.026461
HLA A*0301	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.363330	-0.008210	-4.371539	23084.986525
HLA A*8001	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.444955	0.073404	-4.371551	27858.352756
HLA A*0201	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.396918	0.025261	-4.371657	24941.229751
HLA A*0203	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.317400	-0.054260	-4.371659	20768.232787
HLA A*0250	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.457739	0.086012	-4.371727	28690.557098
HLA A*2602	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.544275	0.172544	-4.371732	35016.699789
HLA A*2402	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.422706	0.050897	-4.371809	26467.066609
HLA A*3301	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.543577	0.171585	-4.371992	34960.482335
HLA A*8001	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.410566	0.038504	-4.372062	25737.479953
HLA B*3801	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.545875	0.173777	-4.372098	35145.943951
HLA A*0212	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.364121	-0.008210	-4.372331	23127.111906
HLA A*2402	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.532443	0.160089	-4.372355	34075.576050
HLA B*4403	1:303-311	9	NLSGPRTDP	0.249186	0.054135	-4.675804	0.303321	-4.372483	47402.809471
HLA A*0203	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.361502	-0.010996	-4.372497	22988.028456
HLA A*2301	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.532645	0.160089	-4.372557	34091.433417
HLA B*4801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.423472	0.050897	-4.372575	26513.785745
HLA B*4403	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.627562	0.254868	-4.372694	42419.164147
HLA A*6801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.527967	0.155271	-4.372696	33726.202044
HLA B*4501	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.653324	0.280603	-4.372721	45011.575012
HLA B*5401	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.555212	0.182373	-4.372839	35909.723862
HLA B*2705	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.501881	0.128996	-4.372885	31760.044733
HLA A*0301	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.363156	-0.009859	-4.373014	23075.746720
HLA B*0801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.351408	-0.021825	-4.373234	22459.926902
HLA B*3801	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.544966	0.171585	-4.373381	35072.438424
HLA A*0201	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.325580	-0.047884	-4.373464	21163.156808
HLA A*2402	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.568740	0.195249	-4.373491	37045.921332
HLA A*3301	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.528823	0.155271	-4.373551	33792.681103
HLA A*2603	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.642834	0.269282	-4.373552	43937.339830
HLA B*3801	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.533989	0.160089	-4.373901	34197.091270
HLA B*0803	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.493291	0.119114	-4.374177	31138.048322
HLA A*1101	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.513779	0.139599	-4.374180	32642.160623
HLA B*1502	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.597425	0.223225	-4.374200	39575.395393
HLA B*0803	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.517768	0.143550	-4.374218	32943.392681
HLA A*3002	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.591260	0.216943	-4.374318	39017.569613
HLA A*3001	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.311136	-0.063193	-4.374329	20470.847174

HLA A*0201	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.386500	0.012088	-4.374412	24350.071819
HLA B*4402	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.373118	-0.001305	-4.374422	23611.173902
HLA B*4403	1:76-84	9	DTGEAETPA	0.744072	-0.471214	-4.647368	0.272858	-4.374510	44398.496675
HLA B*0803	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.514122	0.139599	-4.374523	32667.953016
HLA A*0202	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.565935	0.191384	-4.374551	36807.397814
HLA B*4403	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.638017	0.263371	-4.374646	43452.754804
HLA A*3001	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.295430	-0.079239	-4.374668	19743.743889
HLA B*5801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.352978	-0.021825	-4.374803	22541.239555
HLA A*0202	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.460960	0.086012	-4.374948	28904.144862
HLA B*0803	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.516373	0.141319	-4.375054	32837.699852
HLA A*2501	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.504085	0.128996	-4.375089	31921.619926
HLA B*3901	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.497570	0.122446	-4.375124	31446.317896
HLA B*3801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.551582	0.176401	-4.375181	35610.831235
HLA B*5401	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.515118	0.139887	-4.375231	32742.972545
HLA A*0250	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.593659	0.218420	-4.375239	39233.679326
HLA B*4403	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.604549	0.229302	-4.375247	40229.895186
HLA B*4501	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.591772	0.216497	-4.375275	39063.612357
HLA B*1503	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.438017	0.062590	-4.375427	27416.840412
HLA B*1503	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.350436	-0.025025	-4.375460	22409.679826
HLA B*4403	1:565-573	9	DLSGMFWVD	1.250843	-0.982274	-4.644192	0.268569	-4.375623	44074.943222
HLA B*3501	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.482937	0.107303	-4.375634	30404.453935
HLA B*0801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.433647	0.057919	-4.375728	27142.344725
HLA A*0201	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.385431	0.009579	-4.375852	24290.207836
HLA A*0101	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.384985	0.008974	-4.376011	24265.253270
HLA A*3301	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.636152	0.260101	-4.376051	43266.505881
HLA B*5101	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.508197	0.132130	-4.376067	32225.266761
HLA A*3101	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.385986	0.009850	-4.376136	24321.239771
HLA A*2603	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.635435	0.259153	-4.376282	43195.174311
HLA B*5801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.328954	-0.047418	-4.376373	21328.205193
HLA B*5101	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.499012	0.122446	-4.376566	31550.945922
HLA B*0702	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.427593	0.050897	-4.376696	26766.571050
HLA A*2301	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.534022	0.157255	-4.376767	34199.681403
HLA B*0801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.402056	0.025261	-4.376795	25238.072679
HLA A*2602	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.618890	0.242067	-4.376823	41580.543100
HLA B*5401	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.548471	0.171585	-4.376886	35356.673090
HLA B*5301	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.518382	0.141319	-4.377062	32989.940983
HLA B*4001	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.389235	0.012088	-4.377147	24503.890722
HLA B*4002	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.646433	0.269282	-4.377152	44303.003521
HLA A*2602	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.546615	0.169330	-4.377285	35205.887745
HLA A*0101	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.375984	-0.001305	-4.377289	23767.524573
HLA A*0206	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.436803	0.059501	-4.377302	27340.265041
HLA B*1502	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.588777	0.211378	-4.377399	38795.093978
HLA B*4001	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.415664	0.038251	-4.377413	26041.404519
HLA B*2705	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.496543	0.119119	-4.377424	31372.062787
HLA A*0101	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.366577	-0.010996	-4.377572	23258.227468
HLA A*0212	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.435541	0.057919	-4.377622	27260.953810
HLA B*4601	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.387285	0.009579	-4.377705	24394.109810
HLA A*6802	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.360738	-0.017067	-4.377805	22947.646094
HLA A*3301	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.564685	0.186843	-4.377842	36701.616173
HLA A*6901	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.353123	-0.025025	-4.378148	22548.801451
HLA A*2603	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.535432	0.157255	-4.378177	34310.871654
HLA B*0803	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.490521	0.112336	-4.378185	30940.073814
HLA A*0101	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.370087	-0.008210	-4.378296	23446.970890
HLA B*4801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.436229	0.057919	-4.378310	27304.199346
HLA A*2603	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.638419	0.260101	-4.378318	43492.971158
HLA A*6801	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.599660	0.221286	-4.378374	39779.527729
HLA B*1801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.500864	0.122446	-4.378418	31685.734469
HLA A*3101	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.403792	0.025261	-4.378531	25339.174136
HLA B*1509	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.549197	0.170651	-4.378546	35415.826705
HLA B*3801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.569943	0.191384	-4.378559	37148.675709
HLA A*2601	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.403870	0.025261	-4.378609	25343.698250
HLA A*0203	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.390711	0.012088	-4.378623	24587.282072
HLA A*2501	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.282599	-0.096147	-4.378746	19168.978542
HLA A*2603	1:195-203	9	ARSDVYSLG	0.781389	-0.515245	-4.644948	0.266144	-4.378804	44151.787993
HLA B*5801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.361861	-0.017067	-4.378928	23007.063823

HLA A*2501	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.498089	0.119114	-4.378975	31483.937142
HLA B*5701	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.313182	-0.065831	-4.379013	20567.533696
HLA A*0216	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.498225	0.119119	-4.379106	31493.817519
HLA A*2602	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.600468	0.221286	-4.379182	39853.626432
HLA A*0212	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.391484	0.012088	-4.379396	24631.082800
HLA A*2603	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.603170	0.223276	-4.379893	40102.343566
HLA B*4403	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.487209	0.107303	-4.379906	30704.962521
HLA B*7301	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.550602	0.170651	-4.379951	35530.586461
HLA B*3801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.502255	0.122274	-4.379981	31787.375599
HLA A*0301	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.366823	-0.013165	-4.379988	23271.442787
HLA B*5801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.351829	-0.028622	-4.380451	22481.686959
HLA A*2603	1:518-526	9	TKFSQASVD	1.042939	-0.773537	-4.649873	0.269402	-4.380471	44655.279938
HLA A*3001	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.284511	-0.096147	-4.380659	19253.578146
HLA B*7301	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.522004	0.141319	-4.380685	33266.295769
HLA B*4403	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.640790	0.260101	-4.380689	43731.030080
HLA A*0101	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.345490	-0.035208	-4.380698	22155.930072
HLA A*3002	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.572128	0.191384	-4.380744	37336.048972
HLA A*6802	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.445418	0.064589	-4.380829	27888.058570
HLA B*0702	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.406527	0.025261	-4.381266	25499.241178
HLA A*3002	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.467306	0.086012	-4.381294	29329.596224
HLA A*0211	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.347041	-0.034337	-4.381378	22235.179812
HLA A*6801	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.641647	0.260101	-4.381546	43817.467101
HLA B*1502	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.564018	0.182373	-4.381645	36645.270793
HLA B*5101	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.441246	0.059501	-4.381745	27621.394234
HLA A*8001	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.439671	0.057919	-4.381752	27521.458243
HLA B*1502	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.553356	0.171585	-4.381771	35756.579925
HLA A*3201	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.598734	0.216943	-4.381791	39694.828112
HLA B*4601	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.407108	0.025261	-4.381846	25533.337126
HLA A*2603	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.614266	0.232368	-4.381898	41140.197384
HLA A*3001	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.293172	-0.088805	-4.381976	19641.364431
HLA A*0211	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.539431	0.157340	-4.382090	34628.252431
HLA B*4501	1:139-147	9	VKPANIMIS	1.254877	-0.994776	-4.642305	0.260101	-4.382204	43883.890735
HLA B*5401	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.539546	0.157255	-4.382291	34637.433063
HLA A*2603	1:125-133	9	ALNFSHQNG	0.859324	-0.595953	-4.645738	0.263371	-4.382366	44232.116688
HLA A*3201	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.392017	0.009579	-4.382437	24661.349455
HLA B*3901	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.489786	0.107303	-4.382483	30887.727463
HLA B*1509	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.554077	0.171585	-4.382492	35816.015082
HLA B*1502	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.553234	0.170651	-4.382583	35746.522505
HLA A*2301	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.530815	0.148101	-4.382714	33948.064078
HLA B*5301	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.604020	0.221286	-4.382734	40180.956140
HLA A*2501	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.456332	0.073404	-4.382927	28597.735148
HLA B*4501	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.652281	0.269282	-4.383000	44903.587368
HLA A*0203	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.447634	0.064589	-4.383045	28030.693730
HLA B*1509	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.574483	0.191384	-4.383098	37538.986361
HLA B*5101	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.495495	0.112336	-4.383159	31296.459188
HLA A*2402	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.574551	0.191384	-4.383166	37544.876194
HLA A*6901	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.334598	-0.048602	-4.383199	21607.164250
HLA A*2602	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.612793	0.229302	-4.383491	41000.886220
HLA B*0801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.393201	0.009579	-4.383621	24728.682452
HLA B*1509	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.329363	-0.054260	-4.383623	21348.291326
HLA B*3801	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.570613	0.186843	-4.383770	37205.996399
HLA B*7301	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.553112	0.169330	-4.383782	35736.467914
HLA B*3501	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.263434	-0.120427	-4.383861	18341.473474
HLA A*0201	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.393741	0.009850	-4.383892	24759.470872
HLA B*0803	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.491320	0.107303	-4.384017	30997.036190
HLA A*2602	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.639051	0.254868	-4.384183	43556.310823
HLA B*4002	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.647413	0.263202	-4.384211	44403.060538
HLA A*0301	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.367279	-0.017067	-4.384346	23295.879417
HLA B*1509	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.526278	0.141914	-4.384364	33595.271695
HLA A*6802	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.335949	-0.048602	-4.384550	21674.482006
HLA B*4002	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.643734	0.259153	-4.384580	44028.471830
HLA B*1509	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.503834	0.119119	-4.384714	31903.147184
HLA A*8001	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.449473	0.064589	-4.384885	28149.681993
HLA B*4001	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.350628	-0.034337	-4.384966	22419.623210
HLA B*1503	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.525477	0.140490	-4.384987	33533.353202

HLA A*2301	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.542389	0.157340	-4.385048	34864.912240
HLA B*4501	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.330801	-0.054260	-4.385061	21419.089499
HLA B*3501	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.267203	-0.117875	-4.385078	18501.323459
HLA A*3101	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.394684	0.009579	-4.385104	24813.241518
HLA B*5401	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.517294	0.132130	-4.385164	32907.411884
HLA B*1801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.533287	0.148101	-4.385186	34141.820245
HLA B*4402	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.443137	0.057919	-4.385218	27741.946632
HLA B*3801	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.557775	0.172544	-4.385232	36122.296546
HLA A*6802	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.321542	-0.063767	-4.385308	20967.260219
HLA A*2902	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.443290	0.057919	-4.385370	27751.703603
HLA B*5301	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.610105	0.224721	-4.385384	40747.918898
HLA A*2902	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.458789	0.073404	-4.385385	28760.021145
HLA A*1101	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.338054	-0.047418	-4.385472	21779.798914
HLA B*0702	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.443520	0.057919	-4.385601	27766.420601
HLA A*0301	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.357054	-0.028622	-4.385676	22753.811239
HLA B*0801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.424320	0.038504	-4.385816	26565.616968
HLA A*0101	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.265481	-0.120427	-4.385907	18428.102682
HLA B*4001	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.395851	0.009850	-4.386001	24880.047020
HLA B*4801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.398100	0.012088	-4.386012	25009.191609
HLA B*4002	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.627142	0.240938	-4.386204	42378.106577
HLA B*4501	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.651226	0.264968	-4.386259	44794.647112
HLA A*0219	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.459736	0.073404	-4.386332	28822.791722
HLA B*1501	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.364509	-0.021825	-4.386334	23147.765116
HLA B*1502	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.609795	0.223276	-4.386519	40718.830978
HLA B*5101	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.487244	0.100651	-4.386592	30707.454278
HLA A*0216	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.460093	0.073404	-4.386689	28846.502542
HLA A*3201	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.528722	0.141914	-4.386808	33784.820987
HLA B*5401	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.557463	0.170651	-4.386812	36096.315351
HLA B*4403	1:364-372	9	DVRGQSSAD	1.188572	-0.907969	-4.667532	0.280603	-4.386928	46508.415691
HLA B*4002	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.651905	0.264968	-4.386938	44864.736436
HLA B*1502	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.509341	0.122274	-4.387067	32310.279904
HLA B*3801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.529048	0.141914	-4.387134	33810.235869
HLA B*4402	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.412417	0.025261	-4.387156	25847.432838
HLA A*0206	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.557942	0.170651	-4.387291	36136.173862
HLA A*0203	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.379088	-0.008210	-4.387297	23937.986697
HLA A*2301	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.529260	0.141914	-4.387346	33826.701743
HLA B*3501	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.445334	0.057919	-4.387415	27882.627732
HLA B*5401	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.542699	0.155271	-4.387428	34889.818353
HLA A*3301	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.642300	0.254868	-4.387432	43883.415924
HLA A*0201	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.396408	0.008974	-4.387434	24911.967275
HLA B*1801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.506601	0.119114	-4.387487	32107.110359
HLA A*0301	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.362580	-0.025025	-4.387605	23045.181859
HLA B*1509	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.536146	0.148535	-4.387611	34367.345956
HLA B*3801	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.557005	0.169330	-4.387675	36058.256401
HLA A*3201	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.579163	0.191384	-4.387778	37945.712824
HLA B*3501	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.397501	0.009579	-4.387921	24974.714672
HLA B*5701	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.413298	0.025261	-4.388037	25899.922969
HLA A*0211	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.527850	0.139599	-4.388251	33717.080527
HLA B*1517	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.380077	-0.008210	-4.388286	23992.569111
HLA A*2501	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.377300	-0.010996	-4.388295	23839.638371
HLA A*0301	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.366511	-0.021825	-4.388336	23254.704651
HLA B*4402	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.426968	0.038504	-4.388464	26728.080839
HLA A*2902	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.427017	0.038504	-4.388514	26731.117526
HLA B*3801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.536719	0.148101	-4.388618	34412.741252
HLA A*0203	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.446654	0.057919	-4.388735	27967.529895
HLA A*0206	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.353563	-0.035208	-4.388771	22571.624472
HLA A*0250	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.584031	0.195249	-4.388782	38373.450172
HLA B*4403	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.599293	0.210423	-4.388870	39745.970249
HLA A*2603	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.618197	0.229302	-4.388895	41514.236915
HLA A*2402	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.546239	0.157255	-4.388985	35175.427338
HLA B*4601	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.398837	0.009850	-4.388988	25051.710956
HLA A*6901	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.345652	-0.043361	-4.389013	22164.202033
HLA B*4601	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.398093	0.008974	-4.389119	25008.785721
HLA B*0702	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.448628	0.059501	-4.389127	28094.912147
HLA B*5701	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.354824	-0.034337	-4.389162	22637.292875

HLA B*0702	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.367444	-0.021825	-4.389269	23304.703057
HLA B*5401	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.563160	0.173777	-4.389384	36572.982087
HLA A*6802	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.427924	0.038504	-4.389420	26786.996229
HLA A*0219	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.427950	0.038504	-4.389446	26788.590338
HLA A*0211	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.526757	0.137283	-4.389475	33632.368487
HLA B*1509	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.454071	0.064589	-4.389483	28449.290185
HLA A*3301	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.614273	0.224721	-4.389552	41140.865081
HLA A*2301	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.538103	0.148535	-4.389568	34522.569748
HLA B*3901	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.486553	0.096922	-4.389631	30658.652665
HLA A*0206	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.529278	0.139599	-4.389680	33828.165765
HLA B*5301	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.608214	0.218420	-4.389794	40570.849156
HLA A*1101	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.447730	0.057919	-4.389811	28036.911781
HLA A*3201	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.561431	0.171585	-4.389846	36427.649759
HLA A*0101	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.346503	-0.043361	-4.389864	22207.650491
HLA B*1509	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.547360	0.157340	-4.390020	35266.315349
HLA A*3101	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.324190	-0.065831	-4.390020	21095.486951
HLA A*0101	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.342189	-0.047884	-4.390073	21988.163586
HLA A*6901	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.361499	-0.028622	-4.390122	22987.904093
HLA A*2403	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.355839	-0.034337	-4.390177	22690.259731
HLA A*1101	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.452941	0.062590	-4.390351	28375.356909
HLA B*7301	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.379355	-0.010996	-4.390351	23952.754462
HLA A*6901	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.389134	-0.001305	-4.390439	24498.191162
HLA B*3501	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.356413	-0.034337	-4.390750	22720.230944
HLA A*3301	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.633441	0.242669	-4.390771	42997.233971
HLA A*3101	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.382649	-0.008210	-4.390859	24135.118782
HLA A*6801	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.633036	0.242067	-4.390969	42957.243613
HLA A*3002	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.327274	-0.063767	-4.391041	21245.865537
HLA B*4403	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.609480	0.218420	-4.391061	40689.323570
HLA B*1502	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.570444	0.179347	-4.391097	37191.507038
HLA A*3201	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.601631	0.210423	-4.391208	39960.493289
HLA A*0250	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.523341	0.132130	-4.391211	33368.854745
HLA B*0802	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.453862	0.062590	-4.391272	28435.595714
HLA A*2301	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.534826	0.143550	-4.391276	34263.015612
HLA B*4403	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.527314	0.135996	-4.391318	33675.517673
HLA A*0211	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.534870	0.143550	-4.391320	34266.537617
HLA A*0219	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.429606	0.038251	-4.391355	26890.956354
HLA B*5401	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.539898	0.148535	-4.391363	34665.552171
HLA A*0250	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.551460	0.160089	-4.391371	35600.814810
HLA B*3801	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.546667	0.155271	-4.391396	35210.078114
HLA B*1502	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.560750	0.169330	-4.391420	36370.544397
HLA A*0203	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.357252	-0.034337	-4.391589	22764.153619
HLA B*4501	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.633798	0.242192	-4.391606	43032.605273
HLA B*4001	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.374901	-0.017067	-4.391967	23708.323198
HLA B*1509	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.478024	0.086012	-4.392013	30062.454384
HLA A*0202	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.404244	0.012088	-4.392156	25365.507578
HLA B*4801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.430703	0.038504	-4.392200	26958.980048
HLA B*3501	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.456809	0.064589	-4.392220	28629.158646
HLA A*6901	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.328456	-0.063767	-4.392223	21303.757971
HLA A*0203	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.430851	0.038504	-4.392348	26968.169855
HLA B*1502	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.363727	-0.028622	-4.392349	23106.102116
HLA A*0301	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.357165	-0.035208	-4.392373	22759.597467
HLA A*2601	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.401462	0.008974	-4.392488	25203.552909
HLA B*1517	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.478562	0.086012	-4.392551	30099.720774
HLA B*7301	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.579419	0.186843	-4.392576	37968.095172
HLA B*4501	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.640895	0.248296	-4.392600	43741.677477
HLA A*3301	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.609720	0.216943	-4.392778	40711.782488
HLA B*0801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.344943	-0.047884	-4.392826	22128.020023
HLA A*0203	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.357665	-0.035208	-4.392873	22785.838613
HLA A*3002	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.550269	0.157340	-4.392929	35503.302195
HLA A*2601	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.391629	-0.001305	-4.392934	24639.345775
HLA A*3201	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.622290	0.229302	-4.392988	41907.317492
HLA B*4801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.357893	-0.035208	-4.393101	22797.798830
HLA B*7301	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.565648	0.172544	-4.393105	36783.112708
HLA A*6801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.327274	-0.065831	-4.393105	21245.865537
HLA A*3301	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.616402	0.223225	-4.393177	41343.006232

HLA A*2601	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.383458	-0.009859	-4.393316	24180.076103
HLA A*0301	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.359002	-0.034337	-4.393339	22856.086659
HLA B*4501	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.656766	0.263202	-4.393564	45369.731097
HLA B*5301	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.562914	0.169330	-4.393584	36552.213129
HLA A*0202	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.550952	0.157255	-4.393698	35559.238271
HLA B*5401	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.551108	0.157340	-4.393767	35571.937060
HLA A*0216	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.458425	0.064589	-4.393836	28735.915032
HLA B*1801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.526048	0.132177	-4.393871	33577.465239
HLA B*7301	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.549153	0.155271	-4.393882	35412.186573
HLA B*4002	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.636340	0.242192	-4.394148	43285.235293
HLA A*3301	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.640668	0.246391	-4.394277	43718.729649
HLA B*7301	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.565942	0.171585	-4.394357	36807.995191
HLA A*0201	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.393135	-0.001305	-4.394440	24724.936912
HLA A*2501	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.346613	-0.047884	-4.394497	22213.297832
HLA A*3001	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.265333	-0.129168	-4.394501	18421.823031
HLA A*0206	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.432804	0.038251	-4.394553	27089.681371
HLA B*5701	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.403541	0.008974	-4.394567	25324.510593
HLA A*6801	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.542739	0.148101	-4.394638	34893.027252
HLA A*0206	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.502055	0.107303	-4.394752	31772.761834
HLA B*5801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.369753	-0.025025	-4.394778	23428.965744
HLA B*5801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.359864	-0.035208	-4.395072	22901.510882
HLA A*0212	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.433711	0.038504	-4.395207	27146.309616
HLA A*6801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.477357	0.082090	-4.395268	30016.301637
HLA A*8001	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.347889	-0.047418	-4.395307	22278.646882
HLA A*2301	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.536630	0.141319	-4.395311	34405.667553
HLA B*7301	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.569159	0.173777	-4.395382	37081.612264
HLA B*5801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.352078	-0.043361	-4.395439	22494.582741
HLA A*6901	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.382323	-0.013165	-4.395488	24116.976608
HLA A*0211	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.517834	0.122274	-4.395560	32948.383222
HLA B*7301	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.539149	0.143550	-4.395599	34605.779525
HLA B*5401	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.434312	0.038504	-4.395809	27183.931444
HLA B*0702	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.370942	-0.025025	-4.395967	23493.188147
HLA A*3101	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.360778	-0.035208	-4.395986	22949.756642
HLA A*2602	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.612937	0.216943	-4.395994	41014.418878
HLA A*2603	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.642397	0.246391	-4.396006	43893.150584
HLA B*5701	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.405952	0.009579	-4.396372	25465.466290
HLA A*2603	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.651259	0.254868	-4.396391	44798.039917
HLA B*4501	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.637352	0.240938	-4.396415	43386.279596
HLA A*0211	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.503779	0.107303	-4.396476	31899.177803
HLA A*2403	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.244025	-0.152648	-4.396673	17539.819769
HLA A*0212	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.349364	-0.047418	-4.396782	22354.465308
HLA B*4002	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.620079	0.223276	-4.396803	41694.521772
HLA B*5801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.348298	-0.048602	-4.396899	22299.628107
HLA B*7301	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.579297	0.182373	-4.396924	37957.415708
HLA A*0211	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.532991	0.135996	-4.396994	34118.555538
HLA B*1502	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.545119	0.148101	-4.397018	35084.773563
HLA B*4501	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.620300	0.223276	-4.397023	41715.730062
HLA A*2402	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.576651	0.179592	-4.397059	37726.899587
HLA B*4002	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.639169	0.242067	-4.397101	43568.094158
HLA B*1503	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.456649	0.059501	-4.397148	28618.628704
HLA A*2501	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.456703	0.059501	-4.397202	28622.189869
HLA A*3101	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.435762	0.038504	-4.397258	27274.820337
HLA A*6801	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.627088	0.229302	-4.397786	42372.833906
HLA A*2603	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.494800	0.096922	-4.397878	31246.383421
HLA A*3101	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.372908	-0.025025	-4.397933	23599.808327
HLA B*4402	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.407568	0.009579	-4.397989	25560.425460
HLA A*0202	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.505314	0.107303	-4.398011	32012.065957
HLA A*2402	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.569612	0.171585	-4.398027	37120.349714
HLA A*3201	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.555381	0.157340	-4.398041	35923.713855
HLA A*2402	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.571828	0.173777	-4.398051	37310.203984
HLA A*2603	1:580-588	9	ALGWTGMLD	0.972669	-0.730602	-4.640125	0.242067	-4.398058	43664.129159
HLA A*2501	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.407956	0.009850	-4.398106	25583.251692
HLA A*2402	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.574605	0.176401	-4.398203	37549.548098
HLA A*2902	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.462795	0.064589	-4.398206	29026.526798
HLA A*6901	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.332521	-0.065831	-4.398352	21504.078094

HLA B*0702	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.471885	0.073404	-4.398481	29640.479868
HLA A*2301	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.538371	0.139887	-4.398484	34543.867329
HLA B*5801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.350661	-0.047884	-4.398545	22421.321302
HLA A*2902	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.369972	-0.028622	-4.398594	23440.756284
HLA B*5701	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.408466	0.009850	-4.398616	25613.302682
HLA B*4002	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.647025	0.248296	-4.398729	44363.442643
HLA A*3002	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.575230	0.176401	-4.398828	37603.621941
HLA B*1503	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.449899	0.050897	-4.399002	28177.259378
HLA A*2501	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.449932	0.050897	-4.399035	28179.393560
HLA A*0201	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.388154	-0.010996	-4.399150	24442.987401
HLA B*1801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.528588	0.128996	-4.399592	33774.404582
HLA A*0301	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.333794	-0.065831	-4.399625	21567.224021
HLA B*1502	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.579278	0.179592	-4.399686	37955.772980
HLA B*4601	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.391507	-0.008210	-4.399717	24632.415351
HLA A*2603	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.640867	0.240938	-4.399930	43738.837918
HLA B*3901	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.345767	-0.054260	-4.400027	22170.078200
HLA B*3801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.539926	0.139887	-4.400039	34667.802686
HLA A*2301	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.539656	0.139599	-4.400058	34646.241262
HLA B*4001	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.409119	0.008974	-4.400145	25651.852769
HLA A*0250	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.591685	0.191384	-4.400301	39055.793936
HLA B*1801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.507774	0.107303	-4.400471	32193.901713
HLA A*0219	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.460131	0.059501	-4.400630	28848.999552
HLA A*2402	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.544221	0.143550	-4.400671	35012.343021
HLA B*1501	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.409694	0.008974	-4.400721	25685.874863
HLA B*5401	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.544296	0.143550	-4.400746	35018.404759
HLA B*4501	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.630264	0.229302	-4.400962	42683.892201
HLA A*0202	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.580335	0.179347	-4.400988	38048.286981
HLA B*4403	1:373-381	9	AIATLQNRG	0.799075	-0.539922	-4.660142	0.259153	-4.400989	45723.810397
HLA A*6801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.513405	0.112336	-4.401069	32614.094811
HLA B*1509	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.520214	0.119114	-4.401100	33129.443206
HLA B*1502	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.596608	0.195249	-4.401359	39500.959205
HLA B*2705	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.487385	0.086012	-4.401373	30717.423332
HLA A*0301	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.352799	-0.048602	-4.401401	22531.973594
HLA A*2902	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.460967	0.059501	-4.401466	28904.613970
HLA A*0301	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.353788	-0.047884	-4.401672	22583.350075
HLA B*0803	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.483767	0.082090	-4.401677	30462.572519
HLA A*3002	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.248346	-0.153340	-4.401686	17715.190602
HLA A*2301	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.524307	0.122446	-4.401861	33443.131752
HLA B*1501	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.427240	0.025261	-4.401979	26744.859233
HLA B*4002	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.626740	0.224721	-4.402018	42338.921098
HLA B*1503	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.488099	0.086012	-4.402087	30767.982963
HLA B*0803	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.539480	0.137283	-4.402197	34632.186689
HLA A*2601	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.385142	-0.017067	-4.402209	24274.050110
HLA B*5701	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.414398	0.012088	-4.402310	25965.580203
HLA B*7301	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.597613	0.195249	-4.402364	39592.526980
HLA A*2402	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.559754	0.157340	-4.402413	36287.213506
HLA A*0101	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.373820	-0.028622	-4.402442	23649.397224
HLA A*2603	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.594061	0.191384	-4.402676	39269.990845
HLA A*0203	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.412582	0.009850	-4.402732	25857.222914
HLA B*1509	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.550840	0.148101	-4.402739	35550.005636
HLA B*3801	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.573406	0.170651	-4.402756	37446.090051
HLA B*4501	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.441126	0.038251	-4.402875	27613.774423
HLA A*2603	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.613312	0.210423	-4.402889	41049.935600
HLA A*8001	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.428199	0.025261	-4.402938	26803.956614
HLA A*2601	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.381155	-0.021825	-4.402981	24052.220028
HLA A*3301	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.575535	0.172544	-4.402991	37630.077328
HLA A*0201	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.368891	-0.034337	-4.403228	23382.495335
HLA B*1501	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.393370	-0.009859	-4.403229	24738.316447
HLA A*3001	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.157888	-0.245356	-4.403244	14384.285928
HLA B*5401	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.465941	0.062590	-4.403351	29237.553760
HLA B*2705	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.415498	0.012088	-4.403410	26031.403881
HLA A*0206	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.543963	0.140490	-4.403472	34991.513801
HLA A*2301	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.539473	0.135996	-4.403477	34631.624625
HLA B*3501	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.381759	-0.021825	-4.403584	24085.684086
HLA A*3002	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.545025	0.141319	-4.403706	35077.182195

HLA B*5401	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.539715	0.135996	-4.403719	34650.927387
HLA B*3801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.543364	0.139599	-4.403765	34943.275528
HLA A*0250	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.590764	0.186843	-4.403921	38973.056990
HLA B*5401	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.545866	0.141914	-4.403952	35145.183417
HLA A*0301	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.356598	-0.047362	-4.403961	22729.943220
HLA A*3301	1:505-513	9	VDVAQKNLN	0.867398	-0.638096	-4.633361	0.229302	-4.404059	42989.325949
HLA A*2501	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.462086	0.057919	-4.404166	28979.142369
HLA A*2301	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.541641	0.137283	-4.404359	34804.984135
HLA A*2601	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.391206	-0.013165	-4.404371	24615.364150
HLA A*3002	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.575037	0.170651	-4.404386	37586.944264
HLA B*1801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.544085	0.139599	-4.404486	35001.358797
HLA B*1509	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.536623	0.132130	-4.404493	34405.109165
HLA A*2902	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.414079	0.009579	-4.404499	25946.483186
HLA A*6901	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.350299	-0.054260	-4.404559	22402.649364
HLA A*8001	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.414163	0.009579	-4.404584	25951.536911
HLA A*6802	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.416696	0.012088	-4.404608	26103.324827
HLA A*6802	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.370366	-0.034337	-4.404704	23462.070366
HLA B*1502	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.596138	0.191384	-4.404753	39458.243156
HLA A*0250	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.455669	0.050897	-4.404772	28554.140027
HLA A*0203	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.430034	0.025261	-4.404773	26917.446223
HLA A*0201	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.395212	-0.009859	-4.405071	24843.463207
HLA A*0206	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.548765	0.143550	-4.405215	35380.590637
HLA B*5301	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.600658	0.195249	-4.405409	39871.094158
HLA A*2603	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.634427	0.228841	-4.405587	43095.041358
HLA B*2705	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.479004	0.073404	-4.405600	30130.349544
HLA A*2403	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.377034	-0.028622	-4.405656	23825.069237
HLA A*6901	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.383876	-0.021825	-4.405701	24203.371770
HLA B*1509	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.502647	0.096922	-4.405725	31816.106927
HLA B*5801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.358363	-0.047362	-4.405725	22822.478892
HLA A*0212	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.394738	-0.010996	-4.405733	24816.329158
HLA B*4403	1:550-558	9	VIELQVSKG	0.831304	-0.562022	-4.675038	0.269282	-4.405757	47319.282422
HLA B*2705	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.465325	0.059501	-4.405825	29196.142071
HLA A*6802	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.414809	0.008974	-4.405836	25990.174253
HLA A*2301	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.546378	0.140490	-4.405888	35186.656545
HLA A*0216	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.444281	0.038251	-4.406030	27815.132375
HLA A*0101	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.396197	-0.009859	-4.406055	24899.840839
HLA B*0802	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.457281	0.050897	-4.406384	28660.306574
HLA B*2705	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.444925	0.038251	-4.406674	27856.393587
HLA B*1501	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.372561	-0.034337	-4.406898	23580.920382
HLA A*6801	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.589284	0.182373	-4.406912	38840.453941
HLA B*4801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.432240	0.025261	-4.406979	27054.531674
HLA B*4001	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.432282	0.025261	-4.407021	27057.166318
HLA B*0802	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.471634	0.064589	-4.407045	29623.327200
HLA A*2501	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.352839	-0.054260	-4.407099	22534.045913
HLA B*1509	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.548563	0.141319	-4.407244	35364.133629
HLA B*0702	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.445782	0.038504	-4.407279	27911.453430
HLA A*6802	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.363978	-0.043361	-4.407339	23119.481143
HLA A*0201	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.394357	-0.013165	-4.407522	24794.589604
HLA B*5401	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.548157	0.140490	-4.407666	35331.051437
HLA B*5801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.353408	-0.054260	-4.407667	22563.566652
HLA B*5101	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.489882	0.082090	-4.407793	30894.579290
HLA B*1503	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.536825	0.128996	-4.407829	34421.119882
HLA B*1501	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.360489	-0.047418	-4.407907	22934.490578
HLA B*4001	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.364638	-0.043361	-4.407999	23154.653617
HLA A*6801	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.631389	0.223225	-4.408164	42794.643982
HLA A*0250	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.579055	0.170651	-4.408404	37936.271022
HLA B*4001	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.400195	-0.008210	-4.408405	25130.168151
HLA B*5301	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.599864	0.191384	-4.408480	39798.254782
HLA B*1501	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.365174	-0.043361	-4.408535	23183.231455
HLA B*2705	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.459449	0.050897	-4.408553	28803.774769
HLA A*2403	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.418155	0.009579	-4.408575	26191.167494
HLA A*2403	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.417565	0.008974	-4.408592	26155.627110
HLA B*5301	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.595520	0.186843	-4.408677	39402.141854
HLA A*2301	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.541042	0.132177	-4.408866	34757.003006
HLA B*4403	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.380394	-0.028622	-4.409016	24010.098125

HLA B*5401	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.541195	0.132177	-4.409018	34769.227205
HLA A*3301	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.582821	0.173777	-4.409044	38266.686970
HLA A*2603	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.633828	0.224721	-4.409107	43035.631800
HLA B*4403	1:399-407	9	VIGTDPAAN	0.832294	-0.567326	-4.674178	0.264968	-4.409211	47225.682019
HLA B*0801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.361810	-0.047418	-4.409228	23004.325742
HLA A*3101	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.361389	-0.047884	-4.409273	22982.059822
HLA A*2301	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.506230	0.096922	-4.409308	32079.678132
HLA A*6901	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.399636	-0.009859	-4.409495	25097.832533
HLA A*0101	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.384477	-0.025025	-4.409502	24236.915007
HLA A*0250	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.549115	0.139599	-4.409517	35409.121490
HLA B*4801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.418554	0.008974	-4.409581	26215.266097
HLA B*4501	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.642044	0.232368	-4.409676	43857.546471
HLA B*0803	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.538707	0.128996	-4.409711	34570.601293
HLA B*3801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.567166	0.157340	-4.409826	36911.886791
HLA B*3801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.542001	0.132130	-4.409871	34833.804600
HLA A*0206	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.528989	0.119114	-4.409875	33805.663437
HLA A*3301	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.631239	0.221286	-4.409953	42779.829633
HLA B*1509	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.542149	0.132177	-4.409972	34845.678786
HLA A*6801	1:315-323	9	QDLDDTDRD	1.097844	-0.851453	-4.656473	0.246391	-4.410081	45339.060816
HLA B*4403	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.626728	0.216497	-4.410231	42337.775869
HLA A*0301	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.366910	-0.043361	-4.410271	23276.101402
HLA A*8001	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.422466	0.012088	-4.410378	26452.465880
HLA A*2402	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.558546	0.148101	-4.410445	36186.450427
HLA B*4403	1:420-428	9	VSTGPEQRE	0.836407	-0.588111	-4.658749	0.248296	-4.410453	45577.360511
HLA B*3901	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.496484	0.086012	-4.410473	31367.820089
HLA A*3201	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.581134	0.170651	-4.410483	38118.335969
HLA B*0803	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.473083	0.062590	-4.410493	29722.372160
HLA B*1801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.511187	0.100651	-4.410536	32447.961315
HLA A*2603	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.582212	0.171585	-4.410627	38213.106716
HLA A*0203	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.363280	-0.047362	-4.410643	23082.364042
HLA B*1501	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.409591	-0.001305	-4.410896	25679.761450
HLA A*2301	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.543053	0.132130	-4.410923	34918.331255
HLA A*2403	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.400090	-0.010996	-4.411085	25124.051081
HLA B*4403	1:544-552	9	TVPVDSVIE	0.892823	-0.629621	-4.674317	0.263202	-4.411115	47240.758082
HLA A*0211	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.540124	0.128996	-4.411128	34683.560380
HLA A*2603	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.598038	0.186843	-4.411195	39631.314571
HLA B*3801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.559810	0.148535	-4.411275	36291.925247
HLA A*6802	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.436582	0.025261	-4.411321	27326.365242
HLA B*5401	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.523708	0.112336	-4.411372	33397.028033
HLA B*4403	1:69-77	9	PAIVAVYDT	0.695921	-0.472645	-4.634716	0.223276	-4.411440	43123.727047
HLA A*0202	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.587856	0.176401	-4.411455	38712.909307
HLA A*0211	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.551984	0.140490	-4.411494	35643.789739
HLA A*2602	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.594129	0.182373	-4.411756	39276.152271
HLA A*0201	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.376560	-0.035208	-4.411768	23799.047479
HLA A*2402	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.551380	0.139599	-4.411782	35594.267133
HLA A*0216	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.469759	0.057919	-4.411840	29495.716237
HLA A*2301	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.512545	0.100651	-4.411894	32549.582159
HLA B*1509	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.549242	0.137283	-4.411959	35419.467210
HLA B*3801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.591427	0.179347	-4.412080	39032.559224
HLA A*2602	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.603560	0.191384	-4.412175	40138.373315
HLA B*4002	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.644582	0.232368	-4.412214	44114.542133
HLA B*4403	1:483-491	9	VVIIIVGSG	0.669002	-0.426810	-4.654757	0.242192	-4.412565	45160.360029
HLA B*3801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.548657	0.135996	-4.412661	35371.787099
HLA B*4002	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.641527	0.228841	-4.412687	43805.379339
HLA A*2602	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.535166	0.122446	-4.412720	34289.903229
HLA B*4801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.401760	-0.010996	-4.412756	25220.875109
HLA B*3801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.544954	0.132177	-4.412778	35071.489747
HLA A*3001	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.303679	-0.109105	-4.412784	20122.343142
HLA A*0202	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.553431	0.140490	-4.412941	35762.770514
HLA A*2403	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.438217	0.025261	-4.412956	27429.450687
HLA A*2403	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.377833	-0.035208	-4.413041	23868.932499
HLA A*0101	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.391223	-0.021825	-4.413048	24616.296332
HLA A*0212	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.438417	0.025261	-4.413156	27442.066762
HLA B*0702	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.378829	-0.034337	-4.413166	23923.745731
HLA A*0301	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.349451	-0.063767	-4.413218	22358.940358

HLA B*1502	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.499233	0.086012	-4.413222	31566.994591
HLA A*3201	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.600087	0.186843	-4.413244	39818.713933
HLA B*4002	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.634531	0.221286	-4.413245	43105.300713
HLA B*1517	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.471382	0.057919	-4.413463	29606.184458
HLA A*0101	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.400421	-0.013165	-4.413586	25143.222877
HLA A*2603	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.632017	0.218420	-4.413597	42856.502959
HLA B*4501	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.636932	0.223225	-4.413707	43344.285954
HLA B*7301	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.562317	0.148535	-4.413782	36502.020793
HLA B*1509	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.553478	0.139599	-4.413880	35766.640175
HLA A*0202	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.571348	0.157340	-4.414008	37269.050507
HLA B*0803	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.500049	0.086012	-4.414037	31626.308805
HLA A*2902	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.348225	-0.065831	-4.414055	22295.888627
HLA B*7301	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.526741	0.112336	-4.414405	33631.094880
HLA A*0206	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.533550	0.119119	-4.414431	34162.513301
HLA A*0201	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.392698	-0.021825	-4.414524	24700.070219
HLA A*2301	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.543533	0.128996	-4.414537	34956.889005
HLA B*4801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.413378	-0.001305	-4.414683	25904.687341
HLA B*0801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.335531	-0.079239	-4.414769	21653.620388
HLA B*5801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.351004	-0.063767	-4.414771	22439.037640
HLA B*1517	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.488318	0.073404	-4.414913	30783.466836
HLA B*1501	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.401755	-0.013165	-4.414920	25220.602226
HLA B*3501	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.403980	-0.010996	-4.414976	25350.143079
HLA B*4001	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.424578	0.009579	-4.414999	26581.430548
HLA B*5301	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.587611	0.172544	-4.415068	38691.134448
HLA B*4002	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.551086	0.135996	-4.415090	35570.205140
HLA A*0219	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.473055	0.057919	-4.415136	29720.442686
HLA B*4501	1:200-208	9	YSLGCVLYE	0.855944	-0.641207	-4.629989	0.214737	-4.415252	42656.883680
HLA A*3201	1:68-76 9		HPAIVAVYD	1.071473	-0.891881	-4.595031	0.179592	-4.415439	39357.829257
HLA A*0216	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.454013	0.038504	-4.415509	28445.442757
HLA A*2402	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.586350	0.170651	-4.415699	38578.895540
HLA B*4601	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.414429	-0.001305	-4.415733	25967.406389
HLA A*2402	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.553194	0.137283	-4.415911	35743.235116
HLA A*2403	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.425831	0.009850	-4.415981	26658.187940
HLA A*0250	1:68-76 9		HPAIVAVYD	1.071473	-0.891881	-4.595574	0.179592	-4.415982	39407.044867
HLA B*1501	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.399068	-0.017067	-4.416134	25064.996122
HLA A*0203	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.425121	0.008974	-4.416148	26614.669711
HLA A*2902	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.454414	0.038251	-4.416163	28471.769557
HLA A*0201	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.399169	-0.017067	-4.416235	25070.827550
HLA A*0212	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.425824	0.009579	-4.416244	26657.755290
HLA B*4002	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.633215	0.216943	-4.416272	42974.909183
HLA B*3901	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.480888	0.064589	-4.416300	30261.361035
HLA A*2603	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.588899	0.172544	-4.416355	38806.009125
HLA A*3101	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.399317	-0.017067	-4.416383	25079.373722
HLA B*1502	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.548751	0.132130	-4.416621	35379.442225
HLA A*3101	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.425596	0.008974	-4.416622	26643.770056
HLA B*5401	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.405721	-0.010996	-4.416717	25451.968864
HLA B*0802	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.474721	0.057919	-4.416802	29834.657657
HLA B*2705	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.481485	0.064589	-4.416896	30302.972112
HLA A*2402	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.596267	0.179347	-4.416920	39469.985462
HLA A*3002	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.536339	0.119119	-4.417220	34382.595068
HLA A*2601	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.353521	-0.063767	-4.417287	22569.426599
HLA A*3301	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.635759	0.218420	-4.417340	43227.434344
HLA A*0211	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.536477	0.119114	-4.417363	34393.571175
HLA A*3101	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.416064	-0.001305	-4.417369	26065.365325
HLA B*0702	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.409283	-0.008210	-4.417493	25661.568767
HLA A*2902	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.442780	0.025261	-4.417519	27719.143719
HLA B*4801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.395908	-0.021825	-4.417733	24883.277589
HLA A*3001	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.264428	-0.153340	-4.417768	18383.493853
HLA B*4403	1:159-167	9	IARAIADSG	0.805700	-0.564762	-4.658803	0.240938	-4.417866	45583.031938
HLA B*4601	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.382765	-0.035208	-4.417973	24141.517477
HLA A*0250	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.566121	0.148101	-4.418020	36823.131968
HLA A*3002	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.555346	0.137283	-4.418063	35920.798824
HLA A*2601	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.383876	-0.034337	-4.418213	24203.371770
HLA A*2902	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.407314	-0.010996	-4.418310	25545.495682
HLA B*5301	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.555658	0.137283	-4.418376	35946.653687

HLA A*2603	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.592172	0.173777	-4.418395	39099.554950
HLA B*1503	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.483005	0.064589	-4.418416	30409.224366
HLA B*3501	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.408600	-0.009859	-4.418458	25621.202113
HLA B*4601	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.396765	-0.021825	-4.418590	24932.460889
HLA A*2301	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.537718	0.119114	-4.418603	34491.954155
HLA A*1101	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.483212	0.064589	-4.418623	30423.704739
HLA A*6801	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.554829	0.135996	-4.418833	35878.072197
HLA A*3201	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.384524	-0.034337	-4.418862	24239.537529
HLA B*4801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.428453	0.009579	-4.418873	26819.621884
HLA A*0250	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.567467	0.148535	-4.418932	36937.455863
HLA B*5101	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.504945	0.086012	-4.418933	31984.887969
HLA B*0802	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.492389	0.073404	-4.418985	31073.429364
HLA A*2403	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.410777	-0.008210	-4.418987	25750.014326
HLA A*2601	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.390370	-0.028622	-4.418992	24568.002536
HLA B*1503	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.538136	0.119114	-4.419022	34525.184533
HLA A*1101	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.478891	0.059501	-4.419391	30122.526471
HLA B*4601	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.409570	-0.009859	-4.419428	25678.511159
HLA A*3101	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.376137	-0.043361	-4.419498	23775.883722
HLA A*3201	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.614764	0.195249	-4.419516	41187.408000
HLA A*0201	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.394566	-0.025025	-4.419591	24806.530581
HLA B*5301	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.590273	0.170651	-4.419623	38929.016350
HLA A*0202	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.551909	0.132177	-4.419732	35637.619746
HLA B*5301	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.602117	0.182373	-4.419744	40005.267995
HLA A*0202	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.429385	0.009579	-4.419806	26877.284983
HLA B*5701	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.398074	-0.021825	-4.419899	25007.703387
HLA B*1501	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.371393	-0.048602	-4.419995	23517.603169
HLA A*0216	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.432118	0.012088	-4.420030	27046.921919
HLA A*1101	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.493458	0.073404	-4.420054	31150.010810
HLA A*0301	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.365923	-0.054260	-4.420183	23223.274566
HLA B*4501	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.644979	0.224721	-4.420257	44154.893234
HLA A*0250	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.596723	0.176401	-4.420321	39511.431688
HLA A*3301	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.577589	0.157255	-4.420334	37808.422780
HLA B*4002	1:482-490	9	NVVIIIVGS	1.078675	-0.862178	-4.636899	0.216497	-4.420402	43341.003249
HLA A*2601	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.373310	-0.047362	-4.420673	23621.650400
HLA A*0250	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.600033	0.179347	-4.420687	39813.759700
HLA B*4001	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.409727	-0.010996	-4.420723	25687.820345
HLA B*4002	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.644055	0.223225	-4.420830	44061.115839
HLA A*2902	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.430734	0.009850	-4.420884	26960.876101
HLA A*0212	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.399180	-0.021825	-4.421006	25071.505712
HLA B*3801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.540185	0.119119	-4.421066	34688.439212
HLA B*5401	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.518017	0.096922	-4.421095	32962.289429
HLA B*4601	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.366859	-0.054260	-4.421118	23273.331302
HLA A*3201	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.603562	0.182373	-4.421189	40138.590459
HLA A*2301	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.543634	0.122274	-4.421360	34965.021805
HLA B*5301	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.600710	0.179347	-4.421363	39875.839801
HLA A*2501	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.486285	0.064589	-4.421696	30639.750464
HLA B*5101	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.486337	0.064589	-4.421748	30643.397350
HLA A*6802	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.396744	-0.025025	-4.421769	24931.246982
HLA A*0202	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.413599	-0.008210	-4.421809	25917.863991
HLA B*4001	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.408656	-0.013165	-4.421821	25624.528917
HLA B*4001	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.411992	-0.009859	-4.421851	25822.135679
HLA B*4601	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.393316	-0.028622	-4.421938	24735.238513
HLA B*5701	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.413785	-0.008210	-4.421995	25928.943167
HLA B*4501	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.650843	0.228841	-4.422002	44755.164068
HLA B*5101	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.495469	0.073404	-4.422065	31294.596829
HLA B*4601	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.397268	-0.025025	-4.422293	24961.342320
HLA A*2902	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.431291	0.008974	-4.422317	26995.465989
HLA A*2501	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.460843	0.038504	-4.422339	28896.327508
HLA B*1517	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.486931	0.064589	-4.422342	30685.367743
HLA A*2301	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.529713	0.107303	-4.422410	33862.038939
HLA A*0201	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.414266	-0.008210	-4.422476	25957.715024
HLA A*6901	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.376188	-0.047418	-4.423607	23778.713638
HLA A*8001	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.461862	0.038251	-4.423611	28964.252670
HLA B*4002	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.618998	0.195249	-4.423749	41590.891909
HLA B*0802	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.462071	0.038251	-4.423820	28978.201740

HLA A*2902	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.376491	-0.047362	-4.423854	23795.314016
HLA B*4501	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.641229	0.216943	-4.424287	43775.292930
HLA A*0219	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.436434	0.012088	-4.424346	27317.053374
HLA B*5101	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.271876	-0.152648	-4.424524	18701.477611
HLA B*5401	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.564192	0.139599	-4.424593	36659.943997
HLA A*6801	1:396-404	9	PDHVIGTDP	0.603278	-0.348410	-4.679634	0.254868	-4.424766	47822.661532
HLA A*0216	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.484415	0.059501	-4.424914	30508.091056
HLA A*2402	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.560964	0.135996	-4.424967	36388.454021
HLA A*2301	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.544151	0.119119	-4.425032	35006.661096
HLA A*2603	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.557287	0.132130	-4.425157	36081.672542
HLA B*3501	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.370954	-0.054260	-4.425213	23493.823634
HLA A*2902	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.390168	-0.035208	-4.425376	24556.574920
HLA A*0216	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.417213	-0.008210	-4.425422	26134.410863
HLA B*5801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.362451	-0.063193	-4.425644	23038.325925
HLA A*3002	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.435529	0.009850	-4.425680	27260.216426
HLA A*6901	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.378355	-0.047362	-4.425717	23897.616198
HLA B*4001	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.400703	-0.025025	-4.425728	25159.550822
HLA B*4002	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.490406	0.064589	-4.425817	30931.873164
HLA A*3301	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.567751	0.141914	-4.425837	36961.642911
HLA A*0202	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.596504	0.170651	-4.425853	39491.557708
HLA B*3801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.545001	0.119114	-4.425887	35075.284610
HLA A*0211	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.464505	0.038504	-4.426002	29141.070262
HLA B*0801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.397428	-0.028622	-4.426050	24970.526600
HLA B*5301	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.602465	0.176401	-4.426064	40037.311583
HLA A*2402	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.526866	0.100651	-4.426214	33640.739108
HLA A*0211	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.485721	0.059501	-4.426221	30599.994442
HLA B*3801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.569793	0.143550	-4.426243	37135.815842
HLA A*1101	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.512266	0.086012	-4.426254	32528.634236
HLA B*1502	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.613181	0.186843	-4.426338	41037.501250
HLA A*0206	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.512442	0.086012	-4.426430	32541.835137
HLA B*0801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.379205	-0.047362	-4.426567	23944.462665
HLA A*2603	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.621905	0.195249	-4.426656	41870.152895
HLA B*4601	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.392430	-0.034337	-4.426768	24684.841707
HLA B*4402	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.436782	0.009850	-4.426932	27338.933903
HLA A*3301	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.622494	0.195249	-4.427245	41927.046247
HLA A*0219	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.417422	-0.009859	-4.427280	26146.997092
HLA B*5101	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.465633	0.038251	-4.427382	29216.840578
HLA A*2601	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.392247	-0.035208	-4.427455	24674.427608
HLA B*0801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.373233	-0.054260	-4.427492	23617.433690
HLA A*0212	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.373301	-0.054260	-4.427560	23621.139243
HLA A*0250	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.584903	0.157340	-4.427562	38450.545672
HLA A*3301	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.379694	-0.047884	-4.427577	23971.421503
HLA B*4501	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.622868	0.195249	-4.427619	41963.126250
HLA B*4001	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.379842	-0.047884	-4.427725	23979.592908
HLA A*0203	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.406015	-0.021825	-4.427840	25469.186226
HLA A*2402	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.569201	0.141319	-4.427882	37085.223373
HLA B*5701	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.414720	-0.013165	-4.427885	25984.831851
HLA A*0216	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.453169	0.025261	-4.427908	28390.251047
HLA A*3001	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.039564	-0.388552	-4.428116	10953.768133
HLA A*3002	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.557146	0.128996	-4.428150	36069.962571
HLA A*0219	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.419976	-0.008210	-4.428185	26301.208783
HLA B*7301	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.550718	0.122446	-4.428271	35540.006320
HLA A*2402	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.570373	0.141914	-4.428459	37185.471470
HLA B*1801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.406699	-0.021825	-4.428524	25509.313376
HLA B*0801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.437594	0.008974	-4.428621	27390.155435
HLA A*3101	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.418785	-0.009859	-4.428643	26229.168307
HLA B*0801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.417692	-0.010996	-4.428688	26163.269174
HLA B*4403	1:157-165	9	FGIARAIAD	1.192738	-0.975795	-4.645787	0.216943	-4.428845	44237.142082
HLA B*0802	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.488357	0.059501	-4.428857	30786.298064
HLA A*2602	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.608642	0.179592	-4.429050	40610.814879
HLA A*2602	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.526104	0.096922	-4.429182	33581.825131
HLA B*0801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.419362	-0.009859	-4.429221	26264.098180
HLA B*5401	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.511340	0.082090	-4.429251	32459.373413
HLA A*0101	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.375011	-0.054260	-4.429271	23714.352156
HLA A*3002	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.551615	0.122274	-4.429341	35613.528446

HLA B*5701	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.428044	-0.001305	-4.429349	26794.387897
HLA A*3201	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.578004	0.148535	-4.429469	37844.643588
HLA B*4002	1:59-67	9	EAQNAAALN	0.802264	-0.591841	-4.640050	0.210423	-4.429626	43656.570834
HLA A*3002	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.468011	0.038251	-4.429760	29377.235831
HLA B*4001	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.381195	-0.048602	-4.429797	24054.432167
HLA B*4801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.439683	0.009850	-4.429833	27522.202693
HLA A*0202	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.565933	0.135996	-4.429937	36807.198691
HLA B*4402	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.375707	-0.054260	-4.429966	23752.357014
HLA B*1509	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.408240	-0.021825	-4.430065	25600.003884
HLA B*3501	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.184738	-0.245356	-4.430094	15301.648518
HLA B*1801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.401636	-0.028622	-4.430258	25213.644712
HLA B*5101	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.468850	0.038504	-4.430346	29434.027805
HLA A*0206	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.567643	0.137283	-4.430361	36952.445969
HLA B*3801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.396060	-0.034337	-4.430398	24892.029153
HLA A*3301	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.481309	0.050897	-4.430412	30290.679427
HLA B*1501	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.367129	-0.063767	-4.430896	23287.815013
HLA A*3101	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.376654	-0.054260	-4.430913	23804.198045
HLA B*4601	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.417809	-0.013165	-4.430974	26170.347151
HLA B*1502	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.493571	0.062590	-4.430980	31158.100730
HLA B*4801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.406032	-0.025025	-4.431056	25470.150742
HLA A*0202	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.396775	-0.034337	-4.431112	24933.000422
HLA B*5401	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.553589	0.122446	-4.431143	35775.735529
HLA A*2402	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.560214	0.128996	-4.431219	36325.710633
HLA B*5301	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.605186	0.173777	-4.431409	40288.918685
HLA A*2603	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.579525	0.148101	-4.431424	37977.339440
HLA A*0212	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.440404	0.008974	-4.431431	27567.950537
HLA A*2601	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.384217	-0.047418	-4.431635	24222.365164
HLA B*4601	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.414729	-0.017067	-4.431796	25985.394158
HLA A*0301	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.368616	-0.063193	-4.431809	23367.699904
HLA A*0216	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.403191	-0.028622	-4.431813	25304.105402
HLA A*3301	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.563947	0.132130	-4.431817	36639.323870
HLA B*0801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.279188	-0.152648	-4.431835	19018.993018
HLA B*4501	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.589101	0.157255	-4.431846	38824.067840
HLA B*4402	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.440867	0.008974	-4.431894	27597.346691
HLA A*8001	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.420916	-0.010996	-4.431911	26358.185057
HLA A*3001	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.314040	-0.117875	-4.431915	20608.186668
HLA B*3501	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.414880	-0.017067	-4.431946	25994.392714
HLA A*0219	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.403330	-0.028622	-4.431952	25312.183343
HLA B*5401	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.441852	0.009850	-4.432002	27659.973751
HLA B*7301	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.569307	0.137283	-4.432024	37094.252684
HLA A*3002	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.483062	0.050897	-4.432165	30413.172875
HLA A*0101	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.368459	-0.063767	-4.432225	23359.231522
HLA A*0201	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.388906	-0.043361	-4.432267	24485.338882
HLA B*5701	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.422426	-0.009859	-4.432285	26450.033209
HLA A*3101	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.410507	-0.021825	-4.432333	25733.999265
HLA B*4402	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.407331	-0.025025	-4.432355	25546.463089
HLA B*4002	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.589681	0.157255	-4.432427	38875.980890
HLA B*4403	1:534-542	9	VTGTNPPAG	0.954403	-0.731178	-4.655808	0.223225	-4.432583	45269.699886
HLA B*5301	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.604288	0.171585	-4.432703	40205.744478
HLA A*1101	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.441746	0.008974	-4.432772	27653.240888
HLA A*0219	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.458134	0.025261	-4.432872	28716.644690
HLA A*1101	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.442465	0.009579	-4.432885	27699.056696
HLA B*4002	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.644314	0.211378	-4.432936	44087.343875
HLA B*1509	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.561983	0.128996	-4.432988	36473.990553
HLA A*2301	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.545370	0.112336	-4.433034	35105.088549
HLA B*5801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.354009	-0.079239	-4.433248	22594.837297
HLA B*1801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.491294	0.057919	-4.433375	30995.191649
HLA A*2603	1:406-414	9	ANTSVSAGD	0.962066	-0.740780	-4.654889	0.221286	-4.433603	45174.043604
HLA A*0211	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.552750	0.119119	-4.433631	35706.707442
HLA B*4402	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.422647	-0.010996	-4.433643	26463.487254
HLA A*6801	1:291-299	9	AERTSLLSS	1.254579	-1.011910	-4.676347	0.242669	-4.433678	47462.085052
HLA A*0219	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.398492	-0.035208	-4.433700	25031.796410
HLA B*1801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.484753	0.050897	-4.433857	30531.866852
HLA B*4001	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.412086	-0.021825	-4.433911	25827.724080
HLA B*4402	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.424073	-0.009859	-4.433932	26550.530964

HLA A*6802	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.386693	-0.047362	-4.434055	24360.876173
HLA B*1509	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.484958	0.050897	-4.434061	30546.240374
HLA A*0202	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.094588	-0.339553	-4.434141	12433.359251
HLA B*0702	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.443764	0.009579	-4.434185	27782.047175
HLA B*2705	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.492199	0.057919	-4.434280	31059.815938
HLA A*2602	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.574067	0.139599	-4.434468	37503.058095
HLA A*2601	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.391373	-0.043361	-4.434734	24624.820779
HLA A*0201	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.380504	-0.054260	-4.434764	24016.203824
HLA B*4403	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.611179	0.176401	-4.434778	40848.785402
HLA A*6901	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.314385	-0.120427	-4.434812	20624.581923
HLA A*3002	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.574417	0.139599	-4.434818	37533.300503
HLA B*4001	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.399728	-0.035208	-4.434936	25103.128375
HLA B*4001	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.406396	-0.028622	-4.435018	25491.517257
HLA B*3501	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.386439	-0.048602	-4.435041	24346.647049
HLA B*4801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.425405	-0.009859	-4.435264	26632.097287
HLA A*2602	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.630670	0.195249	-4.435422	42723.859218
HLA A*3301	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.557890	0.122446	-4.435444	36131.873279
HLA A*2402	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.567638	0.132177	-4.435462	36952.046154
HLA B*0801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.392193	-0.043361	-4.435554	24671.357623
HLA B*4403	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.631105	0.195249	-4.435856	42766.639920
HLA A*0203	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.434618	-0.001305	-4.435923	27203.056236
HLA A*2601	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.370103	-0.065831	-4.435934	23447.858825
HLA A*2602	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.593302	0.157340	-4.435962	39201.430609
HLA A*8001	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.388241	-0.047884	-4.436125	24447.880543
HLA A*2902	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.372434	-0.063767	-4.436201	23574.032600
HLA A*1101	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.425365	-0.010996	-4.436361	26629.648096
HLA B*5301	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.593617	0.157255	-4.436362	39229.859015
HLA B*3801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.573698	0.137283	-4.436415	37471.218299
HLA A*6802	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.435283	-0.001305	-4.436587	27244.735975
HLA A*0206	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.389266	-0.047418	-4.436684	24505.614106
HLA B*4501	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.648120	0.211378	-4.436742	44475.424346
HLA A*2603	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.606081	0.169330	-4.436751	40372.046546
HLA B*0801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.435529	-0.001305	-4.436834	27260.216426
HLA A*0206	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.371034	-0.065831	-4.436864	23498.145396
HLA A*2403	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.435581	-0.001305	-4.436886	27263.461064
HLA B*7301	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.569018	0.132130	-4.436888	37069.577772
HLA A*6802	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.415218	-0.021825	-4.437043	26014.650860
HLA B*4501	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.556248	0.119119	-4.437129	35995.498163
HLA A*3001	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.281438	-0.155719	-4.437158	19117.818123
HLA A*0216	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.446205	0.008974	-4.437232	27938.646284
HLA A*0202	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.402181	-0.035208	-4.437389	25245.310081
HLA B*4501	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.569910	0.132130	-4.437780	37145.862233
HLA B*5101	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.495794	0.057919	-4.437874	31317.968994
HLA B*4403	1:89-97	9	YIVMEYVDG	0.816479	-0.587638	-4.666796	0.228841	-4.437955	46429.729847
HLA A*0202	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.581550	0.143550	-4.438000	38154.853677
HLA B*4402	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.416209	-0.021825	-4.438035	26074.109457
HLA A*3001	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.285486	-0.152648	-4.438134	19296.852992
HLA A*2602	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.617722	0.179347	-4.438376	41468.895036
HLA B*5101	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.501002	0.062590	-4.438412	31695.849646
HLA B*4402	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.430264	-0.008210	-4.438474	26931.720806
HLA A*0212	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.425325	-0.013165	-4.438490	26627.199130
HLA A*1101	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.450853	0.012088	-4.438765	28239.216349
HLA B*4402	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.403567	-0.035208	-4.438775	25326.017669
HLA B*3901	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.512181	0.073404	-4.438777	32522.299706
HLA B*4601	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.390386	-0.048602	-4.438988	24568.932925
HLA A*0206	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.385004	-0.054260	-4.439263	24266.303471
HLA B*1517	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.395903	-0.043361	-4.439264	24883.008359
HLA B*3801	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.580655	0.141319	-4.439335	38076.291116
HLA A*0201	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.390741	-0.048602	-4.439343	24589.011321
HLA B*1509	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.546679	0.107303	-4.439376	35211.030540
HLA A*6801	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.571557	0.132177	-4.439381	37286.999135
HLA A*2301	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.525409	0.086012	-4.439397	33528.092675
HLA A*3201	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.618744	0.179347	-4.439398	41566.598778
HLA A*0203	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.414377	-0.025025	-4.439402	25964.315996
HLA A*2402	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.587945	0.148535	-4.439410	38720.868561

HLA A*3201	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.525453	0.086012	-4.439442	33531.539134
HLA B*0702	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.451565	0.012088	-4.439477	28285.543931
HLA A*0206	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.568531	0.128996	-4.439536	37028.088750
HLA A*2602	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.551895	0.112336	-4.439559	35636.462992
HLA A*0211	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.428634	-0.010996	-4.439629	26830.796233
HLA A*3301	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.540626	0.100651	-4.439975	34723.737354
HLA A*0202	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.499715	0.059501	-4.440214	31602.022669
HLA B*7301	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.588530	0.148101	-4.440429	38773.063134
HLA A*2402	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.572584	0.132130	-4.440454	37375.254416
HLA A*0201	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.393135	-0.047362	-4.440497	24724.936912
HLA A*0219	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.429545	-0.010996	-4.440541	26887.174215
HLA B*4403	1:524-532	9	SVDSPRPAG	0.764201	-0.531833	-4.672931	0.232368	-4.440562	47090.213780
HLA B*0802	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.479110	0.038504	-4.440606	30137.685520
HLA B*3901	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.418850	-0.021825	-4.440676	26233.141721
HLA B*5301	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.569673	0.128996	-4.440678	37125.571322
HLA A*3002	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.580730	0.139887	-4.440842	38082.883319
HLA A*0212	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.423909	-0.017067	-4.440975	26540.478387
HLA A*2601	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.386745	-0.054260	-4.441004	24363.775717
HLA B*3501	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.270685	-0.170363	-4.441048	18650.253222
HLA B*5701	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.424083	-0.017067	-4.441149	26551.105512
HLA B*3901	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.406844	-0.034337	-4.441182	25517.870970
HLA B*5401	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.479502	0.038251	-4.441251	30164.925760
HLA A*0219	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.450420	0.008974	-4.441447	28211.120466
HLA B*1517	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.466712	0.025261	-4.441450	29289.480208
HLA A*0101	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.378463	-0.063193	-4.441656	23903.563977
HLA A*8001	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.413280	-0.028622	-4.441902	25898.802067
HLA B*3901	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.501435	0.059501	-4.441934	31727.416024
HLA A*3301	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.633323	0.191384	-4.441939	42985.605030
HLA B*1502	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.590478	0.148535	-4.441943	38947.343007
HLA B*4403	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.666796	0.224721	-4.442075	46429.729847
HLA B*4601	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.394275	-0.047884	-4.442158	24789.895289
HLA A*0203	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.393619	-0.048602	-4.442221	24752.506660
HLA A*2403	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.425187	-0.017067	-4.442253	26618.701524
HLA A*0212	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.452194	0.009850	-4.442344	28326.583478
HLA A*2602	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.597632	0.155271	-4.442361	39594.240547
HLA A*0250	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.395160	-0.047418	-4.442579	24840.506574
HLA B*5701	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.394115	-0.048602	-4.442717	24780.777447
HLA A*0219	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.388641	-0.054260	-4.442900	24470.375141
HLA A*0216	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.433072	-0.009859	-4.442930	27106.393472
HLA A*0250	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.580342	0.137283	-4.443060	38048.904497
HLA A*6801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.543711	0.100651	-4.443060	34971.264540
HLA B*5401	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.550407	0.107303	-4.443104	35514.636070
HLA B*4403	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.622732	0.179592	-4.443140	41949.961395
HLA A*8001	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.453054	0.009850	-4.443204	28382.726227
HLA B*4601	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.399960	-0.043361	-4.443321	25116.576685
HLA B*7301	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.603482	0.160089	-4.443394	40131.208197
HLA A*2601	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.394980	-0.048602	-4.443581	24830.161131
HLA B*1502	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.562705	0.119119	-4.443585	36534.618201
HLA B*1501	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.396255	-0.047362	-4.443618	24903.208701
HLA A*0216	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.453482	0.009850	-4.443632	28410.685617
HLA A*0212	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.400350	-0.043361	-4.443711	25139.142547
HLA A*3001	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.298531	-0.145362	-4.443893	19885.239636
HLA B*1502	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.603987	0.160089	-4.443899	40177.913012
HLA A*1101	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.378087	-0.065831	-4.443917	23882.882428
HLA B*0803	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.494844	0.050897	-4.443948	31249.595336
HLA A*8001	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.422125	-0.021825	-4.443951	26431.723805
HLA A*3201	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.604084	0.160089	-4.443995	40186.825681
HLA A*6801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.415399	-0.028622	-4.444021	26025.489819
HLA A*0212	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.434279	-0.009859	-4.444138	27181.872653
HLA A*2602	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.563285	0.119119	-4.444166	36583.469946
HLA A*6801	1:525-533	9	VDSPRPAGE	0.958604	-0.763355	-4.639415	0.195249	-4.444166	43592.849537
HLA B*3901	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.495096	0.050897	-4.444199	31267.689656
HLA B*3801	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.556589	0.112336	-4.444253	36023.745330
HLA A*0219	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.454114	0.009850	-4.444264	28452.060655
HLA B*3901	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.502250	0.057919	-4.444331	31787.031668

HLA B*0802	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.433443	-0.010996	-4.444439	27129.572905
HLA A*3101	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.397134	-0.047362	-4.444496	24953.646335
HLA A*0206	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.502447	0.057919	-4.444528	31801.479954
HLA B*3801	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.545189	0.100651	-4.444538	35090.468167
HLA B*4501	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.618340	0.173777	-4.444564	41527.939009
HLA B*0803	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.482937	0.038251	-4.444686	30404.453935
HLA A*0212	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.443778	-0.001305	-4.445083	27782.948977
HLA A*6901	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.366027	-0.079239	-4.445265	23228.803179
HLA B*3501	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.470593	0.025261	-4.445332	29552.417504
HLA B*3501	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.401974	-0.043361	-4.445335	25233.294400
HLA A*3201	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.588930	0.143550	-4.445380	38808.738392
HLA A*0203	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.432238	-0.013165	-4.445403	27054.385312
HLA B*4001	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.379623	-0.065831	-4.445454	23967.531337
HLA A*0216	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.434484	-0.010996	-4.445479	27194.669094
HLA B*5701	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.416903	-0.028622	-4.445525	26115.754802
HLA B*5301	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.600797	0.155271	-4.445526	39883.822383
HLA B*7301	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.552914	0.107303	-4.445611	35720.231856
HLA B*3501	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.454628	0.008974	-4.445655	28485.789657
HLA A*0203	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.435811	-0.009859	-4.445670	27277.919142
HLA B*5101	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.327801	-0.117875	-4.445676	21271.627205
HLA A*2402	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.558085	0.112336	-4.445749	36148.100884
HLA B*1509	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.420742	-0.025025	-4.445766	26347.635150
HLA A*0250	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.585873	0.139887	-4.445986	38536.551164
HLA A*0301	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.366844	-0.079239	-4.446083	23272.575878
HLA B*5301	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.578362	0.132177	-4.446185	37875.776157
HLA A*0201	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.380359	-0.065831	-4.446189	24008.149825
HLA B*4002	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.417617	-0.028622	-4.446239	26158.740274
HLA A*2402	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.586735	0.140490	-4.446245	38613.138766
HLA A*2402	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.586136	0.139887	-4.446249	38559.907827
HLA A*2301	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.528388	0.082090	-4.446298	33758.877310
HLA A*6901	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.383178	-0.063193	-4.446371	24164.514540
HLA A*0250	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.589956	0.143550	-4.446406	38900.595505
HLA A*2603	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.601760	0.155271	-4.446489	39972.385059
HLA A*0202	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.575711	0.128996	-4.446716	37645.348517
HLA A*8001	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.411590	-0.035208	-4.446799	25798.258899
HLA B*5801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.350957	-0.096147	-4.447105	22436.609917
HLA A*3301	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.626542	0.179347	-4.447196	42319.685364
HLA B*0702	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.456282	0.008974	-4.447309	28594.486410
HLA A*3101	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.434164	-0.013165	-4.447329	27174.668113
HLA B*3901	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.412133	-0.035208	-4.447341	25830.518733
HLA A*3002	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.529506	0.082090	-4.447417	33845.922066
HLA A*1101	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.413195	-0.034337	-4.447532	25893.758611
HLA A*2603	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.351758	-0.096147	-4.447906	22478.038552
HLA B*0803	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.512510	0.064589	-4.447921	32546.940921
HLA B*5701	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.422938	-0.025025	-4.447963	26481.245611
HLA B*7301	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.548641	0.100651	-4.447989	35370.447622
HLA A*0250	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.510619	0.062590	-4.448028	32405.508461
HLA A*0301	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.351904	-0.096147	-4.448051	22485.579246
HLA A*0250	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.580265	0.132177	-4.448088	38042.112372
HLA B*2705	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.426404	-0.021825	-4.448229	26693.400329
HLA B*1502	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.588056	0.139599	-4.448457	38730.715167
HLA B*5301	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.486767	0.038251	-4.448516	30673.749633
HLA A*0202	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.588189	0.139599	-4.448591	38742.660154
HLA B*4403	1:431-439	9	DVSTLTYAE	1.031631	-0.820253	-4.659990	0.211378	-4.448612	45707.734775
HLA A*2403	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.427076	-0.021825	-4.448901	26734.733080
HLA B*0802	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.458867	0.009850	-4.449017	28765.156025
HLA A*6801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.499915	0.050897	-4.449018	31616.557903
HLA B*5301	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.592611	0.143550	-4.449061	39139.130001
HLA B*4001	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.394846	-0.054260	-4.449105	24822.505592
HLA B*1509	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.571572	0.122446	-4.449125	37288.209466
HLA A*2602	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.487516	0.038251	-4.449265	30726.730701
HLA A*0206	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.438363	-0.010996	-4.449358	27438.652428
HLA B*4501	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.636258	0.186843	-4.449415	43277.040178
HLA B*5701	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.402061	-0.047418	-4.449479	25238.345751
HLA A*6901	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.213557	-0.236114	-4.449671	16351.477645

HLA B*4801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.436655	-0.013165	-4.449820	27330.948437
HLA A*2603	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.620591	0.170651	-4.449940	41743.723457
HLA A*0250	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.591279	0.141319	-4.449960	39019.258296
HLA B*4002	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.636913	0.186843	-4.450070	43342.410092
HLA B*5301	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.607415	0.157340	-4.450075	40496.293254
HLA B*5701	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.414875	-0.035208	-4.450083	25994.111462
HLA A*3001	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.308201	-0.141893	-4.450094	20332.992914
HLA A*6801	1:383-391	9	KIRTLQKPD	0.935900	-0.711179	-4.675064	0.224721	-4.450343	47322.098419
HLA A*8001	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.386674	-0.063767	-4.450441	24359.821878
HLA B*1509	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.532584	0.082090	-4.450495	34086.638551
HLA B*1517	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.415418	-0.035208	-4.450626	26026.616203
HLA B*4601	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.384877	-0.065831	-4.450707	24259.215494
HLA A*2402	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.573242	0.122446	-4.450796	37431.912192
HLA A*6802	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.441060	-0.009859	-4.450919	27609.591891
HLA A*8001	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.459901	0.008974	-4.450927	28833.708757
HLA B*3801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.591420	0.140490	-4.450930	39031.925743
HLA B*5401	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.551594	0.100651	-4.450943	35611.794501
HLA B*2705	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.439982	-0.010996	-4.450977	27541.118483
HLA B*0702	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.403668	-0.047362	-4.451030	25331.909825
HLA A*3201	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.583328	0.132177	-4.451152	38311.429110
HLA B*4601	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.403830	-0.047418	-4.451248	25341.367545
HLA A*6801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.426284	-0.025025	-4.451309	26686.036519
HLA B*0803	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.524812	0.073404	-4.451408	33482.052965
HLA B*4002	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.642815	0.191384	-4.451431	43935.438302
HLA A*3002	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.510938	0.059501	-4.451438	32429.359422
HLA A*2301	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.514127	0.062590	-4.451536	32668.306478
HLA B*4001	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.404356	-0.047418	-4.451775	25372.095213
HLA B*4801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.443630	-0.008210	-4.451840	27773.481522
HLA B*3501	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.404509	-0.047418	-4.451927	25381.018696
HLA B*2705	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.490822	0.038504	-4.452319	30961.506177
HLA B*4403	1:548-556	9	DSVIELQVS	1.229278	-1.042435	-4.639194	0.186843	-4.452351	43570.686919
HLA A*3101	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.418183	-0.034337	-4.452520	26192.867845
HLA B*4501	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.632181	0.179592	-4.452589	42872.735458
HLA B*5301	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.601187	0.148535	-4.452652	39919.655802
HLA B*1503	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.462236	0.009579	-4.452656	28989.177639
HLA B*1503	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.526100	0.073404	-4.452695	33581.461785
HLA B*3801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.582074	0.128996	-4.453078	38200.911670
HLA A*2403	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.439986	-0.013165	-4.453151	27541.416473
HLA A*2501	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.491409	0.038251	-4.453158	31003.409085
HLA B*1517	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.491861	0.038504	-4.453357	31035.629017
HLA B*0802	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.478621	0.025261	-4.453360	30103.791953
HLA A*6802	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.440381	-0.013165	-4.453546	27566.459181
HLA B*0702	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.406337	-0.047418	-4.453755	25488.069833
HLA A*0201	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.390093	-0.063767	-4.453859	24552.324141
HLA B*4002	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.630313	0.176401	-4.453912	42688.741694
HLA B*1801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.466073	0.012088	-4.453985	29246.412729
HLA B*0702	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.425368	-0.028622	-4.453990	26629.792159
HLA B*1509	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.479476	0.025261	-4.454215	30163.130736
HLA A*0219	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.419891	-0.034337	-4.454228	26296.086963
HLA B*2705	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.358121	-0.096147	-4.454268	22809.765325
HLA B*4601	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.406922	-0.047362	-4.454284	25522.426988
HLA A*0202	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.358163	-0.096147	-4.454310	22811.986603
HLA B*7301	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.596347	0.141914	-4.454433	39477.246091
HLA B*7301	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.400200	-0.054260	-4.454460	25130.440055
HLA B*3801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.577060	0.122446	-4.454614	37762.429418
HLA B*3801	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.551606	0.096922	-4.454683	35612.757794
HLA B*5701	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.411372	-0.043361	-4.454733	25785.282551
HLA A*6801	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.596713	0.141914	-4.454800	39510.576687
HLA B*1801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.429836	-0.025025	-4.454861	26905.216889
HLA A*1101	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.480137	0.025261	-4.454875	30209.018959
HLA B*5301	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.594784	0.139887	-4.454897	39335.478849
HLA A*2402	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.537116	0.082090	-4.455027	34444.218220
HLA A*3001	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.219059	-0.236114	-4.455174	16559.968213
HLA A*2602	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.592651	0.137283	-4.455369	39142.729719
HLA A*0202	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.592856	0.137283	-4.455573	39161.156986

HLA A*2603	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.591636	0.135996	-4.455640	39051.357150
HLA A*6801	1:322-330	9	RDRSIGSVG	0.890456	-0.672036	-4.674317	0.218420	-4.455897	47240.758082
HLA B*0801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.442775	-0.013165	-4.455940	27718.843806
HLA A*8001	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.454765	-0.001305	-4.456069	28494.729148
HLA B*0702	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.446269	-0.009859	-4.456127	27942.727497
HLA B*5401	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.412836	-0.043361	-4.456197	25872.334877
HLA A*3002	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.596723	0.140490	-4.456232	39511.431688
HLA B*0702	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.421026	-0.035208	-4.456234	26364.887868
HLA A*1101	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.494823	0.038504	-4.456320	31248.073862
HLA A*2602	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.507229	0.050897	-4.456332	32153.520677
HLA A*0250	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.592512	0.135996	-4.456516	39130.238000
HLA A*0250	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.585715	0.128996	-4.456720	38522.585637
HLA B*4403	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.648299	0.191384	-4.456914	44493.714246
HLA A*0301	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.368217	-0.088805	-4.457021	23346.218950
HLA B*0702	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.408494	-0.048602	-4.457095	25614.965518
HLA B*4501	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.569492	0.112336	-4.457156	37110.109460
HLA A*2603	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.639646	0.182373	-4.457273	43615.967248
HLA A*6801	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.648658	0.191384	-4.457274	44530.557519
HLA B*0801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.422948	-0.034337	-4.457285	26481.818660
HLA B*4801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.422971	-0.034337	-4.457309	26483.251336
HLA A*2602	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.617577	0.160089	-4.457488	41454.988157
HLA A*2601	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.394573	-0.063193	-4.457766	24806.933186
HLA A*2602	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.634202	0.176401	-4.457800	43072.665787
HLA B*3501	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.456515	-0.001305	-4.457820	28609.805119
HLA A*2403	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.409953	-0.047884	-4.457836	25701.164763
HLA A*2902	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.449758	-0.008210	-4.457968	28168.114711
HLA B*5801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.369478	-0.088805	-4.458283	23414.140907
HLA A*0206	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.213007	-0.245356	-4.458363	16330.791176
HLA B*0702	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.441518	-0.017067	-4.458585	27638.733401
HLA A*0250	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.571139	0.112336	-4.458803	37251.110519
HLA A*0206	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.415467	-0.043361	-4.458828	26029.573194
HLA B*1801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.497199	0.038251	-4.458947	31419.450248
HLA B*5801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.305690	-0.153340	-4.459030	20215.743093
HLA A*0202	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.448087	-0.010996	-4.459083	28059.976103
HLA B*5101	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.448092	-0.010996	-4.459088	28060.279708
HLA A*2403	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.404873	-0.054260	-4.459133	25402.310439
HLA B*3901	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.468758	0.009579	-4.459179	29427.818302
HLA B*5301	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.601121	0.141914	-4.459207	39913.609355
HLA A*3002	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.468892	0.009579	-4.459312	29436.894171
HLA A*2402	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.556392	0.096922	-4.459469	36007.378754
HLA A*0212	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.434460	-0.025025	-4.459485	27193.197933
HLA B*0801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.393690	-0.065831	-4.459520	24756.524235
HLA A*0201	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.396347	-0.063193	-4.459540	24908.463476
HLA A*0101	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.363567	-0.096147	-4.459714	23097.603581
HLA A*0203	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.363581	-0.096147	-4.459728	23098.353326
HLA B*5801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.349294	-0.110482	-4.459775	22350.837547
HLA B*0702	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.458543	-0.001305	-4.459847	28743.688989
HLA B*1801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.469505	0.009579	-4.459926	29478.487866
HLA B*1501	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.351018	-0.108943	-4.459961	22439.766008
HLA B*1801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.451851	-0.008210	-4.460061	28304.218735
HLA B*5301	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.592404	0.132130	-4.460274	39120.501461
HLA B*4402	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.371496	-0.088805	-4.460301	23523.201851
HLA B*5701	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.412988	-0.047362	-4.460351	25881.434297
HLA A*0250	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.600848	0.140490	-4.460358	39888.569541
HLA A*2402	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.582720	0.122274	-4.460446	38257.786208
HLA A*0250	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.579738	0.119114	-4.460624	37996.040284
HLA B*7301	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.600346	0.139599	-4.460747	39842.416616
HLA B*1501	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.364695	-0.096147	-4.460842	23157.660151
HLA A*0219	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.470429	0.009579	-4.460849	29541.228352
HLA A*2601	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.351942	-0.109105	-4.461047	22487.525642
HLA B*4601	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.381858	-0.079239	-4.461096	24091.157345
HLA A*0206	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.534546	0.073404	-4.461142	34240.964976
HLA B*1502	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.580333	0.119114	-4.461218	38048.081144
HLA B*1801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.499724	0.038504	-4.461221	31602.706530
HLA B*4001	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.460027	-0.001305	-4.461332	28842.133294

HLA B*5301	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.601838	0.140490	-4.461347	39979.521820
HLA A*0211	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.453141	-0.008210	-4.461351	28388.408050
HLA A*8001	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.451609	-0.009859	-4.461468	28288.451492
HLA A*6901	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.352531	-0.108943	-4.461474	22518.081794
HLA B*4403	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.635466	0.173777	-4.461689	43198.212272
HLA B*4501	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.641058	0.179347	-4.461711	43758.008521
HLA A*2602	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.603696	0.141914	-4.461782	40150.969651
HLA B*1801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.407575	-0.054260	-4.461835	25560.840300
HLA B*4501	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.634383	0.172544	-4.461839	43090.611938
HLA B*1503	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.544087	0.082090	-4.461998	35001.548151
HLA A*0216	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.426792	-0.035208	-4.462000	26717.238342
HLA A*2902	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.460868	-0.001305	-4.462173	28898.047144
HLA A*2902	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.413595	-0.048602	-4.462196	25917.583567
HLA A*2603	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.408061	-0.054260	-4.462321	25589.480565
HLA B*7301	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.591406	0.128996	-4.462410	39030.658814
HLA A*3002	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.500946	0.038504	-4.462442	31691.734608
HLA B*1502	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.603830	0.141319	-4.462511	40163.352661
HLA B*0803	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.520470	0.057919	-4.462551	33148.984668
HLA A*3201	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.500850	0.038251	-4.462598	31684.705988
HLA A*2403	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.414269	-0.048602	-4.462870	25957.855452
HLA A*3301	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.639371	0.176401	-4.462969	43588.368950
HLA B*1502	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.620319	0.157340	-4.462978	41717.535521
HLA A*2301	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.536397	0.073404	-4.462993	34387.245533
HLA A*2902	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.438008	-0.025025	-4.463033	27416.247130
HLA B*1502	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.603562	0.140490	-4.463072	40138.590459
HLA B*5301	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.599357	0.135996	-4.463360	39751.776248
HLA B*1501	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.400177	-0.063193	-4.463370	25129.080563
HLA A*2902	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.415488	-0.047884	-4.463372	26030.840579
HLA A*0211	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.475626	0.012088	-4.463538	29896.862258
HLA B*4002	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.642904	0.179347	-4.463558	43944.471293
HLA B*1501	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.052598	-0.410971	-4.463569	11287.518794
HLA A*6801	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.595861	0.132130	-4.463730	39433.062357
HLA B*4002	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.643400	0.179592	-4.463808	43994.661959
HLA B*5401	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.528538	0.064589	-4.463950	33770.567768
HLA B*4402	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.333087	-0.130925	-4.464012	21532.133036
HLA A*0206	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.473845	0.009579	-4.464265	29774.515340
HLA A*2402	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.571604	0.107303	-4.464301	37291.033724
HLA B*2705	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.410098	-0.054260	-4.464358	25709.786717
HLA A*0212	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.401196	-0.063193	-4.464390	25188.150245
HLA B*5301	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.502920	0.038504	-4.464416	31836.079300
HLA B*0801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.400851	-0.063767	-4.464618	25168.127238
HLA A*3002	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.453797	-0.010996	-4.464792	28431.288704
HLA A*3301	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.546989	0.082090	-4.464899	35236.183906
HLA A*2603	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.644272	0.179347	-4.464925	44083.050947
HLA B*4501	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.641396	0.176401	-4.464995	43792.110343
HLA A*0206	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.529732	0.064589	-4.465143	33863.504489
HLA A*2602	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.594319	0.128996	-4.465324	39293.366892
HLA A*0101	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.386124	-0.079239	-4.465363	24329.003948
HLA A*6801	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.644725	0.179347	-4.465378	44129.102477
HLA B*4801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.448365	-0.017067	-4.465431	28077.894382
HLA B*1517	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.220211	-0.245356	-4.465567	16603.924368
HLA B*4402	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.448517	-0.017067	-4.465584	28087.769508
HLA B*5301	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.577946	0.112336	-4.465610	37839.525551
HLA B*5701	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.411351	-0.054260	-4.465610	25784.027122
HLA B*1509	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.539078	0.073404	-4.465674	34600.163578
HLA A*0250	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.588110	0.122274	-4.465836	38735.534631
HLA A*2501	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.491099	0.025261	-4.465838	30981.277288
HLA A*0219	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.464609	-0.001305	-4.465914	29148.007686
HLA A*0211	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.539332	0.073404	-4.465927	34620.385254
HLA A*3201	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.585058	0.119119	-4.465938	38464.276994
HLA B*1503	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.457741	-0.008210	-4.465951	28690.712311
HLA A*3201	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.588568	0.122446	-4.466122	38776.419407
HLA A*0203	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.449264	-0.017067	-4.466331	28136.131742
HLA A*0202	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.585741	0.119119	-4.466622	38524.878138
HLA B*5101	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.476481	0.009850	-4.466631	29955.793153

HLA B*5301	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.606243	0.139599	-4.466644	40387.119531
HLA B*0801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.370538	-0.096147	-4.466685	23471.337881
HLA B*4001	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.402930	-0.063767	-4.466697	25288.914907
HLA A*3002	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.610249	0.143550	-4.466699	40761.368062
HLA A*2902	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.423533	-0.043361	-4.466894	26517.515360
HLA A*2402	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.586237	0.119114	-4.467123	38568.878878
HLA B*4402	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.404016	-0.063193	-4.467209	25352.200285
HLA A*3002	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.574555	0.107303	-4.467252	37545.282424
HLA A*2402	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.553316	0.086012	-4.467304	35753.291611
HLA B*4601	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.403579	-0.063767	-4.467345	25326.702733
HLA B*4402	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.433107	-0.034337	-4.467444	27108.593200
HLA A*8001	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.442813	-0.025025	-4.467837	27721.243203
HLA B*5701	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.420063	-0.047884	-4.467946	26306.473915
HLA A*3201	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.607909	0.139887	-4.468021	40542.326294
HLA B*4002	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.650423	0.182373	-4.468050	44711.845481
HLA B*3901	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.506601	0.038504	-4.468098	32107.110359
HLA A*0219	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.372030	-0.096147	-4.468177	23552.107143
HLA B*5801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.353605	-0.114630	-4.468235	22573.822559
HLA B*5401	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.541721	0.073404	-4.468317	34811.386622
HLA A*2603	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.600884	0.132177	-4.468707	39891.806563
HLA B*4001	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.421508	-0.047362	-4.468870	26394.143467
HLA B*4501	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.617058	0.148101	-4.468957	41405.454790
HLA B*2705	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.477966	0.008974	-4.468992	30058.388795
HLA B*5801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.351162	-0.117875	-4.469037	22447.172425
HLA B*4501	1:183-191	9	LSPEQARGD	0.989683	-0.798299	-4.660450	0.191384	-4.469066	45756.226139
HLA A*0211	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.433873	-0.035208	-4.469081	27156.444745
HLA B*7301	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.528689	0.059501	-4.469188	33782.262274
HLA B*5401	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.555243	0.086012	-4.469231	35912.249430
HLA B*4002	1:295-303	9	SLLSSAAGN	0.699463	-0.525686	-4.643022	0.173777	-4.469245	43956.359636
HLA B*0803	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.528811	0.059501	-4.469310	33791.767042
HLA A*2403	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.426122	-0.043361	-4.469483	26676.076952
HLA A*0203	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.426190	-0.043361	-4.469551	26680.262404
HLA A*2402	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.459879	-0.009859	-4.469738	28832.304906
HLA B*0802	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.444829	-0.025025	-4.469853	27850.215572
HLA B*5701	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.406140	-0.063767	-4.469906	25476.489903
HLA A*3301	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.543319	0.073404	-4.469914	34939.683967
HLA A*2501	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.435701	-0.034337	-4.470038	27270.984209
HLA B*3501	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.373928	-0.096147	-4.470075	23655.283225
HLA A*0206	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.479960	0.009850	-4.470111	30196.764387
HLA B*4402	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.406598	-0.063767	-4.470365	25503.379956
HLA A*2301	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.534967	0.064589	-4.470378	34274.138964
HLA A*3201	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.611893	0.141319	-4.470574	40916.020844
HLA B*0801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.407427	-0.063193	-4.470620	25552.130062
HLA B*5101	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.495925	0.025261	-4.470664	31327.458329
HLA A*3301	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.628009	0.157340	-4.470668	42462.788329
HLA A*3301	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.533517	0.062590	-4.470926	34159.925983
HLA A*8001	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.436690	-0.034337	-4.471027	27333.166388
HLA A*8001	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.423709	-0.047362	-4.471071	26528.276804
HLA B*0802	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.463070	-0.008210	-4.471280	29044.905158
HLA A*2402	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.590438	0.119119	-4.471319	38943.761258
HLA A*0202	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.590485	0.119114	-4.471370	38947.975115
HLA B*3901	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.496677	0.025261	-4.471416	31381.738283
HLA B*7301	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.603759	0.132177	-4.471583	40156.834812
HLA A*3001	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.283085	-0.188551	-4.471636	19190.456890
HLA B*4801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.424285	-0.047362	-4.471647	26563.461300
HLA B*2705	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.406067	-0.065831	-4.471897	25472.217687
HLA A*0202	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.594338	0.122274	-4.472064	39295.067511
HLA A*2501	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.450272	-0.021825	-4.472098	28201.507105
HLA A*2602	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.604314	0.132177	-4.472137	40208.137144
HLA A*2902	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.455227	-0.017067	-4.472294	28525.113541
HLA A*2301	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.523193	0.050897	-4.472297	33357.483809
HLA B*3501	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.105791	-0.366558	-4.472349	12758.241742
HLA A*2902	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.450597	-0.021825	-4.472422	28222.569216
HLA A*0211	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.443802	-0.028622	-4.472424	27784.452044
HLA B*3801	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.554545	0.082090	-4.472455	35854.594218

HLA B*1502	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.616064	0.143550	-4.472514	41310.811578
HLA B*0802	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.482181	0.009579	-4.472601	30351.535958
HLA B*1517	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.482528	0.009850	-4.472679	30375.847059
HLA A*0101	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.383878	-0.088805	-4.472683	24203.502708
HLA B*1801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.471606	-0.001305	-4.472911	29621.404155
HLA A*2301	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.444476	-0.028622	-4.473098	27827.624752
HLA B*5101	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.482131	0.008974	-4.473158	30348.087986
HLA B*4403	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.614483	0.141319	-4.473163	41160.678360
HLA B*1502	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.555315	0.082090	-4.473226	35918.272655
HLA A*3002	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.546669	0.073404	-4.473265	35210.268597
HLA B*4002	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.621367	0.148101	-4.473266	41818.313561
HLA B*7301	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.592388	0.119119	-4.473269	39119.020026
HLA A*3201	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.612868	0.139599	-4.473270	41007.984762
HLA B*0802	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.456327	-0.017067	-4.473393	28597.425728
HLA B*4002	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.646008	0.172544	-4.473464	44259.643698
HLA B*0702	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.419294	-0.054260	-4.473554	26259.978013
HLA A*3201	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.610885	0.137283	-4.473603	40821.171315
HLA A*0301	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.364509	-0.109105	-4.473614	23147.765116
HLA A*0301	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.358985	-0.114630	-4.473615	22855.221133
HLA B*3901	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.465431	-0.008210	-4.473641	29203.250591
HLA A*3301	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.621749	0.148101	-4.473649	41855.205713
HLA B*3901	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.485898	0.012088	-4.473810	30612.412654
HLA B*4801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.426395	-0.047418	-4.473813	26692.822702
HLA A*0212	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.408000	-0.065831	-4.473831	25585.881476
HLA B*5301	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.555924	0.082090	-4.473834	35968.635223
HLA A*6801	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.622417	0.148535	-4.473882	41919.561833
HLA A*6801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.426016	-0.047884	-4.473900	26669.583585
HLA B*5801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.364918	-0.109105	-4.474023	23169.564845
HLA A*1101	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.483938	0.009850	-4.474088	30474.605232
HLA A*0301	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.363619	-0.110482	-4.474100	23100.352765
HLA A*0216	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.483734	0.009579	-4.474154	30460.265419
HLA A*0201	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.394916	-0.079239	-4.474155	24826.534529
HLA B*4402	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.430835	-0.043361	-4.474196	26967.148611
HLA A*0203	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.394975	-0.079239	-4.474213	24829.892476
HLA A*2603	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.650622	0.176401	-4.474221	44732.410530
HLA A*3301	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.606403	0.132177	-4.474226	40401.979574
HLA A*0301	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.365315	-0.108943	-4.474258	23190.757799
HLA A*0206	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.486356	0.012088	-4.474268	30644.723597
HLA A*2403	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.097859	-0.376448	-4.474307	12527.342910
HLA A*3201	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.614807	0.140490	-4.474316	41191.418943
HLA B*4501	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.656719	0.182373	-4.474346	45364.822458
HLA A*0203	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.410592	-0.063767	-4.474359	25739.011604
HLA B*0702	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.410615	-0.063767	-4.474382	25740.404094
HLA A*2301	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.533975	0.059501	-4.474474	34195.981273
HLA A*2403	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.427116	-0.047418	-4.474534	26737.191936
HLA A*6801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.238492	-0.236114	-4.474606	17317.774859
HLA A*1101	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.446006	-0.028622	-4.474628	27925.801914
HLA A*2403	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.449683	-0.025025	-4.474707	28163.238769
HLA A*3002	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.465076	-0.009859	-4.474935	29179.404394
HLA A*6801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.484605	0.009579	-4.475026	30521.462662
HLA B*3801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.582379	0.107303	-4.475076	38227.787271
HLA B*4601	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.411886	-0.063193	-4.475080	25815.850175
HLA A*3201	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.611090	0.135996	-4.475094	40840.388744
HLA B*1503	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.533190	0.057919	-4.475271	34134.248242
HLA A*0212	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.426733	-0.048602	-4.475334	26713.625154
HLA A*0250	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.582668	0.107303	-4.475365	38253.233131
HLA B*0702	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.462219	-0.013165	-4.475384	28988.079862
HLA A*3301	1:186-194	9	EQARGDSVD	1.036763	-0.900767	-4.611508	0.135996	-4.475512	40879.735357
HLA B*5101	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.409915	-0.065831	-4.475746	25698.940212
HLA A*8001	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.462797	-0.013165	-4.475962	29026.683829
HLA B*0802	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.454163	-0.021825	-4.475988	28455.293211
HLA B*4002	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.636314	0.160089	-4.476225	43282.659518
HLA B*1801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.485421	0.008974	-4.476447	30578.812327
HLA B*4002	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.648261	0.171585	-4.476676	44489.863116
HLA A*8001	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.468669	-0.008210	-4.476879	29421.769277

HLA A*3201	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.577753	0.100651	-4.477102	37822.743248
HLA B*3901	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.487021	0.009850	-4.477171	30691.676560
HLA B*4402	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.428580	-0.048602	-4.477181	26827.457953
HLA A*0202	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.487288	0.009850	-4.477439	30710.610795
HLA B*1801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.442317	-0.035208	-4.477525	27689.617829
HLA A*3001	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.307285	-0.170363	-4.477648	20290.138435
HLA B*2705	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.467886	-0.009859	-4.477745	29368.813876
HLA B*2705	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.469585	-0.008210	-4.477795	29483.910527
HLA A*0216	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.381679	-0.096147	-4.477826	24081.254264
HLA A*2602	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.551279	0.073404	-4.477875	35585.987971
HLA B*0802	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.490077	0.012088	-4.477989	30908.454713
HLA A*2603	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.590562	0.112336	-4.478226	38954.928975
HLA B*1502	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.618127	0.139887	-4.478239	41507.499840
HLA A*2602	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.626789	0.148535	-4.478254	42343.731398
HLA A*0211	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.536184	0.057919	-4.478264	34370.320861
HLA A*2301	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.536498	0.057919	-4.478579	34395.245804
HLA A*0219	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.465525	-0.013165	-4.478690	29209.570729
HLA B*4002	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.648188	0.169330	-4.478858	44482.402499
HLA A*2602	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.619374	0.140490	-4.478884	41626.907833
HLA B*1517	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.453970	-0.025025	-4.478995	28442.672932
HLA A*0250	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.598163	0.119119	-4.479044	39642.679455
HLA A*2902	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.465988	-0.013165	-4.479153	29240.717369
HLA A*6802	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.358786	-0.120427	-4.479212	22844.713791
HLA A*6801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.541806	0.062590	-4.479215	34818.167008
HLA B*5301	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.579896	0.100651	-4.479244	38009.814923
HLA B*4002	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.634766	0.155271	-4.479494	43128.626512
HLA B*0702	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.383418	-0.096147	-4.479565	24177.852409
HLA B*1517	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.491675	0.012088	-4.479587	31022.367805
HLA A*3201	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.586911	0.107303	-4.479608	38628.808905
HLA B*2705	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.489227	0.009579	-4.479647	30847.983450
HLA A*2601	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.400423	-0.079239	-4.479662	25143.358900
HLA A*3301	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.619344	0.139599	-4.479745	41623.980375
HLA A*0201	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.383690	-0.096147	-4.479838	24193.029913
HLA A*0301	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.359418	-0.120427	-4.479844	22877.982995
HLA B*1501	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.350802	-0.129168	-4.479970	22428.600295
HLA A*2501	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.492065	0.012088	-4.479977	31050.239695
HLA A*2601	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.391239	-0.088805	-4.480044	24617.228550
HLA A*2403	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.416959	-0.063193	-4.480152	26119.145822
HLA A*2403	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.432935	-0.047362	-4.480298	27097.889536
HLA A*3101	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.391627	-0.088805	-4.480431	24639.212479
HLA A*1101	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.467391	-0.013165	-4.480556	29335.308895
HLA B*0803	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.492772	0.012088	-4.480684	31100.842369
HLA B*4801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.414854	-0.065831	-4.480685	25992.845865
HLA B*1501	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.370303	-0.110482	-4.480784	23458.643582
HLA A*0206	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.506089	0.025261	-4.480828	32069.266971
HLA A*3002	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.433011	-0.047884	-4.480894	27102.581033
HLA A*0216	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.459111	-0.021825	-4.480936	28781.344674
HLA A*6802	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.417772	-0.063193	-4.480965	26168.081990
HLA B*4002	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.651668	0.170651	-4.481017	44840.229094
HLA A*0219	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.459520	-0.021825	-4.481345	28808.449906
HLA A*2603	1:68-76	9	HPAIVAVYD	1.071473	-0.891881	-4.660944	0.179592	-4.481352	45808.238262
HLA A*3101	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.417685	-0.063767	-4.481452	26162.844556
HLA A*2902	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.361253	-0.120427	-4.481679	22974.849790
HLA B*4801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.433081	-0.048602	-4.481683	27106.980049
HLA B*0801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.361328	-0.120427	-4.481755	22978.827459
HLA B*0802	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.447453	-0.034337	-4.481790	28019.019655
HLA B*5801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.372906	-0.108943	-4.481849	23599.680655
HLA A*6901	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.364044	-0.117875	-4.481919	23122.983476
HLA A*3101	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.367364	-0.114630	-4.481993	23300.416872
HLA B*5801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.352853	-0.129168	-4.482021	22534.777365
HLA A*2603	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.434176	-0.047884	-4.482060	27175.403183
HLA B*0702	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.491962	0.009850	-4.482112	31042.849527
HLA A*3002	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.494224	0.012088	-4.482136	31204.996185
HLA B*4001	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.385997	-0.096147	-4.482145	24321.897656
HLA B*5301	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.589463	0.107303	-4.482160	38856.426538

HLA B*4601	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.386120	-0.096147	-4.482267	24328.740715
HLA B*5801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.361849	-0.120427	-4.482276	23006.441503
HLA A*0101	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.367928	-0.114630	-4.482557	23330.689161
HLA B*4501	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.651969	0.169330	-4.482639	44871.290172
HLA A*6901	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.393842	-0.088805	-4.482647	24765.231219
HLA B*1501	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.403433	-0.079239	-4.482672	25318.209249
HLA B*3801	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.568726	0.086012	-4.482715	37044.718865
HLA B*4002	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.622640	0.139887	-4.482753	41941.111488
HLA A*2601	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.362348	-0.120427	-4.482774	23032.842647
HLA A*2602	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.542330	0.059501	-4.482829	34860.197177
HLA A*0216	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.481553	-0.001305	-4.482858	30307.726621
HLA A*0219	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.465882	-0.017067	-4.482949	29233.599729
HLA A*0211	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.547623	0.064589	-4.483034	35287.689952
HLA B*4403	1:584-592	9	TGMLDKGAD	1.089646	-0.910299	-4.662600	0.179347	-4.483253	45983.283189
HLA B*2705	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.439998	-0.043361	-4.483359	27542.161463
HLA A*3002	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.602789	0.119114	-4.483675	40067.213187
HLA A*8001	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.466629	-0.017067	-4.483696	29283.934883
HLA B*7301	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.534661	0.050897	-4.483764	34250.042931
HLA B*4801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.420580	-0.063193	-4.483773	26337.801878
HLA B*5801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.352870	-0.130925	-4.483795	22535.630755
HLA B*4002	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.603010	0.119119	-4.483891	40087.593732
HLA A*2403	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.374978	-0.108943	-4.483921	23712.556136
HLA A*2402	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.546575	0.062590	-4.483985	35202.650075
HLA A*2501	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.467360	-0.017067	-4.484427	29333.245858
HLA B*1502	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.616686	0.132177	-4.484510	41370.078082
HLA A*3101	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.421327	-0.063193	-4.484520	26383.150974
HLA B*5301	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.607039	0.122446	-4.484593	40461.255547
HLA B*4501	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.626258	0.141319	-4.484939	42291.992108
HLA A*3301	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.624830	0.139887	-4.484942	42153.113281
HLA B*4501	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.656548	0.171585	-4.484963	45346.910433
HLA B*1517	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.248893	-0.236114	-4.485007	17737.534753
HLA B*3501	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.421872	-0.063193	-4.485065	26416.285105
HLA B*7301	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.567263	0.082090	-4.485173	36920.074957
HLA B*4801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.441887	-0.043361	-4.485248	27662.218403
HLA B*5401	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.543173	0.057919	-4.485254	34927.966704
HLA A*2603	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.642777	0.157340	-4.485437	43931.635493
HLA B*1501	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.396735	-0.088805	-4.485539	24930.707487
HLA A*2501	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.494544	0.008974	-4.485570	31227.963551
HLA A*0201	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.396873	-0.088805	-4.485678	24938.666226
HLA A*3201	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.614689	0.128996	-4.485694	41180.278399
HLA B*0802	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.457133	-0.028622	-4.485755	28650.540146
HLA A*0212	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.438417	-0.047362	-4.485779	27442.066762
HLA A*0101	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.376816	-0.109105	-4.485921	23813.085391
HLA B*5301	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.536825	0.050897	-4.485928	34421.119882
HLA A*2501	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.476147	-0.009859	-4.486006	29932.789822
HLA B*1503	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.495920	0.009850	-4.486071	31327.119374
HLA B*2705	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.438694	-0.047418	-4.486112	27459.590462
HLA B*3801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.511479	0.025261	-4.486217	32469.735561
HLA A*3101	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.390184	-0.096147	-4.486332	24557.504876
HLA B*0803	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.478130	-0.008210	-4.486340	30069.773830
HLA B*3501	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.473203	-0.013165	-4.486368	29730.573823
HLA B*4501	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.657215	0.170651	-4.486564	45416.635362
HLA A*6802	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.372103	-0.114630	-4.486732	23556.057317
HLA A*1101	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.443534	-0.043361	-4.486895	27767.321895
HLA B*4402	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.439486	-0.047418	-4.486904	27509.698601
HLA B*4601	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.398198	-0.088805	-4.487003	25014.874727
HLA B*2705	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.496950	0.009850	-4.487100	31401.437984
HLA B*7301	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.573117	0.086012	-4.487106	37421.181098
HLA B*1509	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.485966	-0.001305	-4.487271	30617.215714
HLA A*2603	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.627010	0.139599	-4.487411	42365.269914
HLA A*0219	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.444159	-0.043361	-4.487520	27807.308683
HLA A*3101	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.377163	-0.110482	-4.487645	23832.159296
HLA B*4402	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.421827	-0.065831	-4.487658	26413.569970
HLA A*0301	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.369807	-0.117875	-4.487682	23431.881132
HLA A*0219	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.462866	-0.025025	-4.487890	29031.238090

HLA A*0101	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.379207	-0.108943	-4.488150	23944.592203
HLA A*2602	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.588915	0.100651	-4.488264	38807.478707
HLA A*1101	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.487079	-0.001305	-4.488384	30695.827805
HLA A*2602	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.607688	0.119114	-4.488573	40521.714563
HLA B*0702	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.440832	-0.047884	-4.488716	27595.107303
HLA B*0702	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.300077	-0.188668	-4.488745	19956.151402
HLA B*3501	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.441459	-0.047362	-4.488822	27634.995592
HLA B*5701	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.425795	-0.063193	-4.488989	26656.024760
HLA B*1517	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.487935	-0.001305	-4.489239	30756.333573
HLA A*3301	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.637895	0.148535	-4.489360	43440.532645
HLA B*5101	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.380262	-0.109105	-4.489368	24002.825277
HLA A*3201	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.611649	0.122274	-4.489375	40893.006801
HLA B*0802	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.498387	0.008974	-4.489414	31505.575800
HLA B*1502	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.626836	0.137283	-4.489554	42348.313144
HLA A*2602	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.633253	0.143550	-4.489703	42978.629175
HLA A*1101	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.479855	-0.009859	-4.489713	30189.414030
HLA B*4501	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.649809	0.160089	-4.489721	44648.757751
HLA A*3301	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.464804	-0.025025	-4.489829	29161.098686
HLA A*3002	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.515123	0.025261	-4.489862	32743.326818
HLA A*0301	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.359004	-0.130925	-4.489929	22856.210308
HLA A*6901	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.337318	-0.152648	-4.489966	21742.950489
HLA A*2603	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.638894	0.148535	-4.490358	43540.526152
HLA B*3501	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.426615	-0.063767	-4.490382	26706.400243
HLA B*1503	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.427330	-0.063193	-4.490523	26750.357894
HLA B*1503	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.455361	-0.035208	-4.490570	28533.911006
HLA B*1502	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.619668	0.128996	-4.490672	41655.066972
HLA B*3801	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.553264	0.062590	-4.490674	35749.036595
HLA A*6801	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.630407	0.139599	-4.490809	42697.980348
HLA B*4001	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.381898	-0.108943	-4.490840	24093.373065
HLA A*2501	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.489760	-0.001305	-4.491065	30885.889427
HLA A*2402	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.503265	0.012088	-4.491177	31861.407130
HLA A*2601	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.380723	-0.110482	-4.491204	24028.289889
HLA B*3901	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.500335	0.008974	-4.491362	31647.189263
HLA B*0802	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.442803	-0.048602	-4.491405	27720.643334
HLA A*8001	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.442883	-0.048602	-4.491485	27725.742634
HLA A*3101	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.255390	-0.236114	-4.491504	18004.853227
HLA B*3501	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.443713	-0.047884	-4.491596	27778.740820
HLA B*4403	1:109-117	9	PMTPKRAIE	1.045405	-0.863032	-4.674112	0.182373	-4.491740	47218.528962
HLA B*3501	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-3.985521	-0.506277	-4.491798	9672.098030
HLA A*6901	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.361121	-0.130925	-4.492046	22967.890526
HLA A*1101	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.483910	-0.008210	-4.492120	30472.626926
HLA B*2705	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.457824	-0.034337	-4.492161	28696.145300
HLA A*2501	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.443722	-0.048602	-4.492324	27779.341947
HLA B*0803	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.481575	-0.010996	-4.492570	30309.202309
HLA A*2402	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.531109	0.038504	-4.492605	33971.028750
HLA B*4403	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.652718	0.160089	-4.492629	44948.793866
HLA A*8001	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.449271	-0.043361	-4.492632	28136.588386
HLA B*4801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.428901	-0.063767	-4.492668	26847.348622
HLA B*1509	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.484626	-0.008210	-4.492836	30522.948758
HLA A*2601	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.383916	-0.108943	-4.492859	24205.597811
HLA A*2603	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.634218	0.141319	-4.492899	43074.296947
HLA B*1509	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.505128	0.012088	-4.493040	31998.387524
HLA A*2603	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.633581	0.140490	-4.493091	43011.192852
HLA A*0250	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.531593	0.038251	-4.493341	34008.908430
HLA B*5801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.351505	-0.141893	-4.493397	22464.909189
HLA B*3501	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.340060	-0.153340	-4.493400	21880.655373
HLA B*0803	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.518755	0.025261	-4.493494	33018.330227
HLA A*2501	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.465053	-0.028622	-4.493675	29177.825863
HLA B*4501	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.642235	0.148535	-4.493699	43876.769104
HLA B*4801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.445980	-0.047884	-4.493863	27924.140133
HLA B*4501	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.649234	0.155271	-4.493963	44589.618469
HLA B*1509	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.532265	0.038251	-4.494013	34061.568703
HLA A*3301	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.634521	0.140490	-4.494031	43104.367943
HLA B*4403	1:347-355	9	TIAINTFGG	0.703989	-0.531445	-4.666700	0.172544	-4.494156	46419.432622
HLA B*4402	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.446417	-0.047884	-4.494300	27952.252645

HLA B*0801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.385363	-0.108943	-4.494306	24286.397322
HLA B*5701	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.415173	-0.079239	-4.494412	26011.977007
HLA B*4001	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.431223	-0.063193	-4.494416	26991.231089
HLA B*4403	1:463-471	9	LVGKVIGTN	0.819884	-0.650554	-4.663838	0.169330	-4.494508	46114.569122
HLA A*3301	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.638085	0.143550	-4.494535	43459.572502
HLA B*4001	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.374412	-0.120427	-4.494839	23681.660247
HLA A*3101	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.415765	-0.079239	-4.495004	26047.463112
HLA B*5101	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.507095	0.012088	-4.495007	32143.607228
HLA B*4002	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.627306	0.132177	-4.495129	42394.157876
HLA A*2602	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.635134	0.139887	-4.495247	43165.273483
HLA B*7301	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.614640	0.119114	-4.495525	41175.600269
HLA B*4501	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.507795	0.012088	-4.495707	32195.469240
HLA B*3901	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.494433	-0.001305	-4.495738	31220.024388
HLA A*2301	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.534292	0.038504	-4.495789	34220.964918
HLA B*7301	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.470960	-0.025025	-4.495984	29577.368579
HLA A*0211	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.441817	-0.054260	-4.496076	27657.729282
HLA B*5101	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.487932	-0.008210	-4.496142	30756.167185
HLA A*0301	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.367209	-0.129168	-4.496377	23292.098880
HLA B*1509	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.555891	0.059501	-4.496390	35965.911117
HLA B*1801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.449133	-0.047418	-4.496551	28127.609086
HLA B*1801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.479676	-0.017067	-4.496743	30177.004157
HLA B*4002	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.645564	0.148535	-4.497029	44214.412710
HLA B*1509	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.555116	0.057919	-4.497197	35901.759773
HLA B*0802	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.495920	-0.001305	-4.497225	31327.119374
HLA A*0216	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.480355	-0.017067	-4.497422	30224.221536
HLA B*4601	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.382823	-0.114630	-4.497453	24144.782771
HLA B*4002	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.609950	0.112336	-4.497614	40733.372342
HLA A*2403	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.418514	-0.079239	-4.497753	26212.855239
HLA B*4002	1:150-158	9	NAVKVMDFG	0.669740	-0.528421	-4.639291	0.141319	-4.497972	43580.352207
HLA B*1503	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.536487	0.038504	-4.497983	34394.315445
HLA B*1517	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.480980	-0.017067	-4.498047	30267.746422
HLA B*4002	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.630184	0.132130	-4.498054	42676.041809
HLA A*2603	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.640026	0.141914	-4.498112	43654.209125
HLA A*2501	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.450829	-0.047362	-4.498191	28237.688680
HLA B*4403	1:161-169	9	RAIADSGNS	0.898555	-0.750454	-4.646304	0.148101	-4.498203	44289.823393
HLA A*0216	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.485054	-0.013165	-4.498219	30553.016448
HLA B*4402	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.451104	-0.047362	-4.498466	28255.567581
HLA A*6801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.463373	-0.035208	-4.498581	29065.181966
HLA B*7301	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.620939	0.122274	-4.498665	41777.159521
HLA B*4402	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.388206	-0.110482	-4.498688	24445.896719
HLA B*1517	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.470102	-0.028622	-4.498724	29519.022449
HLA A*2301	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.510894	0.012088	-4.498806	32426.026248
HLA B*0802	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.489114	-0.009859	-4.498973	30839.974050
HLA A*0219	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.433159	-0.065831	-4.498989	27111.819791
HLA A*2403	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.435287	-0.063767	-4.499054	27245.030759
HLA A*3001	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.310405	-0.188668	-4.499073	20436.434432
HLA B*1502	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.537372	0.038251	-4.499121	34464.535204
HLA A*0101	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.381343	-0.117875	-4.499218	24062.631869
HLA A*0212	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.435529	-0.063767	-4.499296	27260.216426
HLA B*1501	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.385008	-0.114630	-4.499638	24266.566029
HLA B*5101	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.471082	-0.028622	-4.499704	29585.690284
HLA A*3002	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.452361	-0.047362	-4.499723	28337.465869
HLA A*2602	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.622067	0.122274	-4.499793	41885.785201
HLA A*3101	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.346503	-0.153340	-4.499842	22207.650491
HLA A*3101	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.379579	-0.120427	-4.500005	23965.067891
HLA A*3301	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.637362	0.137283	-4.500079	43387.218466
HLA A*0216	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.456733	-0.043361	-4.500094	28624.202897
HLA B*4801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.403992	-0.096147	-4.500139	25350.828796
HLA B*5301	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.597063	0.096922	-4.500141	39542.437955
HLA B*1801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.525576	0.025261	-4.500314	33540.973360
HLA B*5101	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.478490	-0.021825	-4.500315	30094.673277
HLA B*1801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.382506	-0.117875	-4.500381	24127.155428
HLA B*1517	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.478562	-0.021825	-4.500388	30099.720774
HLA A*2501	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.465182	-0.035208	-4.500390	29186.508839
HLA A*0206	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.492199	-0.008210	-4.500409	31059.815938

HLA B*0803	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.538914	0.038504	-4.500410	34587.063245
HLA A*0219	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.437237	-0.063193	-4.500431	27367.641682
HLA B*2705	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.452608	-0.047884	-4.500491	28353.567210
HLA A*2601	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.369584	-0.130925	-4.500509	23419.841657
HLA B*3901	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.489995	-0.010996	-4.500991	30902.602871
HLA B*4002	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.642932	0.141914	-4.501019	43947.324202
HLA B*7301	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.574466	0.073404	-4.501062	37537.564816
HLA B*5701	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.390612	-0.110482	-4.501093	24581.696099
HLA B*0803	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.479277	-0.021825	-4.501102	30149.263693
HLA B*4403	1:361-369	9	QVPDVRGQS	1.068447	-0.896862	-4.672900	0.171585	-4.501315	47086.902110
HLA B*0802	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.447502	-0.054260	-4.501762	28022.203012
HLA A*1101	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.453181	-0.048602	-4.501783	28391.018998
HLA B*3901	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.488649	-0.013165	-4.501814	30806.957250
HLA A*0219	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.422628	-0.079239	-4.501867	26462.341962
HLA B*3801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.575406	0.073404	-4.502001	37618.882394
HLA B*3801	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.553020	0.050897	-4.502123	35728.928826
HLA B*5101	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.500821	-0.001305	-4.502126	31682.649126
HLA A*6802	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.266277	-0.236114	-4.502391	18461.929955
HLA A*0216	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.436565	-0.065831	-4.502396	27325.330433
HLA A*0203	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.413611	-0.088805	-4.502416	25918.565064
HLA A*2403	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.413935	-0.088805	-4.502740	25937.922175
HLA B*2705	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.501489	-0.001305	-4.502794	31731.364031
HLA B*5101	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.512411	0.009579	-4.502832	32539.546597
HLA A*3301	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.621961	0.119119	-4.502842	41875.589557
HLA A*2603	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.576332	0.073404	-4.502927	37699.152420
HLA A*0201	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.392466	-0.110482	-4.502947	24686.844922
HLA B*2705	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.467762	-0.035208	-4.502970	29360.394336
HLA A*2602	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.565611	0.062590	-4.503020	36779.928965
HLA A*2603	1:119-127	9	IADACQALN	0.752755	-0.592666	-4.663277	0.160089	-4.503188	46054.983196
HLA B*3801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.562740	0.059501	-4.503239	36537.583045
HLA B*4001	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.424047	-0.079239	-4.503286	26548.951021
HLA A*2603	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.646985	0.143550	-4.503435	44359.362808
HLA B*3901	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.486506	-0.017067	-4.503573	30655.335646
HLA B*4501	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.643529	0.139887	-4.503642	44007.754250
HLA B*1801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.493848	-0.009859	-4.503707	31177.997380
HLA A*2301	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.493865	-0.009859	-4.503723	31179.178089
HLA A*0101	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.374610	-0.129168	-4.503778	23692.424365
HLA B*1517	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.393335	-0.110482	-4.503816	24736.309055
HLA A*6801	1:302-310	9	GNLSGPRTD	1.034308	-0.857907	-4.680226	0.176401	-4.503825	47887.902248
HLA A*0206	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.482148	-0.021825	-4.503973	30349.237267
HLA B*5701	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.415169	-0.088805	-4.503973	26011.695564
HLA A*8001	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.449741	-0.054260	-4.504001	28167.048026
HLA B*1502	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.611318	0.107303	-4.504015	40861.825740
HLA A*8001	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.438238	-0.065831	-4.504069	27430.786232
HLA B*1801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.407982	-0.096147	-4.504129	25584.774166
HLA A*6901	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.375021	-0.129168	-4.504189	23714.865330
HLA A*0201	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.395113	-0.109105	-4.504219	24837.819032
HLA A*2602	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.586315	0.082090	-4.504225	38575.765054
HLA A*2603	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.626829	0.122446	-4.504383	42347.625850
HLA B*4403	1:359-367	9	DVQVPDVRG	0.809825	-0.639174	-4.675142	0.170651	-4.504491	47330.547414
HLA A*0211	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.514214	0.009579	-4.504634	32674.846214
HLA A*3201	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.623772	0.119114	-4.504658	42050.618439
HLA B*0702	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.461761	-0.043361	-4.505122	28957.515638
HLA A*0201	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.396666	-0.108943	-4.505609	24926.796495
HLA A*3301	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.634730	0.128996	-4.505735	43125.126837
HLA B*1502	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.451489	-0.054260	-4.505749	28280.647662
HLA B*5301	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.565263	0.059501	-4.505762	36750.492401
HLA A*1101	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.488747	-0.017067	-4.505814	30813.957858
HLA B*4501	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.647782	0.141914	-4.505868	44440.790413
HLA A*2603	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.634878	0.128996	-4.505883	43139.827378
HLA A*3301	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.628168	0.122274	-4.505894	42478.412093
HLA B*7301	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.484133	-0.021825	-4.505958	30488.292037
HLA A*0301	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.364180	-0.141893	-4.506073	23130.239995
HLA B*5701	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.409934	-0.096147	-4.506081	25700.052463
HLA A*0101	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.395837	-0.110482	-4.506319	24879.239443

HLA A*0212	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.417551	-0.088805	-4.506356	26154.778129
HLA A*2403	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.410216	-0.096147	-4.506363	25716.742012
HLA A*6901	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.395891	-0.110482	-4.506373	24882.335296
HLA B*3901	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.397569	-0.108943	-4.506511	24978.633182
HLA B*5801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.361222	-0.145362	-4.506584	22973.234059
HLA B*3801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.571174	0.064589	-4.506586	37254.133508
HLA B*1502	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.564645	0.057919	-4.506726	36698.240950
HLA B*0801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.418225	-0.088805	-4.507030	26195.418578
HLA B*4601	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.397961	-0.109105	-4.507066	25001.210362
HLA A*0202	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.452918	-0.054260	-4.507177	28373.821875
HLA B*0801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.376327	-0.130925	-4.507252	23786.304621
HLA A*0101	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.354077	-0.153340	-4.507417	22598.382407
HLA B*1502	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.398316	-0.109105	-4.507421	25021.642027
HLA B*1517	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.460081	-0.047362	-4.507444	28845.722271
HLA B*0803	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.517026	0.009579	-4.507446	32887.123239
HLA A*2501	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.460067	-0.047418	-4.507486	28844.785973
HLA A*6901	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.392863	-0.114630	-4.507492	24709.425716
HLA A*0301	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.362200	-0.145362	-4.507562	23024.993862
HLA B*1509	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.472510	-0.035208	-4.507719	29683.164127
HLA A*6802	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.376877	-0.130925	-4.507802	23816.435106
HLA A*0201	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.393175	-0.114630	-4.507805	24727.210922
HLA A*2501	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.442207	-0.065831	-4.508037	27682.578229
HLA B*5401	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.459574	-0.048602	-4.508176	28812.034691
HLA A*6801	1:240-248	9	HEGLSADLD	1.041172	-0.900682	-4.648731	0.140490	-4.508241	44538.026212
HLA B*1509	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.546853	0.038504	-4.508349	35225.129457
HLA B*1502	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.559286	0.050897	-4.508389	36248.168876
HLA A*2603	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.590833	0.082090	-4.508743	38979.171828
HLA B*5101	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.499174	-0.009859	-4.509033	31562.725531
HLA A*8001	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.429848	-0.079239	-4.509087	26905.944670
HLA B*4501	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.646480	0.137283	-4.509198	44307.797267
HLA B*5801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.353518	-0.155719	-4.509237	22569.304502
HLA B*4403	1:589-597	9	KGADVDAGG	0.876436	-0.727901	-4.658009	0.148535	-4.509474	45499.757584
HLA A*3002	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.492441	-0.017067	-4.509507	31077.127867
HLA A*6802	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.320994	-0.188551	-4.509545	20940.847550
HLA B*2705	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.492572	-0.017067	-4.509639	31086.544227
HLA A*2301	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.547912	0.038251	-4.509661	35311.178773
HLA A*2601	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.391890	-0.117875	-4.509765	24654.146088
HLA A*0211	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.519667	0.009850	-4.509817	33087.709712
HLA A*2402	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.583375	0.073404	-4.509971	38315.574546
HLA B*0702	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.444305	-0.065831	-4.510135	27816.637183
HLA B*1501	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.401114	-0.109105	-4.510219	25183.381418
HLA A*3301	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.629418	0.119114	-4.510304	42600.843653
HLA B*0803	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.519345	0.008974	-4.510371	33063.195683
HLA B*4002	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.647913	0.137283	-4.510631	44454.255959
HLA B*2705	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.463293	-0.047362	-4.510655	29059.836318
HLA B*4403	1:275-283	9	RVHNGEPPE	0.636065	-0.478810	-4.667964	0.157255	-4.510709	46554.734129
HLA A*2602	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.618115	0.107303	-4.510812	41506.377100
HLA A*0101	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.365545	-0.145362	-4.510907	23203.056083
HLA A*0212	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.431747	-0.079239	-4.510985	27023.813103
HLA B*4501	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.643179	0.132177	-4.511003	43972.295059
HLA B*4601	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.402279	-0.108943	-4.511222	25251.046854
HLA A*1101	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.489410	-0.021825	-4.511235	30861.003162
HLA A*0203	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.448134	-0.063193	-4.511328	28063.012295
HLA B*4402	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.432228	-0.079239	-4.511467	27053.799873
HLA A*0201	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.394021	-0.117875	-4.511896	24775.415577
HLA A*2402	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.571449	0.059501	-4.511949	37277.721238
HLA A*0216	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.457889	-0.054260	-4.512149	28700.492433
HLA A*1101	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.487145	-0.025025	-4.512170	30700.477866
HLA B*5301	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.575037	0.062590	-4.512447	37586.944264
HLA B*0803	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.487523	-0.025025	-4.512548	30727.229390
HLA B*1501	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.381837	-0.130925	-4.512762	24089.984399
HLA A*3101	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.381881	-0.130925	-4.512806	24092.460685
HLA A*0219	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.464294	-0.048602	-4.512896	29126.885219
HLA B*5801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.360278	-0.152648	-4.512925	22923.326722
HLA B*3901	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.488029	-0.025025	-4.513053	30762.989827

HLA B*4403	1:7-15	9	LSDRYELGE	0.877419	-0.745242	-4.645348	0.132177	-4.513171	44192.412239
HLA B*0801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.395421	-0.117875	-4.513296	24855.427721
HLA A*3101	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.404427	-0.109105	-4.513532	25376.213354
HLA B*5101	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.470210	-0.043361	-4.513571	29526.369316
HLA A*3301	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.625932	0.112336	-4.513596	42260.201559
HLA B*0802	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.500662	-0.013165	-4.513827	31670.996095
HLA A*0301	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.360604	-0.153340	-4.513944	22940.570964
HLA A*0219	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.466601	-0.047362	-4.513964	29282.033871
HLA A*0101	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.383274	-0.130925	-4.514199	24169.874956
HLA B*0802	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.466843	-0.047362	-4.514206	29298.354911
HLA B*4002	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.653829	0.139599	-4.514231	45063.959611
HLA B*1509	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.504475	-0.009859	-4.514334	31950.299745
HLA A*2601	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.399841	-0.114630	-4.514470	25109.647868
HLA B*5401	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.485916	-0.028622	-4.514539	30613.737561
HLA A*0211	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.523783	0.008974	-4.514809	33402.810109
HLA B*0802	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.471474	-0.043361	-4.514835	29612.431598
HLA A*3201	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.574522	0.059501	-4.515022	37542.438910
HLA B*2705	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.466432	-0.048602	-4.515034	29270.630388
HLA A*6801	1:574-582	9	AEPRLRALG	0.825573	-0.668233	-4.672491	0.157340	-4.515151	47042.599088
HLA B*3901	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.505445	-0.009859	-4.515304	32021.765603
HLA B*4002	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.502295	-0.013165	-4.515460	31790.299158
HLA B*4403	1:16-24	9	ILGFGGMSE	0.958227	-0.802956	-4.670771	0.155271	-4.515500	46856.676941
HLA A*0203	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.400924	-0.114630	-4.515553	25172.348452
HLA B*3801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.573477	0.057919	-4.515558	37452.167920
HLA B*0802	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.480461	-0.035208	-4.515669	30231.580367
HLA B*0801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.401149	-0.114630	-4.515779	25185.425090
HLA A*2603	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.623211	0.107303	-4.515908	41996.283658
HLA B*1517	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.468509	-0.047418	-4.515927	29410.947808
HLA A*6802	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.427323	-0.088805	-4.516127	26749.923748
HLA B*1509	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.481967	-0.034337	-4.516304	30336.597577
HLA B*0802	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.469355	-0.047418	-4.516773	29468.283211
HLA B*1509	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.526365	0.009579	-4.516786	33601.996996
HLA B*2705	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.503787	-0.013165	-4.516952	31899.695521
HLA B*3901	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.451424	-0.065831	-4.517254	28276.364121
HLA B*1517	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.504090	-0.013165	-4.517255	31921.965313
HLA B*1503	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.516065	-0.001305	-4.517370	32814.436167
HLA A*3002	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.421392	-0.096147	-4.517540	26387.147714
HLA B*4601	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.386651	-0.130925	-4.517576	24358.504075
HLA A*6901	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.372347	-0.145362	-4.517709	23569.314354
HLA B*3901	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.362211	-0.155719	-4.517930	23025.616684
HLA A*0216	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.454266	-0.063767	-4.518033	28462.067376
HLA A*0203	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.409015	-0.109105	-4.518121	25645.747454
HLA A*0219	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.454471	-0.063767	-4.518238	28475.466496
HLA A*3301	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.625661	0.107303	-4.518358	42233.918090
HLA A*2301	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.543747	0.025261	-4.518485	34974.102515
HLA B*1801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.452782	-0.065831	-4.518612	28364.920316
HLA B*5401	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.543920	0.025261	-4.518659	34988.106563
HLA B*1517	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.365409	-0.153340	-4.518749	23195.776719
HLA B*5101	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.505605	-0.013165	-4.518770	32033.547696
HLA A*3201	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.510600	-0.008210	-4.518810	32404.106009
HLA B*4002	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.641424	0.122274	-4.519150	43794.953361
HLA A*0202	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.470661	-0.048602	-4.519263	29557.054252
HLA A*0101	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.377419	-0.141893	-4.519312	23846.216738
HLA A*6801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.410221	-0.109105	-4.519326	25717.020263
HLA B*1503	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.472217	-0.047418	-4.519635	29663.098084
HLA A*6802	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.440440	-0.079239	-4.519678	27570.187721
HLA A*0206	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.558187	0.038504	-4.519683	36156.510823
HLA A*0211	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.509846	-0.009859	-4.519704	32347.882700
HLA A*0301	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.367258	-0.152648	-4.519906	23294.745192
HLA B*5701	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.405291	-0.114630	-4.519921	25426.783636
HLA A*2402	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.584543	0.064589	-4.519954	38418.732822
HLA A*2603	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.642315	0.122274	-4.520041	43884.840373
HLA B*5301	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.593565	0.073404	-4.520161	39225.190250
HLA B*4403	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.639295	0.119119	-4.520176	43580.823739
HLA B*4403	1:440-448	9	AVKKLTAAG	0.688292	-0.556162	-4.652464	0.132130	-4.520334	44922.539394

HLA A*2603	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.660594	0.139887	-4.520706	45771.328334
HLA B*4403	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.660704	0.139887	-4.520817	45782.967851
HLA B*0802	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.455089	-0.065831	-4.520919	28516.010250
HLA B*4001	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.375923	-0.145362	-4.521285	23764.181737
HLA B*4403	1:287-295	9	VLTDAERTS	1.054637	-0.912723	-4.663540	0.141914	-4.521626	46082.896716
HLA B*4403	1:298-306	9	SSAAGNLSG	0.649359	-0.537023	-4.634056	0.112336	-4.521720	43058.221072
HLA A*1101	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.474380	-0.047362	-4.521743	29811.263516
HLA B*1503	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.530745	0.008974	-4.521771	33942.554867
HLA A*6801	1:100-108	9	LRDIVHTEG	0.726007	-0.586120	-4.661686	0.139887	-4.521799	45886.615564
HLA B*4002	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.650841	0.128996	-4.521845	44754.921949
HLA B*5401	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.531541	0.009579	-4.521962	34004.861013
HLA B*1503	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.512120	-0.009859	-4.521979	32517.725535
HLA A*0201	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.391070	-0.130925	-4.521995	24607.641711
HLA A*0219	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.413035	-0.109105	-4.522141	25884.234762
HLA B*4002	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.521025	-0.001305	-4.522330	33191.334127
HLA B*5101	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.497311	-0.025025	-4.522336	31427.610143
HLA A*6901	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.351977	-0.170363	-4.522340	22489.350542
HLA B*3901	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.459353	-0.063193	-4.522546	28797.386644
HLA A*2902	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.468377	-0.054260	-4.522637	29402.039000
HLA A*0211	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.548107	0.025261	-4.522846	35327.037787
HLA B*4001	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.408226	-0.114630	-4.522856	25599.172938
HLA B*1503	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.475529	-0.047362	-4.522892	29890.231706
HLA B*0803	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.468657	-0.054260	-4.522917	29420.973445
HLA B*4801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.443783	-0.079239	-4.523022	27783.249584
HLA A*0201	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.402608	-0.120427	-4.523035	25270.178850
HLA A*0203	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.392195	-0.130925	-4.523120	24671.491092
HLA B*5101	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.468892	-0.054260	-4.523151	29436.894171
HLA A*0250	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.581155	0.057919	-4.523236	38120.191958
HLA A*6801	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.642416	0.119119	-4.523296	43895.050282
HLA B*4403	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.660713	0.137283	-4.523431	45783.958585
HLA A*0202	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.581411	0.057919	-4.523492	38142.677222
HLA A*6801	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.660955	0.137283	-4.523673	45809.477366
HLA B*4402	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.409048	-0.114630	-4.523678	25647.689897
HLA B*4002	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.646139	0.122446	-4.523693	44273.054356
HLA A*3101	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.414762	-0.108943	-4.523705	25987.362326
HLA B*4501	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.663317	0.139599	-4.523718	46059.218981
HLA A*0301	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.368583	-0.155719	-4.524302	23365.930137
HLA A*0206	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.428507	-0.096147	-4.524654	26822.959189
HLA A*0212	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.415617	-0.109105	-4.524723	26038.587050
HLA B*3801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.562998	0.038251	-4.524747	36559.332586
HLA A*0206	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.533721	0.008974	-4.524748	34176.007490
HLA A*0250	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.598156	0.073404	-4.524751	39642.036072
HLA B*1517	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.470506	-0.054260	-4.524766	29546.502710
HLA A*0250	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.584325	0.059501	-4.524824	38399.408462
HLA B*0702	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.414469	-0.110482	-4.524950	25969.794673
HLA A*2601	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.396004	-0.129168	-4.525172	24888.797448
HLA A*2603	1:540-548	9	PAGTTVPVD	1.245620	-1.108337	-4.662464	0.137283	-4.525181	45968.857114
HLA A*3201	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.563745	0.038504	-4.525242	36622.281373
HLA A*0201	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.396194	-0.129168	-4.525362	24899.706134
HLA B*1509	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.508330	-0.017067	-4.525397	32235.205395
HLA B*4501	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.654473	0.128996	-4.525478	45130.807885
HLA A*3301	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.585006	0.059501	-4.525505	38459.699341
HLA B*5101	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.491210	-0.034337	-4.525547	30989.155737
HLA B*0802	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.461869	-0.063767	-4.525636	28964.722754
HLA B*5401	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.537732	0.012088	-4.525644	34493.073759
HLA A*6901	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.370037	-0.155719	-4.525757	23444.307285
HLA B*5801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.355426	-0.170363	-4.525789	22668.665698
HLA B*3901	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.478382	-0.047418	-4.525800	30087.185002
HLA A*0101	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.373181	-0.152648	-4.525829	23614.622967
HLA A*2603	1:284-292	9	APKVLTDAE	0.940306	-0.821187	-4.645005	0.119119	-4.525886	44157.520916
HLA B*1517	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.405503	-0.120427	-4.525930	25439.166698
HLA A*0201	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.380666	-0.145362	-4.526029	24025.170323
HLA B*0803	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.509136	-0.017067	-4.526203	32295.076314
HLA A*2501	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.513152	-0.013165	-4.526317	32595.045003
HLA A*0250	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.518149	-0.008210	-4.526359	32972.276993

HLA A*2501	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.417257	-0.109105	-4.526363	26137.097302
HLA A*2601	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.381118	-0.145362	-4.526480	24050.138201
HLA A*0216	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.501458	-0.025025	-4.526483	31729.132488
HLA B*4002	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.395590	-0.130925	-4.526515	24865.111094
HLA A*0202	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.565078	0.038504	-4.526574	36734.789286
HLA B*1517	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.516772	-0.009859	-4.526631	32867.913957
HLA B*3901	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.478130	-0.048602	-4.526732	30069.773830
HLA B*5301	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.612746	0.086012	-4.526735	40996.450255
HLA A*0216	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.478245	-0.048602	-4.526847	30077.745919
HLA B*4001	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.438050	-0.088805	-4.526855	27418.917000
HLA B*4001	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.417751	-0.109105	-4.526856	26166.807923
HLA A*1101	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.479016	-0.047884	-4.526899	30131.164564
HLA B*4601	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.416529	-0.110482	-4.527011	26093.300409
HLA A*2501	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.463340	-0.063767	-4.527107	29062.980698
HLA B*3501	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.187008	-0.340176	-4.527184	15381.823526
HLA B*4601	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.371588	-0.155719	-4.527307	23528.165434
HLA A*2501	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.116439	-0.410971	-4.527410	13074.909542
HLA A*2602	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.510393	-0.017067	-4.527460	32388.683050
HLA A*0206	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.448261	-0.079239	-4.527500	28071.211653
HLA B*4601	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.407126	-0.120427	-4.527553	25534.442210
HLA A*6802	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.418693	-0.108943	-4.527636	26223.634912
HLA B*0802	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.479801	-0.047884	-4.527684	30185.657872
HLA B*4001	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.398706	-0.129168	-4.527874	25044.122595
HLA B*0803	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.537814	0.009850	-4.527964	34499.605507
HLA B*4501	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.647159	0.119114	-4.528045	44377.124827
HLA B*1501	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.374765	-0.153340	-4.528104	23700.885319
HLA B*4001	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.375516	-0.152648	-4.528164	23741.950987
HLA B*1801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.515149	-0.013165	-4.528314	32745.275392
HLA A*0216	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.480966	-0.047362	-4.528328	30266.763967
HLA B*3501	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.413928	-0.114630	-4.528558	25937.501214
HLA B*5301	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.593304	0.064589	-4.528715	39201.642685
HLA B*1503	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.494513	-0.034337	-4.528850	31225.767410
HLA B*1509	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.518083	-0.010996	-4.529079	32967.282833
HLA B*0803	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.500631	-0.028622	-4.529253	31668.768798
HLA A*2301	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.539250	0.009850	-4.529400	34613.830639
HLA A*0216	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.450214	-0.079239	-4.529452	28197.693187
HLA B*4002	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.648762	0.119114	-4.529647	44541.158618
HLA B*5101	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.481051	-0.048602	-4.529652	30272.659175
HLA B*4501	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.651978	0.122274	-4.529704	44872.261178
HLA B*7301	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.567970	0.038251	-4.529719	36980.243720
HLA B*5701	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.420725	-0.109105	-4.529831	26346.637404
HLA B*5101	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.513076	-0.017067	-4.530143	32589.402753
HLA A*8001	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.467210	-0.063193	-4.530403	29323.091481
HLA A*3002	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.482030	-0.048602	-4.530632	30341.029076
HLA A*0212	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.434498	-0.096147	-4.530645	27195.551829
HLA B*5701	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.377335	-0.153340	-4.530675	23841.572996
HLA B*5401	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.529527	-0.001305	-4.530832	33847.570030
HLA B*4001	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.420387	-0.110482	-4.530868	26326.120733
HLA A*8001	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.434759	-0.096147	-4.530906	27211.887600
HLA B*2705	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.505885	-0.025025	-4.530909	32054.176790
HLA B*3801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.569678	0.038504	-4.531174	37125.973015
HLA B*1503	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.416625	-0.114630	-4.531255	26099.088688
HLA B*1509	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.540307	0.008974	-4.531333	34698.198937
HLA B*4002	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.543662	0.012088	-4.531574	34967.291762
HLA B*4501	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.654034	0.122446	-4.531588	45085.174423
HLA A*2603	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.650775	0.119114	-4.531661	44748.143125
HLA B*5101	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.496635	-0.035208	-4.531843	31378.682541
HLA B*1801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.483999	-0.047884	-4.531883	30478.892004
HLA A*6901	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.378768	-0.153340	-4.532108	23920.380922
HLA B*0801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.378850	-0.153340	-4.532190	23924.910582
HLA A*0250	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.596779	0.064589	-4.532190	39516.562080
HLA B*1501	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.411969	-0.120427	-4.532395	25820.738768
HLA B*0803	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.522712	-0.009859	-4.532570	33320.509956
HLA A*6801	1:282-290	9	PEAPKVLTD	1.255655	-1.112105	-4.676253	0.143550	-4.532703	47451.815579
HLA A*0212	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.387548	-0.145362	-4.532910	24408.894865

HLA A*0202	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.597573	0.064589	-4.532984	39588.885898
HLA B*1801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.489784	-0.043361	-4.533145	30887.560365
HLA A*2402	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.485806	-0.047418	-4.533224	30605.954555
HLA B*4402	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.404262	-0.129168	-4.533430	25366.605398
HLA B*1503	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.520379	-0.013165	-4.533544	33141.991445
HLA A*3002	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.591502	0.057919	-4.533583	39039.316987
HLA B*1801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.485014	-0.048602	-4.533616	30550.206674
HLA B*0803	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.454452	-0.079239	-4.533691	28474.234130
HLA B*1503	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.424628	-0.109105	-4.533733	26584.450574
HLA B*0702	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.288423	-0.245356	-4.533780	19427.787500
HLA A*0202	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.512130	-0.021825	-4.533955	32518.429211
HLA B*0803	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.499656	-0.034337	-4.533993	31597.748872
HLA A*6801	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.663084	0.128996	-4.534088	46034.557234
HLA A*2403	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.404951	-0.129168	-4.534119	25406.845825
HLA B*5401	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.543100	0.008974	-4.534127	34922.109545
HLA B*7301	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.572671	0.038504	-4.534168	37382.736416
HLA B*0803	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.490855	-0.043361	-4.534216	30963.851242
HLA A*2902	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.471190	-0.063193	-4.534383	29593.053744
HLA B*4001	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.381064	-0.153340	-4.534403	24047.145890
HLA A*2403	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.425300	-0.109105	-4.534405	26625.614625
HLA B*4601	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.405510	-0.129168	-4.534678	25439.579570
HLA B*4801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.445876	-0.088805	-4.534681	27917.493998
HLA A*2402	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.592618	0.057919	-4.534699	39139.765221
HLA B*0803	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.499546	-0.035208	-4.534754	31589.715698
HLA A*2902	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.424334	-0.110482	-4.534816	26566.479284
HLA B*5701	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.405714	-0.129168	-4.534882	25451.555790
HLA B*3801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.547304	0.012088	-4.535216	35261.736762
HLA A*6801	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.608693	0.073404	-4.535289	40615.648567
HLA B*3901	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.446809	-0.088805	-4.535614	27977.517560
HLA A*2301	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.545325	0.009579	-4.535746	35101.480356
HLA A*3101	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.406642	-0.129168	-4.535810	25506.001530
HLA A*2601	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.394061	-0.141893	-4.535953	24777.694230
HLA B*3901	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.195795	-0.340176	-4.535971	15696.213535
HLA A*6802	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.418110	-0.117875	-4.535985	26188.475497
HLA A*3002	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.507416	-0.028622	-4.536039	32167.439448
HLA A*6802	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.383406	-0.152648	-4.536054	24177.198420
HLA B*1502	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.600703	0.064589	-4.536114	39875.192635
HLA B*1801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.501876	-0.034337	-4.536214	31759.701098
HLA B*1509	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.427135	-0.109105	-4.536240	26738.349123
HLA B*1502	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.528191	-0.008210	-4.536400	33743.539726
HLA B*1801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.473309	-0.063193	-4.536502	29737.812464
HLA A*8001	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.416099	-0.120427	-4.536526	26067.480572
HLA B*0803	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.535237	-0.001305	-4.536542	34295.468817
HLA B*4002	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.633488	0.096922	-4.536565	43001.886428
HLA B*5701	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.427654	-0.108943	-4.536597	26770.336224
HLA A*0250	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.502417	-0.034337	-4.536754	31799.243480
HLA A*2301	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.545847	0.008974	-4.536873	35143.662397
HLA B*5801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.348455	-0.188551	-4.537006	22307.712353
HLA B*5101	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.489377	-0.047884	-4.537261	30858.665886
HLA B*5101	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.489908	-0.047418	-4.537326	30896.417843
HLA B*7301	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.536151	-0.001305	-4.537456	34367.717805
HLA A*0201	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.384127	-0.153340	-4.537467	24217.386144
HLA B*4403	1:233-241	9	PIPPSARHE	1.037252	-0.897653	-4.677096	0.139599	-4.537498	47544.063683
HLA A*3101	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.385145	-0.152648	-4.537792	24274.181430
HLA A*3001	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.198248	-0.339553	-4.537800	15785.115380
HLA A*1101	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.474317	-0.063767	-4.538084	29806.909392
HLA B*0801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.427656	-0.110482	-4.538138	26770.481049
HLA B*0702	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.475189	-0.063193	-4.538382	29866.793988
HLA A*2902	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.449821	-0.088805	-4.538626	28172.229444
HLA B*4403	1:609-617	9	PAGTGVNRD	1.237333	-1.108337	-4.667684	0.128996	-4.538689	46524.772916
HLA B*4402	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.429790	-0.108943	-4.538732	26902.305961
HLA B*1517	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.393410	-0.145362	-4.538772	24740.591688
HLA B*4801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.429846	-0.108943	-4.538789	26905.799112
HLA A*3301	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.530690	-0.008210	-4.538900	33938.331744
HLA B*1503	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.521993	-0.017067	-4.539059	33265.395946

HLA A*3101	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.421266	-0.117875	-4.539141	26379.440257
HLA A*1101	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.150628	-0.388552	-4.539180	14145.828830
HLA A*3002	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.548281	0.008974	-4.539308	35341.183154
HLA B*4801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.430367	-0.109105	-4.539473	26938.132265
HLA A*0301	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.369276	-0.170363	-4.539639	23403.250001
HLA B*1502	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.599239	0.059501	-4.539738	39741.025067
HLA B*5801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.351192	-0.188668	-4.539860	22448.751158
HLA B*1502	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.613277	0.073404	-4.539873	41046.604601
HLA A*0206	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.530091	-0.009859	-4.539950	33891.545357
HLA A*0212	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.409201	-0.130925	-4.540126	25656.710308
HLA A*6802	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.429693	-0.110482	-4.540175	26896.339545
HLA B*1509	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.550081	0.009850	-4.540231	35487.940005
HLA B*1503	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.461017	-0.079239	-4.540255	28907.897943
HLA B*5301	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.370014	-0.170363	-4.540377	23443.039009
HLA B*0803	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.527216	-0.013165	-4.540381	33667.866948
HLA A*3201	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.511763	-0.028622	-4.540385	32490.997098
HLA B*4001	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.422579	-0.117875	-4.540454	26459.335808
HLA A*0212	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.431566	-0.108943	-4.540509	27012.558368
HLA A*0216	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.477334	-0.063193	-4.540527	30014.677832
HLA B*4801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.430050	-0.110482	-4.540532	26918.465586
HLA B*5701	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.420117	-0.120427	-4.540543	26309.747366
HLA A*3201	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.552872	0.012088	-4.540784	35716.753660
HLA A*3002	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.605517	0.064589	-4.540928	40319.662569
HLA B*3801	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.551112	0.009579	-4.541533	35572.321942
HLA A*3301	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.524920	-0.017067	-4.541987	33490.386174
HLA A*2301	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.540814	-0.001305	-4.542119	34738.768732
HLA A*8001	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.433147	-0.109105	-4.542252	27111.086441
HLA B*4801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.424477	-0.117875	-4.542353	26575.247755
HLA B*4402	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.433356	-0.109105	-4.542461	27124.143033
HLA B*0802	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.463321	-0.079239	-4.542560	29061.722905
HLA A*2501	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.499297	-0.043361	-4.542658	31571.605824
HLA A*2403	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.428091	-0.114630	-4.542720	26797.287148
HLA A*2902	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.463674	-0.079239	-4.542912	29085.315581
HLA A*0250	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.581475	0.038504	-4.542971	38148.249016
HLA A*6801	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.602559	0.059501	-4.543058	40045.976417
HLA A*6801	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.662379	0.119114	-4.543265	45959.905274
HLA A*6802	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.154947	-0.388552	-4.543499	14287.187756
HLA B*3901	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.495751	-0.047884	-4.543635	31314.919461
HLA A*0206	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.496329	-0.047362	-4.543692	31356.622124
HLA B*5701	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.426110	-0.117875	-4.543985	26675.355389
HLA B*4601	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.398901	-0.145362	-4.544263	25055.370452
HLA B*4402	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.426423	-0.117875	-4.544298	26694.555620
HLA A*3002	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.536094	-0.008210	-4.544304	34363.255882
HLA A*2301	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.536177	-0.008210	-4.544386	34369.763047
HLA A*0212	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.429829	-0.114630	-4.544459	26904.780230
HLA B*1502	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.554319	0.009579	-4.544740	35835.977992
HLA A*6801	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.583143	0.038251	-4.544891	38295.059022
HLA A*8001	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.403177	-0.141893	-4.545069	25303.284061
HLA A*6801	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.667583	0.122446	-4.545137	46513.951338
HLA A*0250	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.557254	0.012088	-4.545166	36078.939875
HLA B*0702	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.430572	-0.114630	-4.545202	26950.813960
HLA A*8001	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.434730	-0.110482	-4.545212	27210.121098
HLA A*0206	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.543930	-0.001305	-4.545235	34988.863699
HLA B*0802	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.436190	-0.109105	-4.545295	27301.688345
HLA A*2603	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.583838	0.038504	-4.545335	38356.431066
HLA B*1501	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.356798	-0.188551	-4.545349	22740.397774
HLA B*7301	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.554338	0.008974	-4.545364	35837.528975
HLA A*0101	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.389707	-0.155719	-4.545427	24530.550444
HLA B*4002	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.491221	-0.054260	-4.545481	30989.993988
HLA B*1501	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.400141	-0.145362	-4.545503	25127.041463
HLA B*2705	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.430927	-0.114630	-4.545556	26972.838893
HLA A*2602	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.498216	-0.047362	-4.545578	31493.136014
HLA A*0202	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.134671	-0.410971	-4.545642	13635.488346
HLA A*2501	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.466409	-0.079239	-4.545647	29269.046922
HLA A*2403	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.427778	-0.117875	-4.545654	26778.013025

HLA B*5301	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.603607	0.057919	-4.545688	40142.716433
HLA B*5401	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.510790	-0.035208	-4.545999	32418.308633
HLA A*6801	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.511782	-0.034337	-4.546119	32492.403310
HLA A*2301	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.497584	-0.048602	-4.546186	31447.338639
HLA B*4601	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.310210	-0.236114	-4.546324	20427.260108
HLA B*0801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.417380	-0.129168	-4.546548	26144.451074
HLA A*2902	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.437660	-0.108943	-4.546603	27394.304725
HLA B*4501	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.457873	-0.088805	-4.546678	28699.405588
HLA B*4403	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.668986	0.122274	-4.546712	46664.420479
HLA A*0203	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.401631	-0.145362	-4.546993	25213.371908
HLA B*3501	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.401708	-0.145362	-4.547071	25217.873560
HLA B*3901	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.483487	-0.063767	-4.547254	30442.967733
HLA A*0216	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.401927	-0.145362	-4.547289	25230.564361
HLA A*2603	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.556878	0.009579	-4.547298	36047.724097
HLA B*7301	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.484145	-0.063193	-4.547338	30489.116739
HLA A*2301	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.536367	-0.010996	-4.547363	34384.827212
HLA A*3101	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.391657	-0.155719	-4.547377	24640.945380
HLA A*0212	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.391744	-0.155719	-4.547464	24645.878151
HLA A*0203	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.438913	-0.108943	-4.547855	27473.409399
HLA A*1101	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.439216	-0.108943	-4.548158	27492.589115
HLA A*1101	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.459487	-0.088805	-4.548292	28806.268081
HLA B*5301	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.395710	-0.152648	-4.548358	24871.972433
HLA B*0801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.359695	-0.188668	-4.548363	22892.592205
HLA B*4601	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.430501	-0.117875	-4.548377	26946.440287
HLA A*2601	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.392663	-0.155719	-4.548382	24698.065931
HLA B*4002	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.649365	0.100651	-4.548714	44603.129109
HLA B*4501	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.645928	0.096922	-4.549006	44251.503495
HLA A*0202	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.558109	0.008974	-4.549135	36150.056509
HLA A*0212	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.360804	-0.188668	-4.549472	22951.122395
HLA B*4801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.434914	-0.114630	-4.549543	27221.605412
HLA B*3501	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.460751	-0.088805	-4.549556	28890.231440
HLA A*0203	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.138618	-0.410971	-4.549589	13759.980908
HLA A*2402	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.559537	0.009850	-4.549688	36269.157498
HLA A*2402	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.521187	-0.028622	-4.549809	33203.726179
HLA A*0201	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.397202	-0.152648	-4.549850	24957.561540
HLA B*0801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.407996	-0.141893	-4.549888	25585.604644
HLA B*5401	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.540117	-0.009859	-4.549975	34682.997481
HLA A*3301	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.588554	0.038504	-4.550050	38775.160771
HLA A*2402	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.588554	0.038251	-4.550302	38775.160771
HLA B*1517	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.502553	-0.047884	-4.550437	31809.222808
HLA B*3501	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.362021	-0.188551	-4.550572	23015.529045
HLA A*0211	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.507243	-0.043361	-4.550604	32154.564376
HLA B*0802	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.487448	-0.063193	-4.550642	30721.910461
HLA B*0803	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.502842	-0.047884	-4.550726	31830.396229
HLA A*0203	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.440275	-0.110482	-4.550757	27559.749081
HLA A*3201	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.615368	0.064589	-4.550779	41244.712390
HLA A*0201	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.395167	-0.155719	-4.550887	24840.909731
HLA A*0250	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.541113	-0.009859	-4.550971	34762.644410
HLA B*4403	1:41-49	9	VLRADLARD	0.810769	-0.688323	-4.673483	0.122446	-4.551037	47150.118768
HLA B*0702	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.462316	-0.088805	-4.551120	28994.510289
HLA B*1801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.430807	-0.120427	-4.551234	26965.397996
HLA B*3901	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.507882	-0.043361	-4.551243	32201.914320
HLA A*0211	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.395550	-0.155719	-4.551270	24862.824402
HLA B*4402	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.455143	-0.096147	-4.551290	28519.558645
HLA B*1509	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.485519	-0.065831	-4.551350	30585.761092
HLA A*0212	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.440879	-0.110482	-4.551361	27598.093194
HLA A*2902	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.436901	-0.114630	-4.551531	27346.477874
HLA A*6901	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.409779	-0.141893	-4.551671	25690.877828
HLA B*2705	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.431286	-0.120427	-4.551713	26995.173906
HLA B*0803	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.487951	-0.063767	-4.551718	30757.498314
HLA B*5701	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.420817	-0.130925	-4.551742	26352.196754
HLA B*1517	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.463049	-0.088805	-4.551853	29043.491025
HLA A*0206	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.396201	-0.155719	-4.551920	24900.110251
HLA A*0219	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.437294	-0.114630	-4.551923	27371.195254
HLA A*6801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.141376	-0.410971	-4.552347	13847.651547

HLA B*4402	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.363990	-0.188551	-4.552541	23120.106521
HLA B*1502	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.561612	0.008974	-4.552639	36442.827275
HLA B*3501	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.442162	-0.110482	-4.552643	27679.732941
HLA B*4402	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.432301	-0.120427	-4.552728	27058.337354
HLA B*1502	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.591267	0.038504	-4.552764	39018.202861
HLA A*0301	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.364265	-0.188551	-4.552816	23134.745187
HLA B*0702	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.422278	-0.130925	-4.553203	26441.019965
HLA A*0250	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.542255	-0.010996	-4.553250	34854.162825
HLA A*0203	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.424113	-0.129168	-4.553281	26552.972878
HLA A*0212	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.435424	-0.117875	-4.553299	27253.580871
HLA A*3301	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.565644	0.012088	-4.553556	36782.714725
HLA A*2403	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.422746	-0.130925	-4.553671	26469.500847
HLA B*1517	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.457530	-0.096147	-4.553677	28676.746490
HLA B*2705	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.464896	-0.088805	-4.553700	29167.251910
HLA A*3101	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.365165	-0.188551	-4.553715	23182.729785
HLA A*0211	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.552454	-0.001305	-4.553759	35682.376400
HLA A*6801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.506387	-0.047418	-4.553806	32091.307922
HLA A*2601	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.401431	-0.152648	-4.554079	25201.780441
HLA B*4801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.433715	-0.120427	-4.554142	27146.603334
HLA A*2403	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.400844	-0.153340	-4.554184	25167.718771
HLA B*5301	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.445094	-0.109105	-4.554199	27867.246100
HLA A*6901	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.365698	-0.188668	-4.554366	23211.216705
HLA A*1101	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.458228	-0.096147	-4.554375	28722.859517
HLA B*4403	1:281-289	9	PPEAPKVLT	0.902000	-0.782886	-4.673492	0.119114	-4.554378	47151.139087
HLA A*2902	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.445277	-0.109105	-4.554383	27879.007761
HLA B*5101	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.507059	-0.047362	-4.554422	32140.998933
HLA A*3201	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.628053	0.073404	-4.554649	42467.153214
HLA A*3002	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.529760	-0.025025	-4.554785	33865.702934
HLA A*2403	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.409577	-0.145362	-4.554939	25678.927916
HLA A*6801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.434672	-0.120427	-4.555098	27206.441253
HLA A*2601	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.401847	-0.153340	-4.555187	25225.923973
HLA A*8001	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.440602	-0.114630	-4.555231	27580.481106
HLA B*4501	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.526685	-0.028622	-4.555307	33626.728591
HLA B*1509	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.542229	-0.013165	-4.555394	34852.088758
HLA B*5801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.319300	-0.236114	-4.555414	20859.326236
HLA A*6801	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.593981	0.038504	-4.555477	39262.768335
HLA A*2301	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.520355	-0.035208	-4.555563	33140.198548
HLA A*2902	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.413705	-0.141893	-4.555597	25924.174334
HLA A*3301	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.459527	-0.096147	-4.555674	28808.917461
HLA A*0201	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.413858	-0.141893	-4.555750	25933.291986
HLA A*0301	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.367089	-0.188668	-4.555757	23285.673375
HLA A*0206	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.507205	-0.048602	-4.555807	32151.781254
HLA B*4501	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.656534	0.100651	-4.555882	45345.438526
HLA B*1502	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.530944	-0.025025	-4.555969	33958.166620
HLA B*1501	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.414208	-0.141893	-4.556100	25954.204552
HLA B*3801	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.545128	-0.010996	-4.556124	35085.532790
HLA B*1501	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.438520	-0.117875	-4.556395	27448.599715
HLA B*5401	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.548220	-0.008210	-4.556430	35336.212515
HLA B*1503	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.367921	-0.188551	-4.556471	23330.310515
HLA B*1501	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.400867	-0.155719	-4.556587	25169.080353
HLA B*4001	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.425725	-0.130925	-4.556650	26651.698927
HLA A*2603	1:130-138	9	HQNGIIHRD	0.875899	-0.813309	-4.619398	0.062590	-4.556807	41629.159863
HLA A*6801	1:362-370	9	VPDVRGQSS	1.301546	-1.179272	-4.679394	0.122274	-4.557120	47796.279852
HLA A*8001	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.448325	-0.108943	-4.557267	28075.312230
HLA A*1101	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.503030	-0.054260	-4.557290	31844.175124
HLA A*2601	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.368672	-0.188668	-4.557340	23370.734101
HLA A*0101	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.368889	-0.188551	-4.557439	23382.368839
HLA B*1501	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.404953	-0.152648	-4.557601	25406.983274
HLA A*2402	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.549397	-0.008210	-4.557607	35432.116084
HLA A*2602	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.448614	-0.109105	-4.557719	28094.000219
HLA A*0206	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.540723	-0.017067	-4.557789	34731.440123
HLA B*4601	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.404551	-0.153340	-4.557891	25383.490370
HLA A*2402	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.546984	-0.010996	-4.557980	35235.802660
HLA A*2603	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.549977	-0.008210	-4.558187	35479.493634
HLA B*3901	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.510840	-0.047362	-4.558202	32421.991811

HLA B*7301	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.616193	0.057919	-4.558274	41323.105187
HLA A*0211	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.541385	-0.017067	-4.558452	34784.466455
HLA A*0219	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.469663	-0.088805	-4.558467	29489.174652
HLA A*2501	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.495338	-0.063193	-4.558531	31285.117448
HLA B*4403	1:205-213	9	VLYEVLTGE	0.661214	-0.564292	-4.655526	0.096922	-4.558603	45240.320936
HLA A*0216	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.444342	-0.114630	-4.558972	27819.045046
HLA B*1509	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.448562	-0.110482	-4.559043	28090.656739
HLA A*2402	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.584505	0.025261	-4.559244	38415.407508
HLA A*2603	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.660011	0.100651	-4.559359	45709.960293
HLA A*1101	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.444753	-0.114630	-4.559383	27845.394659
HLA B*0803	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.510809	-0.048602	-4.559411	32419.711699
HLA A*2403	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.439028	-0.120427	-4.559454	27480.693141
HLA B*4601	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.406828	-0.152648	-4.559476	25516.904646
HLA B*3801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.549707	-0.009859	-4.559566	35457.427384
HLA A*0301	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.323546	-0.236114	-4.559660	21064.240072
HLA A*2301	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.546712	-0.013165	-4.559877	35213.697469
HLA A*0206	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.546895	-0.013165	-4.560060	35228.559777
HLA B*1503	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.511646	-0.048602	-4.560247	32482.209651
HLA A*6802	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.431227	-0.129168	-4.560395	26991.523130
HLA B*1801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.496771	-0.063767	-4.560538	31388.529887
HLA A*2403	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.450070	-0.110482	-4.560552	28188.389392
HLA A*1101	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.497412	-0.063193	-4.560606	31434.921848
HLA A*0203	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.440188	-0.120427	-4.560615	27554.233111
HLA A*6801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.543596	-0.017067	-4.560663	34961.995426
HLA B*0803	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.513574	-0.047418	-4.560993	32626.800867
HLA A*2601	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.390795	-0.170363	-4.561158	24592.071059
HLA A*6901	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.372617	-0.188551	-4.561168	23583.982265
HLA B*5101	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.497636	-0.063767	-4.561402	31451.081648
HLA A*6802	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.408202	-0.153340	-4.561542	25597.788089
HLA A*0203	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.405844	-0.155719	-4.561563	25459.129872
HLA B*5701	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.416360	-0.145362	-4.561722	26083.138735
HLA A*2602	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.626317	0.064589	-4.561728	42297.712369
HLA B*4002	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.647779	0.086012	-4.561768	44440.549994
HLA A*2403	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.420034	-0.141893	-4.561927	26304.766189
HLA B*1517	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.431058	-0.130925	-4.561983	26981.011655
HLA B*4403	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.600334	0.038251	-4.562083	39841.338915
HLA B*4002	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.600339	0.038251	-4.562087	39841.769992
HLA A*0250	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.587365	0.025261	-4.562103	38669.162640
HLA A*0212	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.441683	-0.120427	-4.562109	27649.201957
HLA A*0216	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.420385	-0.141893	-4.562277	26325.978312
HLA B*4403	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.621973	0.059501	-4.562472	41876.722284
HLA B*2705	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.409499	-0.153340	-4.562839	25674.343960
HLA A*2301	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.515496	-0.047418	-4.562915	32771.503840
HLA A*0201	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.392623	-0.170363	-4.562986	24695.794601
HLA A*8001	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.445282	-0.117875	-4.563157	27879.309407
HLA B*4002	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.645714	0.082090	-4.563625	44229.723845
HLA B*0702	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.434597	-0.129168	-4.563765	27201.731778
HLA A*0250	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.573834	0.009850	-4.563984	37482.977621
HLA A*0219	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.443752	-0.120427	-4.564179	27781.295696
HLA B*3501	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.433382	-0.130925	-4.564307	27125.757206
HLA B*5401	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.539360	-0.025025	-4.564385	34622.632837
HLA A*2301	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.547398	-0.017067	-4.564464	35269.368071
HLA A*0206	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.411137	-0.153340	-4.564477	25771.336772
HLA A*3201	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.517134	-0.047418	-4.564552	32895.308380
HLA B*3801	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.556345	-0.008210	-4.564554	36003.483046
HLA B*1509	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.501395	-0.063193	-4.564588	31724.498247
HLA B*4801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.433673	-0.130925	-4.564598	27143.959981
HLA A*2301	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.542861	-0.021825	-4.564686	34902.844538
HLA A*0202	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.554977	-0.009859	-4.564836	35890.302353
HLA A*0202	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.590255	0.025261	-4.564993	38927.331573
HLA A*0203	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.412037	-0.153340	-4.565377	25824.790019
HLA B*4501	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.530420	-0.035208	-4.565629	33917.224010
HLA A*2902	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.447836	-0.117875	-4.565711	28043.738058
HLA B*4601	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.423850	-0.141893	-4.565743	26536.889104
HLA B*1509	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.502147	-0.063767	-4.565913	31779.466139

HLA A*3201	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.624047	0.057919	-4.566128	42077.243099
HLA B*0801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.420873	-0.145362	-4.566235	26355.618475
HLA A*3101	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.424545	-0.141893	-4.566438	26579.417388
HLA A*0211	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.553365	-0.013165	-4.566530	35757.353690
HLA A*2301	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.541679	-0.025025	-4.566704	34807.996923
HLA B*5701	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.424853	-0.141893	-4.566746	26598.260777
HLA A*0212	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.413475	-0.153340	-4.566815	25910.433779
HLA A*0212	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.437703	-0.129168	-4.566871	27396.972457
HLA A*2501	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.449022	-0.117875	-4.566898	28120.458134
HLA B*4001	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.411200	-0.155719	-4.566920	25775.101389
HLA A*8001	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.478151	-0.088805	-4.566956	30071.237932
HLA A*6802	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.421641	-0.145362	-4.567004	26402.283717
HLA A*0219	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.458080	-0.108943	-4.567022	28713.071774
HLA A*6802	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.411330	-0.155719	-4.567049	25782.771754
HLA B*7301	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.576675	0.009579	-4.567095	37728.940625
HLA B*4501	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.653169	0.086012	-4.567157	44995.506377
HLA A*2602	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.531964	-0.035208	-4.567172	34037.990396
HLA B*7301	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.559298	-0.008210	-4.567508	36249.149382
HLA A*2602	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.519211	-0.048602	-4.567813	33053.001766
HLA B*3801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.576912	0.008974	-4.567938	37749.561306
HLA B*5701	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.415340	-0.152648	-4.567988	26021.970181
HLA B*1517	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.488891	-0.079239	-4.568129	30824.128242
HLA B*3501	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.438981	-0.129168	-4.568149	27477.719952
HLA B*1517	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.459059	-0.109105	-4.568165	28777.919393
HLA B*0802	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.472177	-0.096147	-4.568324	29660.370151
HLA A*2603	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.627865	0.059501	-4.568365	42448.777783
HLA A*2403	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.412709	-0.155719	-4.568428	25864.777792
HLA A*6801	1:271-279	9	ADLVRVHNG	0.718174	-0.610871	-4.675806	0.107303	-4.568503	47403.065916
HLA B*0802	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.448383	-0.120427	-4.568810	28079.109595
HLA B*0702	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.415502	-0.153340	-4.568842	26031.685537
HLA A*0101	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.380274	-0.188668	-4.568942	24003.474549
HLA B*3801	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.551876	-0.017067	-4.568942	35634.920710
HLA B*4801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.439834	-0.129168	-4.569002	27531.733435
HLA B*1503	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.505271	-0.063767	-4.569038	32008.948838
HLA B*7301	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.505443	-0.063767	-4.569210	32021.592369
HLA A*2902	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.424059	-0.145362	-4.569421	26549.669165
HLA B*5401	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.556288	-0.013165	-4.569453	35998.808753
HLA B*3801	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.579475	0.009850	-4.569625	37973.025168
HLA A*0219	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.413992	-0.155719	-4.569711	25941.290104
HLA A*3002	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.548279	-0.021825	-4.570104	35340.991963
HLA A*2603	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.535904	-0.034337	-4.570241	34348.201167
HLA A*0211	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.548568	-0.021825	-4.570393	35364.516263
HLA A*2603	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.628434	0.057919	-4.570515	42504.387827
HLA B*0802	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.439667	-0.130925	-4.570592	27521.160468
HLA B*5301	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.596793	0.025261	-4.571532	39517.844782
HLA B*3801	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.546575	-0.025025	-4.571600	35202.650075
HLA B*4002	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.645047	0.073404	-4.571642	44161.821097
HLA B*0702	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.463065	-0.108943	-4.572008	29044.590901
HLA B*4001	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.430116	-0.141893	-4.572009	26922.543420
HLA A*0219	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.441109	-0.130925	-4.572034	27612.728730
HLA A*3301	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.630027	0.057919	-4.572108	42660.576144
HLA A*0250	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.581096	0.008974	-4.572123	38115.036656
HLA A*3301	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.636944	0.064589	-4.572355	43345.458408
HLA A*0206	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.508664	-0.063767	-4.572431	32259.978131
HLA A*2602	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.561459	-0.010996	-4.572455	36430.014670
HLA B*4801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.417142	-0.155719	-4.572861	26130.169679
HLA A*6801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.524429	-0.048602	-4.573031	33452.541105
HLA B*0803	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.525712	-0.047362	-4.573074	33551.499282
HLA B*1503	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.525550	-0.047884	-4.573433	33538.977437
HLA B*4403	1:182-190	9	YLSPEQARG	0.729067	-0.628416	-4.674195	0.100651	-4.573543	47227.470453
HLA B*0802	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.484753	-0.088805	-4.573558	30531.866852
HLA B*7301	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.556617	-0.017067	-4.573684	36026.084020
HLA A*0216	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.484953	-0.088805	-4.573758	30545.909872
HLA A*2402	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.526436	-0.047362	-4.573798	33607.450931
HLA B*5101	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.453449	-0.120427	-4.573876	28408.533917

HLA A*0211	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.508225	-0.065831	-4.574055	32227.358850
HLA A*0202	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.572793	-0.001305	-4.574098	37393.254191
HLA A*2602	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.612641	0.038504	-4.574137	40986.471088
HLA B*4403	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.656362	0.082090	-4.574273	45327.534155
HLA A*6801	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.632350	0.057919	-4.574431	42889.438156
HLA A*2403	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.329300	-0.245356	-4.574656	21345.173273
HLA B*0801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.419198	-0.155719	-4.574917	26254.154053
HLA A*2301	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.540655	-0.034337	-4.574992	34725.991646
HLA A*0206	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.549989	-0.025025	-4.575014	35480.453348
HLA B*4501	1:94-102	9	YVDGVTLRD	0.968389	-0.886299	-4.657281	0.082090	-4.575191	45423.515454
HLA A*2902	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.315586	-0.259643	-4.575229	20681.676499
HLA B*4801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.429912	-0.145362	-4.575274	26909.875028
HLA A*2402	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.585121	0.009579	-4.575542	38469.895766
HLA A*3101	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.430323	-0.145362	-4.575685	26935.363493
HLA A*0203	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.457859	-0.117875	-4.575734	28698.474039
HLA A*0101	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.330383	-0.245356	-4.575739	21398.473695
HLA B*1502	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.566043	-0.009859	-4.575902	36816.558655
HLA A*8001	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.445437	-0.130925	-4.576362	27889.265567
HLA A*0219	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.431030	-0.145362	-4.576392	26979.260140
HLA B*5101	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.513271	-0.063193	-4.576465	32604.039359
HLA B*4403	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.650188	0.073404	-4.576783	44687.663410
HLA B*4501	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.551803	-0.025025	-4.576828	35628.945001
HLA A*3301	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.615115	0.038251	-4.576863	41220.621462
HLA B*2705	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.447730	-0.129168	-4.576898	28036.911781
HLA B*0803	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.511244	-0.065831	-4.577074	32452.174545
HLA B*0801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.388601	-0.188551	-4.577151	24468.124750
HLA B*5401	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.542866	-0.034337	-4.577203	34903.222181
HLA B*3901	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.481260	-0.096147	-4.577407	30287.238369
HLA A*2902	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.424078	-0.153340	-4.577418	26550.818236
HLA A*0201	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.388751	-0.188668	-4.577419	24476.597886
HLA B*4801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.424217	-0.153340	-4.577556	26559.294171
HLA B*4403	1:272-280	9	DLVRVHNGE	0.792093	-0.706081	-4.663681	0.086012	-4.577669	46097.857345
HLA B*1801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.498467	-0.079239	-4.577706	31511.371350
HLA B*3901	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.498568	-0.079239	-4.577807	31518.702543
HLA A*3002	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.534454	-0.043361	-4.577815	34233.741385
HLA B*5401	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.530430	-0.047418	-4.577848	33917.957972
HLA B*0702	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.435971	-0.141893	-4.577864	27287.955783
HLA B*4402	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.422405	-0.155719	-4.578124	26448.745414
HLA A*0101	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.407977	-0.170363	-4.578340	25584.497345
HLA B*4002	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.638071	0.059501	-4.578571	43458.161856
HLA A*3002	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.524330	-0.054260	-4.578590	33444.941037
HLA B*4501	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.636591	0.057919	-4.578672	43310.298557
HLA A*3101	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.333477	-0.245356	-4.578833	21551.478472
HLA A*0219	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.425532	-0.153340	-4.578872	26639.878565
HLA B*4601	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.390398	-0.188551	-4.578949	24569.597510
HLA B*4501	1:617-625	9	DGIITLRFG	0.844392	-0.770988	-4.652481	0.073404	-4.579076	44924.240608
HLA B*4402	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.433852	-0.145362	-4.579214	27155.122557
HLA A*0212	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.426672	-0.152648	-4.579319	26709.867957
HLA A*0201	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.390797	-0.188551	-4.579348	24592.204100
HLA A*0203	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.426780	-0.152648	-4.579428	26716.515665
HLA B*2705	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.516448	-0.063193	-4.579641	32843.385090
HLA A*0219	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.450709	-0.129168	-4.579877	28229.898854
HLA B*7301	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.566790	-0.013165	-4.579955	36879.950341
HLA B*1501	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.320468	-0.259643	-4.580111	20915.486483
HLA A*0211	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.555142	-0.025025	-4.580166	35903.896306
HLA B*5301	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.589174	0.008974	-4.580200	38830.579437
HLA B*1501	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.191989	-0.388552	-4.580541	15559.252640
HLA B*1509	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.533188	-0.047362	-4.580550	34134.063580
HLA B*5401	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.563539	-0.017067	-4.580605	36604.850744
HLA A*2301	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.526483	-0.054260	-4.580742	33611.087379
HLA B*2705	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.517000	-0.063767	-4.580767	32885.166225
HLA B*3801	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.552317	-0.028622	-4.580940	35671.181970
HLA A*2602	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.638905	0.057919	-4.580986	43541.703915
HLA A*2602	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.606320	0.025261	-4.581059	40394.330340
HLA A*2301	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.537732	-0.043361	-4.581093	34493.073759

HLA A*2601	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.392834	-0.188551	-4.581385	24707.821665
HLA A*1101	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.502196	-0.079239	-4.581434	31783.076735
HLA A*2402	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.590710	0.008974	-4.581737	38968.207974
HLA A*0211	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.533157	-0.048602	-4.581759	34131.663065
HLA B*2705	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.502595	-0.079239	-4.581834	31812.320477
HLA B*3801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.580633	-0.001305	-4.581938	38074.437264
HLA A*0250	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.591646	0.009579	-4.582066	39052.202214
HLA B*5301	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.574020	-0.008210	-4.582229	37499.000567
HLA B*1503	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.486111	-0.096147	-4.582259	30627.486853
HLA A*2501	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.493456	-0.088805	-4.582260	31149.842293
HLA B*4501	1:37-45	9	VAVKVLRAD	0.825160	-0.765659	-4.642270	0.059501	-4.582769	43880.329775
HLA A*0219	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.472334	-0.110482	-4.582816	29671.122873
HLA A*2902	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.452143	-0.130925	-4.583068	28323.212318
HLA B*1801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.452300	-0.130925	-4.583225	28333.480283
HLA B*1503	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.539945	-0.043361	-4.583306	34669.303110
HLA B*5701	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.427745	-0.155719	-4.583465	26775.984977
HLA A*2602	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.573644	-0.009859	-4.583502	37466.556141
HLA A*8001	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.454555	-0.129168	-4.583723	28481.012804
HLA A*1101	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.430384	-0.153340	-4.583724	26939.152410
HLA B*4403	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.529875	-0.054260	-4.584135	33874.681399
HLA A*3002	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.438849	-0.145362	-4.584211	27469.396733
HLA A*2501	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.453620	-0.130925	-4.584545	28419.755285
HLA B*0802	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.474416	-0.110482	-4.584897	29813.682749
HLA B*5301	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.594777	0.009850	-4.584928	39334.840452
HLA B*5101	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.496296	-0.088805	-4.585101	31354.247312
HLA B*5401	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.537791	-0.047362	-4.585153	34497.739167
HLA A*2603	1:405-413	9	AANTSVSAG	0.661890	-0.623639	-4.623613	0.038251	-4.585361	42035.152020
HLA A*2603	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.574405	-0.010996	-4.585401	37532.285262
HLA B*1501	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.396786	-0.188668	-4.585454	24933.674855
HLA B*4801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.443586	-0.141893	-4.585478	27770.626891
HLA B*3801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.572671	-0.013165	-4.585836	37382.736416
HLA B*5801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.340493	-0.245356	-4.585849	21902.446650
HLA A*2301	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.538503	-0.047362	-4.585865	34554.334109
HLA B*1517	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.522721	-0.063193	-4.585914	33321.231005
HLA B*1502	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.574945	-0.010996	-4.585941	37579.014793
HLA A*3301	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.557378	-0.028622	-4.586000	36089.286061
HLA A*3002	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.209568	-0.376448	-4.586016	16201.960887
HLA A*0211	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.538977	-0.047362	-4.586339	34592.115643
HLA A*3301	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.596128	0.009579	-4.586549	39457.389306
HLA B*4403	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.573385	-0.013165	-4.586550	37444.266883
HLA A*2301	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.538672	-0.047884	-4.586555	34567.796060
HLA B*4402	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.444800	-0.141893	-4.586693	27848.407632
HLA A*0301	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.327192	-0.259643	-4.586836	21241.843095
HLA A*0250	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.490728	-0.096147	-4.586875	30954.806969
HLA A*0211	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.433624	-0.153340	-4.586964	27140.876394
HLA A*0216	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.478137	-0.108943	-4.587080	30070.261856
HLA A*1101	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.476666	-0.110482	-4.587148	29968.598433
HLA A*2402	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.521328	-0.065831	-4.587158	33214.505637
HLA B*5401	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.532955	-0.054260	-4.587215	34115.786987
HLA B*4001	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.416973	-0.170363	-4.587336	26119.993646
HLA B*4501	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.638262	0.050897	-4.587365	43477.209440
HLA A*0203	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.398983	-0.188551	-4.587534	25060.115038
HLA B*5301	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.599859	0.012088	-4.587771	39797.824176
HLA B*3501	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.432139	-0.155719	-4.587858	27048.238839
HLA B*5101	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.491978	-0.096147	-4.588125	31044.025118
HLA B*0802	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.473833	-0.114630	-4.588463	29773.709967
HLA A*2603	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.571426	-0.017067	-4.588492	37275.704609
HLA B*5301	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.598109	0.009579	-4.588529	39637.747124
HLA A*0219	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.470795	-0.117875	-4.588670	29566.169979
HLA B*4002	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.646708	0.057919	-4.588789	44331.054295
HLA B*4403	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.601041	0.012088	-4.588953	39906.268471
HLA B*1509	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.509895	-0.079239	-4.589134	32351.557876
HLA A*0202	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.541792	-0.047362	-4.589154	34817.036852
HLA A*0216	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.480501	-0.109105	-4.589606	30234.360837
HLA A*8001	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.444392	-0.145362	-4.589754	27822.205683

HLA A*0216	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.434157	-0.155719	-4.589876	27174.227081
HLA B*1801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.542588	-0.047362	-4.589951	34880.948229
HLA A*2402	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.556260	-0.034337	-4.590597	35996.471834
HLA B*5801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.330970	-0.259643	-4.590613	21427.434117
HLA B*1503	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.331022	-0.259643	-4.590665	21429.984510
HLA B*1503	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.438046	-0.152648	-4.590693	27418.620335
HLA B*5701	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.420335	-0.170363	-4.590698	26322.987649
HLA A*2902	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.461592	-0.129168	-4.590760	28946.238534
HLA B*0702	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.472912	-0.117875	-4.590787	29710.636462
HLA B*5701	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.402383	-0.188551	-4.590934	25257.058206
HLA A*3201	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.599942	0.008974	-4.590968	39805.360453
HLA B*0801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.354869	-0.236114	-4.590983	22639.619835
HLA B*3901	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.470605	-0.120427	-4.591032	29553.216892
HLA A*2402	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.556053	-0.035208	-4.591261	35979.339063
HLA B*0802	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.438617	-0.152648	-4.591264	27454.688640
HLA A*2603	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.527758	-0.063767	-4.591525	33709.967457
HLA A*0216	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.460972	-0.130925	-4.591897	28904.926713
HLA A*0212	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.403409	-0.188551	-4.591960	25316.839599
HLA B*1502	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.617344	0.025261	-4.592083	41432.791679
HLA B*0803	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.528910	-0.063193	-4.592103	33799.445923
HLA A*2902	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.436467	-0.155719	-4.592186	27319.122404
HLA B*0801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.421876	-0.170363	-4.592240	26416.570925
HLA A*0216	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.438934	-0.153340	-4.592274	27474.747084
HLA B*1502	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.602127	0.009850	-4.592277	40006.133701
HLA B*4402	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.439629	-0.152648	-4.592277	27518.778389
HLA B*4002	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.643254	0.050897	-4.592358	43979.908046
HLA B*7301	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.582631	-0.009859	-4.592489	38249.922142
HLA A*0206	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.447314	-0.145362	-4.592676	28010.077875
HLA A*0202	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.579644	-0.013165	-4.592809	37987.818999
HLA B*1503	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.482446	-0.110482	-4.592928	30370.096054
HLA B*5401	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.545058	-0.047884	-4.592941	35079.838987
HLA B*1517	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.484128	-0.108943	-4.593071	30487.962162
HLA B*5301	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.583326	-0.009859	-4.593185	38311.221850
HLA A*0206	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.462363	-0.130925	-4.593288	28997.647601
HLA B*4601	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.423422	-0.170363	-4.593786	26510.773746
HLA A*2501	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.473429	-0.120427	-4.593856	29746.018388
HLA A*2402	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.592649	-0.001305	-4.593954	39142.517961
HLA A*2402	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.572373	-0.021825	-4.594198	37357.061207
HLA B*3901	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.441556	-0.152648	-4.594203	27641.125865
HLA B*1517	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.479812	-0.114630	-4.594442	30186.474389
HLA B*3801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.540229	-0.054260	-4.594489	34692.004947
HLA A*8001	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.441154	-0.153340	-4.594494	27615.567130
HLA B*0802	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.485691	-0.108943	-4.594634	30597.842464
HLA B*1503	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.505873	-0.088805	-4.594678	32053.309754
HLA A*6802	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.453005	-0.141893	-4.594897	28379.501915
HLA B*1801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.506277	-0.088805	-4.595082	32083.149270
HLA A*2603	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.659712	0.064589	-4.595124	45678.565780
HLA B*0802	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.477414	-0.117875	-4.595289	30020.199127
HLA B*5301	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.594098	-0.001305	-4.595403	39273.390132
HLA A*0219	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.453665	-0.141893	-4.595558	28422.676642
HLA A*2301	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.529784	-0.065831	-4.595614	33867.535081
HLA B*3801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.573914	-0.021825	-4.595739	37489.872733
HLA A*0203	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.453886	-0.141893	-4.595778	28437.134090
HLA A*0206	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.481264	-0.114630	-4.595894	30287.566072
HLA A*2501	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.486024	-0.110482	-4.596506	30621.356888
HLA B*0702	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.408005	-0.188551	-4.596556	25586.158311
HLA B*7301	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.561419	-0.035208	-4.596628	36426.664424
HLA B*1501	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.426472	-0.170363	-4.596835	26697.588499
HLA A*1101	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.467863	-0.129168	-4.597031	29367.225099
HLA A*0206	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.533954	-0.063193	-4.597147	34194.316345
HLA B*3801	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.562164	-0.035208	-4.597373	36489.187377
HLA B*1509	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.479610	-0.117875	-4.597486	30172.433384
HLA A*1101	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.489072	-0.109105	-4.598177	30836.971061
HLA A*3101	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.338714	-0.259643	-4.598357	21812.933282
HLA B*3901	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.483790	-0.114630	-4.598420	30464.220555

HLA A*0212	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.428251	-0.170363	-4.598614	26807.146945
HLA B*4601	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.409955	-0.188668	-4.598623	25701.303803
HLA A*0219	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.445999	-0.152648	-4.598646	27925.348692
HLA B*4403	1:210-218	9	LTGEPPFTG	0.714135	-0.663238	-4.650009	0.050897	-4.599112	44669.293783
HLA B*2705	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.488644	-0.110482	-4.599126	30806.623927
HLA A*0211	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.536245	-0.063193	-4.599438	34375.155632
HLA B*5701	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.410817	-0.188668	-4.599485	25752.382615
HLA A*2501	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.490719	-0.108943	-4.599662	30954.137128
HLA A*0216	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.470537	-0.129168	-4.599705	29548.580746
HLA A*3201	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.625008	0.025261	-4.599747	42170.448163
HLA A*0250	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.598616	-0.001305	-4.599921	39684.092333
HLA B*0702	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.429562	-0.170363	-4.599925	26888.192431
HLA B*5101	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.429743	-0.170363	-4.600106	26899.395349
HLA B*0702	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.454854	-0.145362	-4.600216	28500.587576
HLA A*0216	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.489767	-0.110482	-4.600249	30886.390699
HLA B*0702	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.444624	-0.155719	-4.600343	27837.110664
HLA A*0202	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.575408	-0.025025	-4.600433	37619.085908
HLA B*4801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.447794	-0.152648	-4.600441	28041.007348
HLA B*1502	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.534715	-0.065831	-4.600546	34254.304841
HLA B*4002	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.625870	0.025261	-4.600609	42254.257778
HLA B*4402	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.447519	-0.153340	-4.600859	28023.264211
HLA A*3101	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.412248	-0.188668	-4.600916	25837.366913
HLA B*5301	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.572359	-0.028622	-4.600981	37355.848641
HLA B*0702	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.480581	-0.120427	-4.601007	30239.922542
HLA A*1101	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.480952	-0.120427	-4.601379	30265.781544
HLA B*1509	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.553972	-0.047418	-4.601390	35807.296913
HLA A*1101	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.470635	-0.130925	-4.601560	29555.295400
HLA A*2301	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.537871	-0.063767	-4.601637	34504.085135
HLA A*0250	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.584684	-0.017067	-4.601751	38431.205311
HLA A*8001	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.446177	-0.155719	-4.601896	27936.832603
HLA B*4001	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.413454	-0.188668	-4.602121	25909.172257
HLA B*1801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.449612	-0.152648	-4.602260	28158.668340
HLA A*6901	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.357237	-0.245356	-4.602594	22763.414721
HLA A*3201	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.548427	-0.054260	-4.602686	35353.039039
HLA A*6802	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.357355	-0.245356	-4.602711	22769.572932
HLA A*8001	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.450113	-0.152648	-4.602760	28191.134455
HLA B*2705	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.494189	-0.108943	-4.603132	31202.464054
HLA A*3101	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.433013	-0.170363	-4.603376	27102.727655
HLA B*1502	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.568348	-0.035208	-4.603556	37012.467253
HLA A*3201	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.578585	-0.025025	-4.603609	37895.247016
HLA A*2402	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.555842	-0.047884	-4.603725	35961.825346
HLA A*2403	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.433624	-0.170363	-4.603987	27140.876394
HLA B*3801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.560740	-0.043361	-4.604101	36369.757363
HLA A*2902	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.451644	-0.152648	-4.604292	28290.747146
HLA A*2402	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.587254	-0.017067	-4.604321	38659.331684
HLA A*0301	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.359051	-0.245356	-4.604407	22858.683433
HLA B*0803	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.515630	-0.088805	-4.604435	32781.610940
HLA B*7301	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.614551	0.009850	-4.604701	41167.136433
HLA A*2601	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.368661	-0.236114	-4.604775	23370.101944
HLA A*3301	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.556359	-0.048602	-4.604960	36004.651714
HLA B*1501	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.359810	-0.245356	-4.605166	22898.661482
HLA A*2402	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.345725	-0.259643	-4.605368	22167.919427
HLA A*3301	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.558015	-0.047418	-4.605433	36142.234644
HLA B*1509	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.562500	-0.043361	-4.605861	36517.426850
HLA B*2705	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.474968	-0.130925	-4.605893	29851.609701
HLA B*7301	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.617988	0.012088	-4.605900	41494.253446
HLA A*0250	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.266380	-0.339553	-4.605933	18466.325066
HLA A*6802	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.435741	-0.170363	-4.606104	27273.492386
HLA A*0216	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.485691	-0.120427	-4.606118	30597.842464
HLA B*0801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.360785	-0.245356	-4.606141	22950.129112
HLA A*8001	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.417762	-0.188551	-4.606313	26167.515730
HLA B*1517	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.488447	-0.117875	-4.606322	30792.627632
HLA A*0206	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.477315	-0.129168	-4.606483	30013.378852
HLA B*3901	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.488903	-0.117875	-4.606778	30824.962029
HLA A*2602	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.619337	0.012088	-4.607249	41623.304837

HLA B*3801	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.560113	-0.047418	-4.607531	36317.261339
HLA A*3201	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.617415	0.009850	-4.607565	41439.516629
HLA B*4501	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.617175	0.009579	-4.607596	41416.656251
HLA B*1503	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.231289	-0.376448	-4.607737	17032.898885
HLA A*6801	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.619947	0.012088	-4.607859	41681.892172
HLA B*2705	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.462525	-0.145362	-4.607887	29008.473931
HLA A*0203	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.371962	-0.236114	-4.608076	23548.412418
HLA B*4801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.372135	-0.236114	-4.608250	23557.841484
HLA B*4001	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.363001	-0.245356	-4.608357	23067.508934
HLA A*0216	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.490578	-0.117875	-4.608453	30944.091251
HLA B*4403	1:211-219	9	TGEPPFTGD	1.013618	-0.955699	-4.666380	0.057919	-4.608461	46385.292321
HLA B*3901	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.455444	-0.153340	-4.608783	28539.314303
HLA B*3801	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.560303	-0.048602	-4.608905	36333.179088
HLA B*1502	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.574628	-0.034337	-4.608966	37551.579542
HLA B*0802	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.455798	-0.153340	-4.609138	28562.637402
HLA B*1502	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.587496	-0.021825	-4.609322	38680.879384
HLA A*2601	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.198755	-0.410971	-4.609726	15803.571638
HLA A*3201	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.350177	-0.259643	-4.609821	22396.348066
HLA B*3501	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.468023	-0.141893	-4.609915	29378.030480
HLA B*5101	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.495286	-0.114630	-4.609916	31281.394191
HLA B*4002	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.648557	0.038504	-4.610054	44520.199793
HLA A*3301	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.635548	0.025261	-4.610287	43206.392460
HLA A*3002	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.609051	-0.001305	-4.610355	40649.060678
HLA B*1502	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.562648	-0.047884	-4.610532	36529.874951
HLA A*1101	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.465325	-0.145362	-4.610688	29196.142071
HLA A*6801	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.588878	-0.021825	-4.610703	38804.119746
HLA A*0206	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.501651	-0.109105	-4.610756	31743.211000
HLA B*5301	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.599777	-0.010996	-4.610773	39790.289326
HLA A*0203	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.422116	-0.188668	-4.610784	26431.151841
HLA B*5101	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.479897	-0.130925	-4.610822	30192.353958
HLA A*0216	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.458178	-0.152648	-4.610826	28719.596565
HLA A*0211	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.547076	-0.063767	-4.610843	35243.237694
HLA A*3201	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.594065	-0.017067	-4.611132	39270.415740
HLA A*2301	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.548150	-0.063193	-4.611343	35330.478031
HLA A*6802	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.422978	-0.188668	-4.611646	26483.681154
HLA B*1502	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.610345	-0.001305	-4.611650	40770.410159
HLA A*3301	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.493782	-0.117875	-4.611658	31173.274992
HLA A*2402	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.563200	-0.048602	-4.611802	36576.345789
HLA B*2705	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.502753	-0.109105	-4.611858	31823.853343
HLA A*2402	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.557834	-0.054260	-4.612094	36127.182317
HLA B*0702	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.271949	-0.340176	-4.612125	18704.614235
HLA B*1502	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.548537	-0.063767	-4.612304	35362.029215
HLA B*0803	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.481542	-0.130925	-4.612467	30306.906824
HLA B*4402	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.442171	-0.170363	-4.612534	27680.331925
HLA A*0250	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.583918	-0.028622	-4.612540	38363.486853
HLA A*0211	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.533477	-0.079239	-4.612716	34156.784503
HLA A*1101	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.457130	-0.155719	-4.612850	28650.385150
HLA B*0802	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.467670	-0.145362	-4.613032	29354.200367
HLA B*4801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.442681	-0.170363	-4.613044	27712.846220
HLA A*2501	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.460561	-0.152648	-4.613208	28877.574484
HLA B*3801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.565947	-0.047362	-4.613309	36808.393447
HLA B*3801	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.549580	-0.063767	-4.613347	35447.070577
HLA A*0203	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.443027	-0.170363	-4.613390	27734.893729
HLA B*5301	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.495516	-0.117875	-4.613392	31297.983018
HLA A*0250	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.578221	-0.035208	-4.613429	37863.483927
HLA B*5101	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.504618	-0.108943	-4.613561	31960.845187
HLA A*0202	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.596906	-0.017067	-4.613973	39528.107898
HLA B*1517	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.458434	-0.155719	-4.614154	28736.536871
HLA A*3301	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.579196	-0.035208	-4.614404	37948.586882
HLA A*0250	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.601262	-0.013165	-4.614427	39926.567150
HLA A*2902	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.426155	-0.188551	-4.614706	26678.097433
HLA B*5701	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.369368	-0.245356	-4.614724	23408.188273
HLA B*5301	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.571369	-0.043361	-4.614730	37270.865145
HLA B*1517	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.462203	-0.152648	-4.614851	28986.982126
HLA B*4501	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.653648	0.038504	-4.615145	45045.191612

HLA A*1101	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.379217	-0.236114	-4.615331	23945.110359
HLA B*5301	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.602401	-0.013165	-4.615566	40031.463880
HLA A*2402	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.602425	-0.013165	-4.615590	40033.629596
HLA B*5401	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.519460	-0.096147	-4.615607	33071.961387
HLA A*2602	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.593833	-0.021825	-4.615658	39249.388960
HLA B*1509	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.567794	-0.047884	-4.615677	36965.242337
HLA A*0219	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.427283	-0.188551	-4.615833	26747.463721
HLA A*0206	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.507005	-0.108943	-4.615948	32136.999960
HLA B*3501	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.356342	-0.259643	-4.615986	22716.543826
HLA B*3901	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.485247	-0.130925	-4.616172	30566.573106
HLA B*3901	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.471101	-0.145362	-4.616463	29586.970754
HLA A*3002	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.603433	-0.013165	-4.616598	40126.649243
HLA A*2301	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.537429	-0.079239	-4.616667	34469.010278
HLA B*7301	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.568792	-0.047884	-4.616676	37050.330709
HLA B*5101	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.506352	-0.110482	-4.616834	32088.703871
HLA A*2602	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.569471	-0.047418	-4.616889	37108.302650
HLA B*0803	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.506655	-0.110482	-4.617137	32111.105614
HLA A*0250	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.595334	-0.021825	-4.617160	39385.305716
HLA B*4403	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.627090	0.009850	-4.617240	42373.063139
HLA B*3901	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.428612	-0.188668	-4.617280	26829.489900
HLA A*6801	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.570467	-0.047362	-4.617830	37193.519112
HLA B*1509	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.569260	-0.048602	-4.617861	37090.239386
HLA B*5301	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.596213	-0.021825	-4.618038	39465.074618
HLA B*4501	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.643384	0.025261	-4.618122	43992.995946
HLA B*1801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.509510	-0.108943	-4.618453	32322.867598
HLA B*2705	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.500605	-0.117875	-4.618481	31666.884284
HLA A*3002	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.358988	-0.259643	-4.618631	22855.344778
HLA A*2602	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.555146	-0.063767	-4.618913	35904.284780
HLA B*1503	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.498733	-0.120427	-4.619160	31530.640691
HLA A*2402	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.594195	-0.025025	-4.619219	39282.102151
HLA A*3001	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.279049	-0.340176	-4.619225	19012.923439
HLA B*1502	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.242940	-0.376448	-4.619388	17496.036030
HLA B*5101	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.430800	-0.188668	-4.619468	26964.960360
HLA B*4801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.430953	-0.188668	-4.619620	26974.444061
HLA B*3501	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.231110	-0.388552	-4.619662	17025.897221
HLA A*3201	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.610209	-0.009859	-4.620067	40757.619489
HLA B*4402	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.431415	-0.188668	-4.620083	27003.207350
HLA A*3201	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.524060	-0.096147	-4.620208	33424.140165
HLA A*0101	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.384240	-0.236114	-4.620354	24223.675603
HLA A*0301	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.232012	-0.388552	-4.620564	17061.303540
HLA B*0802	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.491463	-0.129168	-4.620632	31007.267001
HLA A*3301	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.610799	-0.009859	-4.620657	40813.001126
HLA B*5301	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.585617	-0.035208	-4.620825	38513.833709
HLA B*5401	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.557954	-0.063193	-4.621147	36137.151339
HLA A*6802	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.282143	-0.339553	-4.621696	19148.870898
HLA B*0803	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.512621	-0.109105	-4.621726	32555.217515
HLA B*0803	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.512971	-0.108943	-4.621913	32581.469991
HLA A*0211	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.533160	-0.088805	-4.621964	34131.847714
HLA A*2603	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.491041	-0.130925	-4.621966	30977.087439
HLA B*3801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.468829	-0.153340	-4.622168	29432.594726
HLA A*2501	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.507611	-0.114630	-4.622241	32181.886540
HLA B*7301	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.575063	-0.047418	-4.622481	37589.181083
HLA A*1101	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.469846	-0.152648	-4.622494	29501.620864
HLA A*0219	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.433911	-0.188668	-4.622578	27158.795461
HLA A*2602	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.631709	0.008974	-4.622735	42826.141509
HLA B*5301	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.605677	-0.017067	-4.622743	40334.497791
HLA A*8001	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.452490	-0.170363	-4.622853	28345.898764
HLA A*6801	1:461-469	9	PELVGKVIG	0.925445	-0.860856	-4.687514	0.064589	-4.622925	48698.312861
HLA B*4501	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.609915	-0.013165	-4.623080	40730.067030
HLA A*2902	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.452826	-0.170363	-4.623189	28367.836037
HLA B*4403	1:530-538	9	PAGEVTGTN	0.806792	-0.768288	-4.661937	0.038504	-4.623434	45913.185094
HLA A*2602	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.622280	-0.001305	-4.623585	41906.410646
HLA A*0206	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.284380	-0.339553	-4.623933	19247.746085
HLA B*1517	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.495002	-0.129168	-4.624170	31260.924198
HLA B*0803	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.528153	-0.096147	-4.624300	33740.619071

HLA A*0202	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.560844	-0.063767	-4.624611	36378.415673
HLA A*3201	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.576219	-0.048602	-4.624820	37689.364176
HLA A*0216	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.436417	-0.188551	-4.624968	27316.018918
HLA B*5301	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.599984	-0.025025	-4.625009	39809.236808
HLA A*0250	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.599993	-0.025025	-4.625018	39810.098272
HLA B*4501	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.635271	0.009850	-4.625421	43178.819730
HLA A*0211	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.510927	-0.114630	-4.625556	32428.482238
HLA A*3201	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.624395	-0.001305	-4.625700	42110.946306
HLA B*1503	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.494793	-0.130925	-4.625718	31245.876307
HLA A*0201	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.380448	-0.245356	-4.625804	24013.085827
HLA B*4001	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.437510	-0.188551	-4.626061	27384.821557
HLA A*0202	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.537274	-0.088805	-4.626078	34456.705223
HLA B*0802	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.470800	-0.155719	-4.626519	29566.489880
HLA B*1501	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.286990	-0.339553	-4.626543	19363.780842
HLA B*1509	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.537868	-0.088805	-4.626673	34503.898472
HLA A*0201	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.390591	-0.236114	-4.626705	24580.499270
HLA B*5301	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.578296	-0.048602	-4.626897	37870.039286
HLA B*0803	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.512296	-0.114630	-4.626926	32530.922008
HLA A*0202	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.563783	-0.063193	-4.626976	36625.451470
HLA B*3801	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.579301	-0.047884	-4.627185	37957.826401
HLA B*1517	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.439138	-0.188551	-4.627689	27487.681402
HLA B*5401	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.563973	-0.063767	-4.627740	36641.504297
HLA B*1502	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.610846	-0.017067	-4.627912	40817.417241
HLA B*4002	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.637554	0.009579	-4.627975	43406.469779
HLA A*2301	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.539221	-0.088805	-4.628026	34611.583628
HLA B*3801	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.562394	-0.065831	-4.628225	36508.537947
HLA A*3101	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.239726	-0.388552	-4.628278	17367.030576
HLA B*3801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.539499	-0.088805	-4.628303	34633.685572
HLA A*2603	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.653698	0.025261	-4.628436	45050.309382
HLA A*0250	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.585081	-0.043361	-4.628442	38466.357925
HLA B*2705	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.383230	-0.245356	-4.628586	24167.390713
HLA A*0206	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.539802	-0.088805	-4.628606	34657.864016
HLA A*3002	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.513993	-0.114630	-4.628622	32658.234312
HLA B*4002	1:121-129	9	DACQALNFS	1.030074	-1.020224	-4.638532	0.009850	-4.628682	43504.266647
HLA B*1502	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.615624	-0.013165	-4.628789	41269.040658
HLA B*4402	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.369177	-0.259643	-4.628821	23397.933028
HLA A*3201	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.581134	-0.047884	-4.629018	38118.335969
HLA B*4402	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.392973	-0.236114	-4.629087	24715.709251
HLA B*4801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.440609	-0.188551	-4.629160	27580.928732
HLA B*4001	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.369539	-0.259643	-4.629183	23417.434505
HLA B*4501	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.627950	-0.001305	-4.629255	42457.045743
HLA B*3901	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.518896	-0.110482	-4.629378	33029.049496
HLA A*3301	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.575119	-0.054260	-4.629379	37594.061879
HLA A*2501	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.487631	-0.141893	-4.629524	30734.876963
HLA A*3201	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.616945	-0.013165	-4.630110	41394.704238
HLA A*3002	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.477653	-0.152648	-4.630301	30036.769105
HLA A*2402	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.566584	-0.063767	-4.630350	36862.397072
HLA A*3002	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.219572	-0.410971	-4.630543	16579.509829
HLA B*3801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.551474	-0.079239	-4.630713	35601.970408
HLA B*0803	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.510316	-0.120427	-4.630743	32382.901333
HLA A*3301	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.639758	0.008974	-4.630785	43627.294681
HLA A*0212	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.488999	-0.141893	-4.630891	30831.799932
HLA A*2402	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.587548	-0.043361	-4.630909	38685.483362
HLA B*4403	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.656386	0.025261	-4.631124	45329.986391
HLA B*1801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.516587	-0.114630	-4.631216	32853.869828
HLA A*1101	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.513356	-0.117875	-4.631231	32610.389810
HLA A*8001	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.442803	-0.188668	-4.631471	27720.643334
HLA A*2403	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.443055	-0.188668	-4.631722	27736.694300
HLA A*0211	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.486779	-0.145362	-4.632141	30674.579352
HLA A*2403	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.443807	-0.188551	-4.632357	27784.752667
HLA B*4002	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.621632	-0.010996	-4.632628	41843.885643
HLA B*2705	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.491036	-0.141893	-4.632928	30976.752276
HLA B*5301	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.598638	-0.034337	-4.632975	39686.024559
HLA A*2501	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.503817	-0.129168	-4.632985	31901.939059
HLA B*4501	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.625201	-0.008210	-4.633411	42189.159584

HLA A*2602	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.555212	-0.079239	-4.634451	35909.723862
HLA A*2603	1:516-524	9	GFTKFSQAS	1.031721	-1.019633	-4.646814	0.012088	-4.634726	44341.847783
HLA A*0250	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.586235	-0.048602	-4.634836	38568.670226
HLA B*5301	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.569187	-0.065831	-4.635017	37084.019631
HLA A*0211	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.526158	-0.108943	-4.635101	33586.003892
HLA A*2603	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.569410	-0.065831	-4.635241	37103.083470
HLA A*3301	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.572046	-0.063767	-4.635813	37328.980205
HLA B*1503	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.526877	-0.108943	-4.635820	33641.649084
HLA A*2501	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.480132	-0.155719	-4.635851	30208.692106
HLA B*4403	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.634895	-0.001305	-4.636200	43141.461081
HLA B*3901	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.507292	-0.129168	-4.636460	32158.217589
HLA B*5301	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.589042	-0.047418	-4.636461	38818.817347
HLA A*3002	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.526001	-0.110482	-4.636482	33573.832429
HLA B*5101	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.480820	-0.155719	-4.636540	30256.613799
HLA B*1502	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.557338	-0.079239	-4.636577	36085.967150
HLA A*0202	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.522037	-0.114630	-4.636667	33268.815402
HLA B*1502	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.589317	-0.047418	-4.636735	38843.395768
HLA A*0250	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.582501	-0.054260	-4.636761	38238.542804
HLA A*6801	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.582544	-0.054260	-4.636803	38242.266578
HLA B*4403	1:264-272	9	QTAAEMRAD	0.817373	-0.807794	-4.646457	0.009579	-4.636877	44305.400329
HLA B*5401	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.548182	-0.088805	-4.636987	35333.154007
HLA B*4001	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.400886	-0.236114	-4.637000	25170.169672
HLA A*2902	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.401069	-0.236114	-4.637184	25180.793004
HLA B*4501	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.627532	-0.009859	-4.637390	42416.180973
HLA B*7301	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.590057	-0.047362	-4.637420	38909.645818
HLA B*3901	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.392090	-0.245356	-4.637446	24665.485672
HLA B*5401	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.131583	-0.506277	-4.637861	13538.902891
HLA A*6901	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.378554	-0.259643	-4.638198	23908.607819
HLA A*2601	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.392896	-0.245356	-4.638252	24711.297240
HLA B*1509	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.523724	-0.114630	-4.638354	33398.292776
HLA A*3002	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.529809	-0.108943	-4.638752	33869.550557
HLA A*2603	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.647742	0.008974	-4.638768	44436.703465
HLA B*0803	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.521130	-0.117875	-4.639006	33199.415375
HLA A*2501	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.493846	-0.145362	-4.639208	31177.828711
HLA B*7301	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.560029	-0.079239	-4.639267	36310.189023
HLA A*3002	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.483637	-0.155719	-4.639357	30453.509915
HLA B*4002	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.618009	-0.021825	-4.639834	41496.273809
HLA B*0802	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.498075	-0.141893	-4.639967	31482.915211
HLA B*4501	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.649213	0.008974	-4.640239	44587.447498
HLA A*0250	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.593067	-0.047362	-4.640429	39180.228805
HLA B*4002	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.649424	0.008974	-4.640451	44609.161967
HLA A*0250	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.498599	-0.141893	-4.640491	31520.919285
HLA A*2602	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.578080	-0.063193	-4.641273	37851.195686
HLA B*4501	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.510363	-0.130925	-4.641288	32386.405281
HLA A*2301	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.532460	-0.108943	-4.641402	34076.866490
HLA A*0250	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.575937	-0.065831	-4.641768	37664.904682
HLA A*2501	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.488654	-0.153340	-4.641993	30807.290576
HLA B*1502	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.598732	-0.043361	-4.642093	39694.613368
HLA B*0803	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.512975	-0.129168	-4.642143	32581.822518
HLA B*1801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.486494	-0.155719	-4.642214	30654.506447
HLA B*1801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.531804	-0.110482	-4.642286	34025.471060
HLA B*1801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.453688	-0.188668	-4.642356	28424.214319
HLA A*2301	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.546272	-0.096147	-4.642420	35178.091572
HLA A*3002	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.553678	-0.088805	-4.642482	35783.090910
HLA B*4801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.397226	-0.245356	-4.642582	24958.911753
HLA A*3201	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.578857	-0.063767	-4.642624	37919.035533
HLA B*5101	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.497577	-0.145362	-4.642939	31446.828264
HLA A*6801	1:384-392	9	IRTLQKPDS	0.874257	-0.848996	-4.668260	0.025261	-4.642999	46586.478797
HLA A*0212	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.397787	-0.245356	-4.643143	24991.203586
HLA B*7301	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.594653	-0.048602	-4.643255	39323.563821
HLA B*5101	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.514178	-0.129168	-4.643346	32672.194812
HLA A*0216	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.303923	-0.339553	-4.643476	20133.667731
HLA B*4002	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.618768	-0.025025	-4.643793	41568.847546
HLA A*2301	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.529201	-0.114630	-4.643831	33822.127085
HLA A*6801	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.652899	0.008974	-4.643925	44967.521702

HLA A*3301	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.642669	-0.001305	-4.643974	43920.704250
HLA A*3301	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.609969	-0.034337	-4.644306	40735.135284
HLA B*3801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.581428	-0.063193	-4.644621	38144.121683
HLA A*3301	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.622882	-0.021825	-4.644707	41964.488367
HLA A*2602	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.616125	-0.028622	-4.644747	41316.622647
HLA B*5701	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.408752	-0.236114	-4.644866	25630.213208
HLA B*4002	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.609826	-0.035208	-4.645034	40721.694775
HLA A*3201	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.623223	-0.021825	-4.645048	41997.419650
HLA A*0201	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.385521	-0.259643	-4.645164	24295.201827
HLA A*0206	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.456618	-0.188551	-4.645169	28616.616068
HLA A*3001	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.234362	-0.410971	-4.645333	17153.853418
HLA A*2902	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.456837	-0.188668	-4.645505	28631.017273
HLA B*5301	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.598365	-0.047362	-4.645727	39661.127521
HLA B*1801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.516589	-0.129168	-4.645757	32854.047565
HLA A*0211	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.536661	-0.109105	-4.645766	34408.087339
HLA A*0219	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.475525	-0.170363	-4.645888	29889.908302
HLA B*4501	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.634928	-0.010996	-4.645923	43144.728672
HLA A*2301	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.536966	-0.109105	-4.646071	34432.294562
HLA A*0211	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.515236	-0.130925	-4.646161	32751.830535
HLA A*0101	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.386918	-0.259643	-4.646562	24373.531264
HLA A*0212	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.410512	-0.236114	-4.646626	25734.277703
HLA A*0206	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.494194	-0.152648	-4.646841	31202.801660
HLA A*2602	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.612622	-0.034337	-4.646959	40984.697268
HLA B*1509	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.550929	-0.096147	-4.647076	35557.314608
HLA A*0250	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.491609	-0.155719	-4.647328	31017.668989
HLA A*0202	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.568097	-0.079239	-4.647335	36991.048485
HLA A*6901	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.258785	-0.388552	-4.647337	18146.153957
HLA A*1101	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.458799	-0.188551	-4.647349	28760.643506
HLA B*0802	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.458900	-0.188551	-4.647450	28767.334736
HLA A*0202	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.388105	-0.259643	-4.647748	24440.210648
HLA B*5301	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.459273	-0.188668	-4.647941	28792.090248
HLA B*4601	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.402658	-0.245356	-4.648014	25273.049899
HLA B*1509	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.527613	-0.120427	-4.648039	33698.662587
HLA A*2603	1:559-567	9	NQFVMPDLS	0.863303	-0.891925	-4.619419	-0.028622	-4.648041	41631.186795
HLA B*3901	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.478109	-0.170363	-4.648472	30068.309798
HLA B*1509	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.519686	-0.129168	-4.648854	33089.141750
HLA B*1517	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.507045	-0.141893	-4.648938	32139.955675
HLA B*4002	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.640120	-0.009859	-4.649979	43663.656725
HLA B*3801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.494663	-0.155719	-4.650383	31236.580670
HLA A*0203	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.405524	-0.245356	-4.650880	25440.405336
HLA B*5301	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.603405	-0.047884	-4.651288	40124.044359
HLA B*0802	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.481187	-0.170363	-4.651550	30282.159426
HLA B*2705	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.499381	-0.152648	-4.652029	31577.755183
HLA A*0202	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.498801	-0.153340	-4.652141	31535.587820
HLA B*4403	1:488-496	9	VGSGPATKD	0.884534	-0.875560	-4.661136	0.008974	-4.652163	45828.563804
HLA B*4002	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.644140	-0.008210	-4.652350	44069.697842
HLA A*2301	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.541869	-0.110482	-4.652351	34823.253165
HLA B*5401	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.543540	-0.108943	-4.652483	34957.456348
HLA A*0216	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.463857	-0.188668	-4.652525	29097.591341
HLA B*7301	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.618197	-0.034337	-4.652534	41514.236915
HLA B*0803	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.497091	-0.155719	-4.652810	31411.632336
HLA B*7301	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.609518	-0.043361	-4.652879	40692.845718
HLA B*5101	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.511018	-0.141893	-4.652911	32435.324905
HLA B*5301	1:425-433	9	EQREIPDVS	1.020396	-1.074656	-4.598936	-0.054260	-4.653195	39713.300446
HLA B*0801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.393699	-0.259643	-4.653342	24757.059961
HLA A*2501	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.464947	-0.188551	-4.653498	29170.723531
HLA B*2705	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.464959	-0.188551	-4.653510	29171.512594
HLA A*2602	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.640454	-0.013165	-4.653619	43697.212219
HLA A*3002	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.574830	-0.079239	-4.654069	37569.054497
HLA A*3002	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.545067	-0.109105	-4.654172	35080.598107
HLA B*0803	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.501644	-0.152648	-4.654292	31742.695823
HLA A*0206	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.536513	-0.117875	-4.654388	34396.362269
HLA A*2601	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.394848	-0.259643	-4.654491	24822.639879
HLA A*0250	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.575284	-0.079239	-4.654522	37608.301155
HLA B*0801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.278304	-0.376448	-4.654752	18980.345456

HLA A*2603	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.632947	-0.021825	-4.654772	42948.413551
HLA B*1509	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.499118	-0.155719	-4.654837	31558.627777
HLA B*1502	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.418829	-0.236114	-4.654943	26231.864486
HLA A*2902	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.244359	-0.410971	-4.655330	17553.299110
HLA B*4601	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.395854	-0.259643	-4.655497	24880.181619
HLA A*3301	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.535368	-0.120427	-4.655795	34305.860334
HLA A*2403	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.419830	-0.236114	-4.655944	26292.388492
HLA B*4501	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.608675	-0.047884	-4.656558	40613.890796
HLA A*0212	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.396963	-0.259643	-4.656606	24943.793539
HLA B*5301	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.592863	-0.063767	-4.656629	39161.792564
HLA B*1801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.486386	-0.170363	-4.656749	30646.878872
HLA B*7301	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.546282	-0.110482	-4.656763	35178.852818
HLA A*0250	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.593140	-0.063767	-4.656907	39186.800138
HLA A*2301	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.536517	-0.120427	-4.656944	34396.734432
HLA A*1101	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.468518	-0.188668	-4.657186	29411.584255
HLA A*2603	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.656000	-0.001305	-4.657305	45289.786473
HLA B*1517	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.468934	-0.188668	-4.657602	29439.760817
HLA A*0202	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.548796	-0.108943	-4.657738	35383.078990
HLA B*0702	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.421705	-0.236114	-4.657819	26406.140502
HLA A*2602	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.592024	-0.065831	-4.657854	39086.231193
HLA A*2301	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.505215	-0.152648	-4.657863	32004.793151
HLA A*6901	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.317689	-0.340176	-4.657865	20782.056908
HLA A*0203	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.398299	-0.259643	-4.657943	25020.694495
HLA A*0211	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.528872	-0.129168	-4.658040	33796.520429
HLA A*1101	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.412697	-0.245356	-4.658053	25864.078173
HLA B*3801	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.549014	-0.109105	-4.658120	35400.885393
HLA B*1502	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.610855	-0.047362	-4.658217	40818.300522
HLA A*0216	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.488134	-0.170363	-4.658497	30770.479835
HLA A*2301	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.398983	-0.259643	-4.658626	25060.115038
HLA B*4501	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.636967	-0.021825	-4.658792	43347.803413
HLA A*2602	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.548326	-0.110482	-4.658807	35344.815987
HLA B*1509	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.549865	-0.108943	-4.658807	35470.281704
HLA B*5401	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.538474	-0.120427	-4.658901	34552.090961
HLA B*4403	1:356-364	9	ITRDVQVPD	0.769352	-0.780348	-4.647967	-0.010996	-4.658963	44459.787633
HLA A*2603	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.649349	-0.009859	-4.659207	44601.440056
HLA B*1502	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.610655	-0.048602	-4.659257	40799.534926
HLA B*5401	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.548871	-0.110482	-4.659352	35389.204914
HLA B*1503	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.541724	-0.117875	-4.659599	34811.574948
HLA B*4501	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.611019	-0.048602	-4.659621	40833.761022
HLA A*1101	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.517886	-0.141893	-4.659778	32952.304891
HLA A*3301	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.613078	-0.047362	-4.660440	41027.734046
HLA A*0211	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.540013	-0.120427	-4.660440	34674.742692
HLA A*3201	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.594846	-0.065831	-4.660676	39341.012053
HLA A*0250	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.597505	-0.063193	-4.660698	39582.675412
HLA B*3901	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.518819	-0.141893	-4.660711	33023.153467
HLA A*3301	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.647627	-0.013165	-4.660792	44424.925542
HLA B*3801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.546188	-0.114630	-4.660817	35171.241094
HLA B*1503	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.507795	-0.153340	-4.661135	32195.469240
HLA A*2501	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.491069	-0.170363	-4.661432	30979.098496
HLA A*2301	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.543704	-0.117875	-4.661580	34970.696973
HLA A*3001	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.295079	-0.366558	-4.661638	19727.835393
HLA B*1503	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.532521	-0.129168	-4.661689	34081.659981
HLA A*0211	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.551732	-0.110482	-4.662214	35623.163011
HLA B*1509	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.531564	-0.130925	-4.662490	34006.700688
HLA B*4002	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.474016	-0.188551	-4.662567	29786.276271
HLA B*5101	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.474035	-0.188551	-4.662586	29787.565423
HLA A*1101	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.492330	-0.170363	-4.662694	31069.227053
HLA B*5301	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.542671	-0.120427	-4.663097	34887.553426
HLA A*0211	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.521476	-0.141893	-4.663368	33225.827834
HLA B*5301	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.600191	-0.063193	-4.663384	39828.193313
HLA A*3201	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.616289	-0.047362	-4.663652	41332.271894
HLA B*4403	1:260-268	9	ENRYQTAAE	0.849920	-0.874945	-4.639105	-0.025025	-4.664130	43561.730761
HLA A*3201	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.549808	-0.114630	-4.664438	35465.676636
HLA A*6801	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.654614	-0.009859	-4.664473	45145.459423
HLA B*1801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.511183	-0.153340	-4.664523	32447.610237

HLA B*4002	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.648033	-0.017067	-4.665100	44466.522773
HLA A*3201	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.622048	-0.043361	-4.665409	41883.972461
HLA A*2402	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.602352	-0.063193	-4.665545	40026.916257
HLA A*1101	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.255206	-0.410971	-4.666177	17997.257297
HLA A*0219	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.406654	-0.259643	-4.666297	25506.691462
HLA B*5401	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.551678	-0.114630	-4.666308	35618.730788
HLA A*0301	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.326788	-0.339553	-4.666341	21222.086734
HLA B*3801	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.570324	-0.096147	-4.666471	37181.247155
HLA B*4403	1:215-223	9	PFTGDSPVS	1.180931	-1.190790	-4.657072	-0.009859	-4.666930	45401.650198
HLA A*3301	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.601224	-0.065831	-4.667055	39923.111326
HLA B*0802	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.421907	-0.245356	-4.667263	26418.428829
HLA B*2705	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.496971	-0.170363	-4.667334	31402.966926
HLA B*0803	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.514070	-0.153340	-4.667410	32664.065188
HLA A*0212	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.327890	-0.339553	-4.667443	21276.000586
HLA B*7301	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.601652	-0.065831	-4.667483	39962.438973
HLA B*5701	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.408226	-0.259643	-4.667869	25599.172938
HLA B*3801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.557491	-0.110482	-4.667973	36098.658752
HLA A*8001	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.432019	-0.236114	-4.668133	27040.777141
HLA A*0206	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.557977	-0.110482	-4.668459	36139.106371
HLA B*0803	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.526722	-0.141893	-4.668615	33629.639387
HLA B*4501	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.634319	-0.034337	-4.668657	43084.318281
HLA B*3801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.559824	-0.108943	-4.668767	36293.103278
HLA B*5401	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.432757	-0.236114	-4.668871	27086.750487
HLA B*5101	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.515656	-0.153340	-4.668996	32783.561792
HLA B*4403	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.635355	-0.034337	-4.669693	43187.229884
HLA B*4002	1:401-409	9	GTDPAANTS	1.101859	-1.136196	-4.635466	-0.034337	-4.669803	43198.212272
HLA A*3002	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.606729	-0.063193	-4.669923	40432.372262
HLA B*0801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.303491	-0.366558	-4.670049	20113.636255
HLA B*4501	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.573916	-0.096147	-4.670064	37490.075550
HLA A*2402	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.574095	-0.096147	-4.670242	37505.492823
HLA B*0802	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.481915	-0.188668	-4.670583	30332.987204
HLA B*2705	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.481995	-0.188668	-4.670663	30338.567052
HLA B*3801	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.550377	-0.120427	-4.670804	35512.138465
HLA B*1502	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.607972	-0.063193	-4.671165	40548.248622
HLA A*2301	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.542708	-0.129168	-4.671876	34890.573362
HLA A*2603	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.624900	-0.047418	-4.672318	42159.955146
HLA B*4403	1:415-423	9	EITVNVSTG	0.706157	-0.714367	-4.664195	-0.008210	-4.672405	46152.504872
HLA A*2402	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.551998	-0.120427	-4.672425	35644.946731
HLA B*7301	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.576407	-0.096147	-4.672554	37705.679329
HLA A*0206	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.261759	-0.410971	-4.672730	18270.862078
HLA A*2601	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.284291	-0.388552	-4.672843	19243.789621
HLA B*1503	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.531257	-0.141893	-4.673149	33982.608831
HLA A*2402	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.296943	-0.376448	-4.673391	19812.650437
HLA A*0211	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.555677	-0.117875	-4.673552	35948.209460
HLA A*3002	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.553130	-0.120427	-4.673557	35738.014590
HLA A*2301	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.542736	-0.130925	-4.673661	34892.838485
HLA A*3301	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.630612	-0.043361	-4.673973	42718.081325
HLA A*2402	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.594853	-0.079239	-4.674091	39341.650549
HLA B*4501	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.657544	-0.017067	-4.674610	45451.046246
HLA B*0803	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.529624	-0.145362	-4.674986	33855.078439
HLA B*4403	1:252-260	9	LKALAKNPE	0.605485	-0.627310	-4.653559	-0.021825	-4.675384	45035.932363
HLA B*4403	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.641102	-0.035208	-4.676310	43762.506546
HLA A*0219	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.440327	-0.236114	-4.676441	27563.029370
HLA A*2603	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.613388	-0.063193	-4.676581	41057.042635
HLA B*5401	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.520921	-0.155719	-4.676641	33183.434364
HLA B*3801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.545758	-0.130925	-4.676683	35136.438454
HLA A*0206	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.557143	-0.120427	-4.677570	36069.767437
HLA A*0201	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.338247	-0.339553	-4.677799	21789.462813
HLA B*5401	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.548742	-0.129168	-4.677910	35378.676638
HLA B*4501	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.630522	-0.047418	-4.677941	42709.300424
HLA A*2402	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.569039	-0.109105	-4.678144	37071.382697
HLA B*4002	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.612666	-0.065831	-4.678497	40988.910215
HLA A*3201	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.615481	-0.063193	-4.678674	41255.423988
HLA B*4403	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.630130	-0.048602	-4.678732	42670.732068
HLA B*5801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.247526	-0.432915	-4.680441	17681.774968

HLA A*6801	1:498-506	9	PDVAGQTVD	1.091996	-1.093301	-4.679138	-0.001305	-4.680443	47768.103749
HLA A*2402	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.591648	-0.088805	-4.680453	39052.413482
HLA A*2301	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.527213	-0.153340	-4.680553	33667.684809
HLA A*0250	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.591883	-0.088805	-4.680687	39073.546121
HLA A*0216	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.445526	-0.236114	-4.681641	27894.999514
HLA A*2301	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.539781	-0.141893	-4.681673	34656.176600
HLA B*5101	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.445867	-0.236114	-4.681981	27916.889883
HLA A*0202	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.552846	-0.129168	-4.682014	35714.628263
HLA A*2603	1:567-575	9	SGMFWVDAE	0.687099	-0.722307	-4.646858	-0.035208	-4.682067	44346.405822
HLA A*2602	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.638750	-0.043361	-4.682111	43526.160008
HLA A*2402	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.571828	-0.110482	-4.682309	37310.203984
HLA A*2501	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.493686	-0.188668	-4.682354	31166.361356
HLA B*3901	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.493841	-0.188551	-4.682392	31177.491376
HLA A*6802	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.422840	-0.259643	-4.682483	26475.229350
HLA A*2603	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.670311	-0.013165	-4.683476	46807.019345
HLA B*4002	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.640120	-0.043361	-4.683481	43663.656725
HLA B*4801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.423848	-0.259643	-4.683491	26536.745543
HLA A*3201	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.250583	-0.432915	-4.683498	17806.662982
HLA A*3201	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.447538	-0.236114	-4.683652	28024.477059
HLA B*5401	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.553135	-0.130925	-4.684060	35738.401269
HLA B*7301	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.566403	-0.117875	-4.684278	36847.044816
HLA A*0202	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.575190	-0.109105	-4.684295	37600.163766
HLA A*0216	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.424893	-0.259643	-4.684537	26600.707081
HLA B*1517	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.514223	-0.170363	-4.684586	32675.553290
HLA B*4403	1:319-327	9	DTDRDRSIG	0.871594	-0.888661	-4.668074	-0.017067	-4.685141	46566.572863
HLA B*5301	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.589613	-0.096147	-4.685760	38869.882241
HLA B*1509	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.534076	-0.152648	-4.686724	34203.937046
HLA B*0802	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.450735	-0.236114	-4.686849	28231.578831
HLA B*3801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.557806	-0.129168	-4.686974	36124.837064
HLA B*4402	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.441725	-0.245356	-4.687081	27651.894512
HLA B*5301	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.598346	-0.088805	-4.687151	39659.411059
HLA B*5401	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.541825	-0.145362	-4.687187	34819.673940
HLA A*0211	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.498662	-0.188551	-4.687213	31525.523788
HLA A*0211	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.534633	-0.152648	-4.687281	34247.819536
HLA B*4501	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.644119	-0.043361	-4.687480	44067.552185
HLA B*1503	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.542405	-0.145362	-4.687767	34866.232573
HLA A*8001	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.442423	-0.245356	-4.687779	27696.359549
HLA B*3901	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.451755	-0.236114	-4.687869	28297.941401
HLA A*0203	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.311972	-0.376448	-4.688420	20510.310388
HLA A*2603	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.579381	-0.109105	-4.688487	37964.808863
HLA B*4002	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.640188	-0.048602	-4.688790	43670.507513
HLA A*0250	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.574377	-0.114630	-4.689006	37529.848795
HLA B*1801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.547137	-0.141893	-4.689029	35248.195255
HLA B*5301	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.580629	-0.108943	-4.689572	38074.025309
HLA A*2501	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.453531	-0.236114	-4.689645	28413.913472
HLA B*4002	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.641802	-0.047884	-4.689686	43833.115038
HLA A*3002	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.560827	-0.129168	-4.689995	36377.038077
HLA B*7301	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.560971	-0.129168	-4.690139	36389.044598
HLA B*1801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.544945	-0.145362	-4.690307	35070.730824
HLA B*5801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.351091	-0.339553	-4.690644	22443.529619
HLA A*2402	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.549056	-0.141893	-4.690949	35404.332828
HLA B*2705	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.454976	-0.236114	-4.691090	28508.606325
HLA B*3801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.546124	-0.145362	-4.691486	35166.104111
HLA B*4002	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.644218	-0.047418	-4.691636	44077.566147
HLA B*1502	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.560935	-0.130925	-4.691860	36386.091808
HLA A*3101	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.281015	-0.410971	-4.691986	19099.210634
HLA A*0211	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.352771	-0.339553	-4.692324	22530.510896
HLA B*4501	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.644998	-0.047362	-4.692360	44156.804260
HLA B*0801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.353168	-0.339553	-4.692721	22551.119314
HLA A*0202	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.582288	-0.110482	-4.692769	38219.722606
HLA B*1801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.504245	-0.188551	-4.692795	31933.365171
HLA A*3001	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.298566	-0.394285	-4.692851	19886.853356
HLA A*2301	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.537741	-0.155719	-4.693461	34493.820182
HLA B*4002	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.646421	-0.047362	-4.693784	44301.805165
HLA A*0202	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.505685	-0.188551	-4.694236	32039.440368

HLA B*5801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.354089	-0.340176	-4.694266	22598.993689
HLA B*1509	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.540937	-0.153340	-4.694276	34748.542617
HLA A*0250	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.585391	-0.108943	-4.694334	38493.836767
HLA A*2402	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.580420	-0.114630	-4.695049	38055.697835
HLA A*2301	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.549846	-0.145362	-4.695208	35468.746615
HLA B*4501	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.629402	-0.065831	-4.695232	42599.230423
HLA A*2603	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.616254	-0.079239	-4.695493	41328.917985
HLA B*4403	1:12-20	9	ELGEILGFG	0.730696	-0.778580	-4.647634	-0.047884	-4.695517	44425.646550
HLA A*2402	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.577668	-0.117875	-4.695544	37815.377759
HLA A*0250	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.575234	-0.120427	-4.695661	37604.028806
HLA B*1502	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.587066	-0.108943	-4.696009	38642.603888
HLA A*2601	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.357160	-0.339553	-4.696713	22759.351215
HLA B*4501	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.633692	-0.063193	-4.696885	43022.130475
HLA A*6801	1:190-198	9	GDSVDARSD	0.931644	-0.944809	-4.683762	-0.013165	-4.696927	48279.391520
HLA B*0702	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.437404	-0.259643	-4.697048	27378.155670
HLA A*0206	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.555250	-0.141893	-4.697142	35912.832279
HLA A*6801	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.653829	-0.043361	-4.697190	45063.959611
HLA A*2902	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.451868	-0.245356	-4.697224	28305.290614
HLA B*3801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.544679	-0.152648	-4.697327	35049.298025
HLA A*6801	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.586902	-0.110482	-4.697383	38627.973004
HLA B*4403	1:297-305	9	LSSAAGNLS	0.872251	-0.938082	-4.631596	-0.065831	-4.697427	42815.022089
HLA B*0702	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.321965	-0.376448	-4.698413	20987.687663
HLA A*0202	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.578155	-0.120427	-4.698582	37857.748918
HLA A*8001	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.438962	-0.259643	-4.698605	27476.530766
HLA A*3301	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.635790	-0.063193	-4.698983	43230.474574
HLA B*7301	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.590151	-0.109105	-4.699257	38918.066604
HLA A*2603	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.655993	-0.043361	-4.699354	45289.051441
HLA B*3801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.581890	-0.117875	-4.699766	38184.795381
HLA A*8001	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.311312	-0.388552	-4.699864	20479.154735
HLA B*5301	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.585370	-0.114630	-4.700000	38491.962587
HLA B*1502	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.611816	-0.088805	-4.700620	40908.716909
HLA B*4501	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.636920	-0.063767	-4.700687	43343.113531
HLA A*2603	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.590248	-0.110482	-4.700729	38926.699800
HLA A*0206	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.512179	-0.188668	-4.700847	32522.123764
HLA A*2501	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.455641	-0.245356	-4.700997	28552.286391
HLA B*1509	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.512966	-0.188551	-4.701517	32581.117469
HLA B*0802	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.442319	-0.259643	-4.701963	27689.767627
HLA B*4403	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.638598	-0.063767	-4.702364	43510.857038
HLA B*4403	1:13-21	9	LGEILGFGG	0.811222	-0.854583	-4.659059	-0.043361	-4.702420	45609.919172
HLA B*4403	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.655197	-0.047362	-4.702559	45206.069591
HLA A*0250	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.593603	-0.109105	-4.702708	39228.585660
HLA A*0219	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.457668	-0.245356	-4.703025	28685.901094
HLA A*2402	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.550403	-0.152648	-4.703050	35514.251812
HLA B*5401	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.336729	-0.366558	-4.703287	21713.446160
HLA B*1509	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.533000	-0.170363	-4.703363	34119.293857
HLA B*4403	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.614609	-0.088805	-4.703414	41172.704551
HLA B*2705	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.443790	-0.259643	-4.703433	27783.700500
HLA B*0803	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.514951	-0.188551	-4.703502	32730.398314
HLA B*3501	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.327223	-0.376448	-4.703671	21243.337056
HLA B*4002	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.624496	-0.079239	-4.703735	42120.743514
HLA B*1509	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.558382	-0.145362	-4.703744	36172.749494
HLA A*3002	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.315605	-0.388552	-4.704157	20682.571603
HLA A*0216	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.458869	-0.245356	-4.704225	28765.311642
HLA B*2705	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.327812	-0.376448	-4.704261	21272.202598
HLA B*1801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.468220	-0.236114	-4.704334	29391.383792
HLA B*1502	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.594195	-0.110482	-4.704676	39282.102151
HLA A*0250	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.573930	-0.130925	-4.704855	37491.292472
HLA B*4002	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.641704	-0.063193	-4.704897	43823.156613
HLA A*2402	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.596251	-0.108943	-4.705193	39468.490793
HLA A*2603	1:236-244	9	PSARHEGLS	1.176077	-1.223439	-4.657838	-0.047362	-4.705200	45481.792281
HLA A*0301	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.365202	-0.340176	-4.705379	23184.736528
HLA A*3201	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.616989	-0.088805	-4.705794	41398.959331
HLA B*7301	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.553241	-0.152648	-4.705889	35747.102664
HLA A*3201	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.626705	-0.079239	-4.705943	42335.485505
HLA A*0203	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.304733	-0.401420	-4.706153	20171.280534

HLA A*0202	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.575899	-0.130925	-4.706824	37661.644616
HLA B*7301	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.575923	-0.130925	-4.706848	37663.682125
HLA B*5301	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.596422	-0.110482	-4.706904	39484.080843
HLA B*1501	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.274684	-0.432915	-4.707599	18822.770898
HLA B*4002	1:407-415	9	NTSVSAGDE	0.542286	-0.606053	-4.643856	-0.063767	-4.707623	44040.859408
HLA B*4403	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.519394	-0.188551	-4.707945	33066.952129
HLA B*0803	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.537786	-0.170363	-4.708149	34497.365911
HLA A*0211	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.537849	-0.170363	-4.708212	34502.405206
HLA A*3201	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.599335	-0.108943	-4.708278	39749.840820
HLA A*3301	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.598060	-0.110482	-4.708541	39633.244227
HLA A*0202	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.563607	-0.145362	-4.708969	36610.594011
HLA B*0702	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.320771	-0.388552	-4.709323	20930.087987
HLA B*7301	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.594716	-0.114630	-4.709346	39329.308116
HLA B*7301	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.600449	-0.108943	-4.709392	39851.901639
HLA B*5401	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.567566	-0.141893	-4.709458	36945.849573
HLA A*6901	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.342971	-0.366558	-4.709530	22027.810812
HLA B*4001	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.333153	-0.376448	-4.709601	21535.394904
HLA A*3301	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.600693	-0.109105	-4.709799	39874.329762
HLA B*4403	1:176-184	9	VIGTAQYLS	0.850095	-0.897513	-4.662532	-0.047418	-4.709950	45976.069585
HLA A*3101	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.370653	-0.339553	-4.710206	23477.560596
HLA B*1517	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.309127	-0.401420	-4.710547	20376.378835
HLA A*0250	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.600552	-0.110482	-4.711034	39861.388921
HLA B*1503	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.466432	-0.245356	-4.711788	29270.630388
HLA A*2603	1:22-30	9	MSEVHLARD	0.778115	-0.826717	-4.663267	-0.048602	-4.711869	46053.986598
HLA B*1502	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.583075	-0.129168	-4.712243	38289.051505
HLA A*2403	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.372295	-0.340176	-4.712472	23566.509359
HLA A*3002	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.523994	-0.188551	-4.712545	33419.077563
HLA A*2301	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.542804	-0.170363	-4.713168	34898.313139
HLA B*0803	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.524577	-0.188668	-4.713245	33463.944444
HLA B*1502	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.593464	-0.120427	-4.713891	39216.066543
HLA A*3301	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.634780	-0.079239	-4.714018	43130.026461
HLA A*3201	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.585422	-0.129168	-4.714590	38496.544079
HLA B*1502	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.600303	-0.114630	-4.714933	39838.537030
HLA B*7301	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.626561	-0.088805	-4.715366	42321.516962
HLA A*2602	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.627243	-0.088805	-4.716047	42387.965941
HLA B*4501	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.601699	-0.114630	-4.716329	39966.763054
HLA B*4601	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.305647	-0.410971	-4.716618	20213.774620
HLA A*3002	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.480750	-0.236114	-4.716864	30251.703650
HLA B*3801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.575305	-0.141893	-4.717197	37610.132310
HLA B*4403	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.654046	-0.063193	-4.717239	45086.393968
HLA B*5401	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.564293	-0.153340	-4.717633	36668.473017
HLA A*3101	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.377694	-0.340176	-4.717871	23861.315147
HLA A*1101	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.458254	-0.259643	-4.717897	28724.568830
HLA A*0250	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.588763	-0.129168	-4.717931	38793.834736
HLA A*0250	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.600705	-0.117875	-4.718580	39875.408356
HLA A*6901	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.307727	-0.410971	-4.718698	20310.785204
HLA A*0202	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.601184	-0.117875	-4.719060	39919.439842
HLA B*1517	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.459424	-0.259643	-4.719067	28802.060743
HLA B*1503	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.530599	-0.188668	-4.719267	33931.171998
HLA B*5401	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.530780	-0.188551	-4.719331	33945.309361
HLA A*2602	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.610686	-0.108943	-4.719629	40802.404399
HLA A*2301	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.531355	-0.188551	-4.719906	33990.331079
HLA B*4501	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.641072	-0.079239	-4.720310	43759.428900
HLA A*6901	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.380988	-0.339553	-4.720541	24042.983293
HLA A*0202	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.565005	-0.155719	-4.720724	36728.629137
HLA A*3201	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.610495	-0.110482	-4.720977	40784.528661
HLA A*0250	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.575805	-0.145362	-4.721167	37653.495685
HLA B*0803	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.485270	-0.236114	-4.721384	30568.226768
HLA B*1502	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.603583	-0.117875	-4.721458	40140.544815
HLA B*1503	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.288903	-0.432915	-4.721818	19449.240180
HLA B*5301	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.592978	-0.129168	-4.722146	39172.175127
HLA A*2602	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.607535	-0.114630	-4.722165	40507.467899
HLA B*7301	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.580345	-0.141893	-4.722237	38049.110338
HLA B*5301	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.577184	-0.145362	-4.722547	37773.258370
HLA B*5801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.356027	-0.366558	-4.722586	22700.081999

HLA A*0202	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.486821	-0.236114	-4.722935	30677.566527
HLA A*3201	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.603355	-0.120427	-4.723782	40119.486219
HLA A*2501	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.335904	-0.388552	-4.724456	21672.254247
HLA A*3201	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.615507	-0.109105	-4.724612	41257.879121
HLA B*5801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.348300	-0.376448	-4.724748	22299.748746
HLA A*2402	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.596248	-0.129168	-4.725416	39468.277273
HLA A*2402	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.594498	-0.130925	-4.725423	39309.525743
HLA A*0212	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.385286	-0.340176	-4.725462	24282.061947
HLA A*0219	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.386195	-0.339553	-4.725747	24332.952785
HLA A*3201	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.572518	-0.153340	-4.725858	37369.593357
HLA A*3002	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.480541	-0.245356	-4.725897	30237.141562
HLA A*0206	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.490498	-0.236114	-4.726612	30938.400035
HLA B*4002	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.630595	-0.096147	-4.726743	42716.463655
HLA A*3101	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.294262	-0.432915	-4.727177	19690.729892
HLA B*5401	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.482061	-0.245356	-4.727417	30343.162992
HLA A*2602	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.607258	-0.120427	-4.727685	40481.617523
HLA A*0201	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.387550	-0.340176	-4.727727	24409.026915
HLA B*1801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.482474	-0.245356	-4.727831	30372.067705
HLA A*0206	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.468706	-0.259643	-4.728350	29424.316083
HLA A*0202	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.586474	-0.141893	-4.728367	38589.958626
HLA A*3002	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.610540	-0.117875	-4.728415	40788.721032
HLA A*0206	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.558168	-0.170363	-4.728531	36154.946035
HLA A*0202	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.575925	-0.152648	-4.728573	37663.885881
HLA B*1503	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.558229	-0.170363	-4.728592	36160.031843
HLA B*1502	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.572908	-0.155719	-4.728628	37403.167880
HLA A*3201	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.587174	-0.141893	-4.729067	38652.221486
HLA A*6801	1:588-596	9	DKGADVDAG	0.707890	-0.771083	-4.666211	-0.063193	-4.729404	46367.228210
HLA A*0101	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.389963	-0.339553	-4.729516	24545.019834
HLA A*3301	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.598915	-0.130925	-4.729840	39711.366892
HLA A*0301	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.363466	-0.366558	-4.730024	23092.231120
HLA A*3002	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.588868	-0.141893	-4.730761	38803.280051
HLA B*1502	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.589404	-0.141893	-4.731297	38851.171670
HLA B*4403	1:15-23	9	EILGFGGMS	0.918520	-1.014667	-4.635280	-0.096147	-4.731427	43179.754111
HLA B*3801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.561128	-0.170363	-4.731491	36402.236656
HLA B*4402	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.152231	-0.579820	-4.732051	14198.116894
HLA A*0301	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.355731	-0.376448	-4.732179	22684.613851
HLA B*4601	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.392675	-0.339553	-4.732227	24698.734009
HLA A*0203	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.343918	-0.388552	-4.732470	22075.887911
HLA B*4403	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.601549	-0.130925	-4.732474	39952.927641
HLA A*2601	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.392383	-0.340176	-4.732560	24682.171006
HLA B*5801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.344289	-0.388552	-4.732841	22094.765619
HLA B*7301	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.544649	-0.188551	-4.733200	35046.833145
HLA A*3301	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.644796	-0.088805	-4.733600	44136.265065
HLA B*7301	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.613202	-0.120427	-4.733629	41039.499374
HLA A*0250	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.580471	-0.153340	-4.733811	38060.227401
HLA B*1509	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.592066	-0.141893	-4.733959	39090.037517
HLA B*0801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.394223	-0.340176	-4.734399	24786.945032
HLA B*1502	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.589275	-0.145362	-4.734637	38839.613460
HLA A*0101	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.394545	-0.340176	-4.734721	24805.322805
HLA B*4002	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.579151	-0.155719	-4.734870	37944.686428
HLA A*0211	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.546472	-0.188668	-4.735140	35194.271605
HLA A*0250	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.582809	-0.152648	-4.735457	38265.651891
HLA B*5701	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.396281	-0.339553	-4.735834	24904.690705
HLA B*1509	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.547346	-0.188668	-4.736014	35265.170647
HLA B*3801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.547708	-0.188551	-4.736259	35294.563111
HLA A*2402	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.583030	-0.153340	-4.736370	38285.116056
HLA B*5301	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.605618	-0.130925	-4.736543	40329.043031
HLA B*3901	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.477228	-0.259643	-4.736871	30007.371798
HLA A*2902	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.397543	-0.339553	-4.737095	24977.146778
HLA A*2301	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.548441	-0.188668	-4.737109	35354.186594
HLA B*0803	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.477500	-0.259643	-4.737144	30026.208748
HLA A*2603	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.648508	-0.088805	-4.737312	44515.142244
HLA B*1501	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.397251	-0.340176	-4.737428	24960.397071
HLA A*3002	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.606666	-0.130925	-4.737591	40426.466857
HLA B*4501	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.549684	-0.188551	-4.738235	35455.509229

HLA B*1502	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.585659	-0.152648	-4.738307	38517.584292
HLA A*6901	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.364091	-0.376448	-4.740539	23125.485466
HLA B*4001	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.400703	-0.340176	-4.740879	25159.550822
HLA A*0212	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.331391	-0.410971	-4.742362	21448.193854
HLA B*1509	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.506380	-0.236114	-4.742495	32090.787095
HLA A*0301	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.331675	-0.410971	-4.742646	21462.238365
HLA B*4501	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.633866	-0.108943	-4.742809	43039.357049
HLA B*4601	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.366612	-0.376448	-4.743060	23260.114911
HLA B*4403	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.664233	-0.079239	-4.743471	46156.499924
HLA A*6802	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.342398	-0.401420	-4.743818	21998.752999
HLA A*3201	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.626065	-0.117875	-4.743941	42273.235079
HLA A*2602	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.588316	-0.155719	-4.744036	38753.979856
HLA A*3101	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.342983	-0.401420	-4.744403	22028.406660
HLA B*1517	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.355865	-0.388552	-4.744417	22691.610041
HLA B*4002	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.634018	-0.110482	-4.744500	43054.494190
HLA A*2402	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.588807	-0.155719	-4.744527	38797.822477
HLA B*5801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.333825	-0.410971	-4.744796	21568.740866
HLA B*1801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.485442	-0.259643	-4.745085	30580.301215
HLA A*2402	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.599838	-0.145362	-4.745200	39795.886507
HLA A*2602	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.614480	-0.130925	-4.745405	41160.455686
HLA B*4501	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.617098	-0.129168	-4.746266	41409.262947
HLA A*2902	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.358262	-0.388552	-4.746814	22817.170425
HLA B*4001	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.407481	-0.339553	-4.747034	25555.309646
HLA B*1501	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.345739	-0.401420	-4.747159	22168.638995
HLA A*2602	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.629284	-0.117875	-4.747160	42587.709126
HLA B*1502	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.559070	-0.188551	-4.747621	36230.132296
HLA A*2603	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.638964	-0.108943	-4.747907	43547.593208
HLA A*0211	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.511935	-0.236114	-4.748049	32503.831038
HLA A*6801	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.630710	-0.117875	-4.748586	42727.788631
HLA B*5301	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.606694	-0.141893	-4.748587	40429.091375
HLA A*3201	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.617953	-0.130925	-4.748878	41490.886393
HLA B*4601	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.408705	-0.340176	-4.748882	25627.440226
HLA B*0801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.338420	-0.410971	-4.749391	21798.187575
HLA B*4403	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.634996	-0.114630	-4.749626	43151.498041
HLA A*0101	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.338707	-0.410971	-4.749678	21812.579268
HLA A*3002	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.410246	-0.339553	-4.749799	25718.550697
HLA B*5701	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.317026	-0.432915	-4.749941	20750.376208
HLA B*4002	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.641027	-0.109105	-4.750132	43754.931192
HLA A*2501	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.490723	-0.259643	-4.750367	30954.472046
HLA A*6801	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.635797	-0.114630	-4.750427	43231.176196
HLA A*3301	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.635825	-0.114630	-4.750455	43233.982797
HLA B*4001	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.383913	-0.366558	-4.750472	24205.466861
HLA A*3301	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.641875	-0.108943	-4.750818	43840.466756
HLA B*4002	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.642087	-0.108943	-4.751029	43861.817439
HLA B*1502	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.598814	-0.153340	-4.752154	39702.130101
HLA B*4002	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.637663	-0.114630	-4.752292	43417.273036
HLA B*4403	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.641868	-0.110482	-4.752350	43839.755245
HLA A*6801	1:312-320	9	LPRQDLDDT	0.399819	-0.479058	-4.673581	-0.079239	-4.752820	47160.833216
HLA B*5301	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.600104	-0.153340	-4.753444	39820.221865
HLA A*2402	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.583150	-0.170363	-4.753513	38295.680543
HLA B*5301	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.598154	-0.155719	-4.753873	39641.821614
HLA B*4601	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.366032	-0.388552	-4.754584	23229.054511
HLA B*5701	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.414499	-0.340176	-4.754675	25971.621155
HLA A*6801	1:413-421	9	GDEITVNVS	1.094912	-1.183717	-4.665885	-0.088805	-4.754689	46332.374339
HLA B*5101	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.495140	-0.259643	-4.754784	31270.903761
HLA A*3301	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.519599	-0.236114	-4.755713	33082.519095
HLA A*2602	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.603132	-0.152648	-4.755780	40098.872529
HLA B*0801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.367845	-0.388552	-4.756397	23326.272004
HLA B*5801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.362150	-0.394285	-4.756435	23022.378195
HLA B*2705	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.417027	-0.339553	-4.756580	26123.243892
HLA B*4501	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.647838	-0.109105	-4.756944	44446.560862
HLA B*4501	1:4-12	9	PSHLSDRYE	0.741948	-0.852430	-4.646511	-0.110482	-4.756992	44310.913480
HLA B*5101	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.512064	-0.245356	-4.757420	32513.503794
HLA B*1509	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.512078	-0.245356	-4.757434	32514.559178
HLA A*2602	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.628678	-0.129168	-4.757846	42528.308735

HLA B*0803	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.512536	-0.245356	-4.757892	32548.877808
HLA A*6801	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.569638	-0.188551	-4.758189	37122.558766
HLA A*2603	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.638224	-0.120427	-4.758651	43473.446293
HLA A*2601	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.382419	-0.376448	-4.758867	24122.326478
HLA B*3801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.570446	-0.188668	-4.759114	37191.708241
HLA A*0216	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.419019	-0.340176	-4.759196	26243.361835
HLA A*6801	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.650406	-0.108943	-4.759349	44710.152310
HLA A*2602	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.606381	-0.153340	-4.759721	40400.012489
HLA A*3301	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.607129	-0.152648	-4.759776	40469.574257
HLA A*0301	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.365548	-0.394285	-4.759832	23203.181609
HLA A*0101	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.393572	-0.366558	-4.760131	24749.828638
HLA A*0101	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.367098	-0.394285	-4.761383	23286.177273
HLA A*3101	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.395095	-0.366558	-4.761653	24836.744096
HLA A*0101	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.385429	-0.376448	-4.761877	24290.076429
HLA A*0301	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.361187	-0.401420	-4.762607	22971.369895
HLA A*3002	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.592310	-0.170363	-4.762674	39112.036873
HLA B*5101	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.422659	-0.340176	-4.762835	26464.203086
HLA A*0211	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.517559	-0.245356	-4.762915	32927.534910
HLA B*7301	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.610000	-0.153340	-4.763340	40738.000228
HLA B*4501	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.607782	-0.155719	-4.763501	40530.484231
HLA A*3201	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.518212	-0.245356	-4.763569	32977.093506
HLA B*4403	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.634406	-0.129168	-4.763574	43092.943155
HLA B*1801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.423446	-0.340176	-4.763622	26512.207988
HLA A*3201	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.608235	-0.155719	-4.763954	40572.824558
HLA A*0101	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.375613	-0.388552	-4.764165	23747.217665
HLA B*4501	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.643898	-0.120427	-4.764325	44045.148228
HLA B*0702	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.353852	-0.410971	-4.764823	22586.648999
HLA A*6801	1:320-328	9	TDRDRSIGS	1.027690	-1.158615	-4.634183	-0.130925	-4.765108	43070.801681
HLA A*3201	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.619823	-0.145362	-4.765185	41669.942681
HLA A*2601	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.398765	-0.366558	-4.765323	25047.509972
HLA A*2602	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.623977	-0.141893	-4.765869	42070.414656
HLA A*0101	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.364885	-0.401420	-4.766305	23167.810085
HLA B*4403	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.645879	-0.120427	-4.766305	44246.476470
HLA B*4002	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.648517	-0.117875	-4.766392	44516.105542
HLA B*7301	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.621296	-0.145362	-4.766658	41811.527139
HLA A*0201	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.390252	-0.376448	-4.766700	24561.357927
HLA A*0250	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.578564	-0.188551	-4.767114	37893.401979
HLA A*0201	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.400677	-0.366558	-4.767235	25158.053653
HLA B*4402	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.427130	-0.340176	-4.767306	26738.059822
HLA A*2602	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.578871	-0.188551	-4.767422	37920.266380
HLA B*0702	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.428140	-0.339553	-4.767693	26800.331698
HLA B*4002	1:290-298	9	DAERTSLLS	1.029050	-1.149477	-4.647326	-0.120427	-4.767753	44394.173449
HLA A*2603	1:541-549	9	AGTTVPVDS	0.993683	-1.108313	-4.653416	-0.114630	-4.768045	45021.072811
HLA A*0202	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.597792	-0.170363	-4.768155	39608.808857
HLA A*2402	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.579694	-0.188551	-4.768244	37992.134952
HLA B*7301	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.598060	-0.170363	-4.768423	39633.244227
HLA A*2602	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.380464	-0.388552	-4.769016	24013.995201
HLA A*6901	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.367763	-0.401420	-4.769183	23321.855683
HLA A*6801	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.616562	-0.152648	-4.769210	41358.217983
HLA B*3501	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.429684	-0.339553	-4.769236	26895.757526
HLA B*4002	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.640087	-0.129168	-4.769255	43660.349833
HLA A*2403	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.430123	-0.339553	-4.769676	26922.980367
HLA A*0202	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.581815	-0.188668	-4.770483	38178.185536
HLA A*3301	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.641415	-0.129168	-4.770583	43794.005668
HLA A*0212	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.394136	-0.376448	-4.770584	24781.984027
HLA A*0250	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.600261	-0.170363	-4.770624	39834.657821
HLA B*3801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.525404	-0.245356	-4.770760	33527.729910
HLA B*5801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.369612	-0.401420	-4.771032	23421.362091
HLA B*7301	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.583204	-0.188668	-4.771872	38300.445873
HLA A*0216	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.361034	-0.410971	-4.772005	22963.293598
HLA B*2705	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.433330	-0.340176	-4.773507	27122.528957
HLA A*3201	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.620962	-0.152648	-4.773610	41779.419680
HLA B*4801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.433575	-0.340176	-4.773751	27137.793157
HLA A*0211	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.514176	-0.259643	-4.773819	32672.018059
HLA B*5301	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.585459	-0.188551	-4.774010	38499.876415

HLA B*4403	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.656477	-0.117875	-4.774352	45339.551378
HLA B*4501	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.656609	-0.117875	-4.774484	45353.289247
HLA B*4601	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.407993	-0.366558	-4.774552	25585.466229
HLA B*4403	1:403-411	9	DPAANTSVS	1.125358	-1.234463	-4.665565	-0.109105	-4.774670	46298.298067
HLA B*3801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.515454	-0.259643	-4.775097	32768.312772
HLA A*2603	1:310-318	9	DPLPRQDLD	0.928272	-1.046147	-4.657351	-0.117875	-4.775226	45430.888138
HLA B*4601	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.373855	-0.401420	-4.775275	23651.316411
HLA B*4402	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.435994	-0.339553	-4.775547	27289.432071
HLA A*1101	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.342736	-0.432915	-4.775651	22015.897233
HLA B*4801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.436457	-0.339553	-4.776010	27318.531237
HLA A*0201	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.365259	-0.410971	-4.776229	23187.746968
HLA A*2602	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.631023	-0.145362	-4.776385	42758.542990
HLA A*6802	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.436399	-0.340176	-4.776575	27314.836731
HLA A*0203	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.437317	-0.340176	-4.777494	27372.676045
HLA A*6901	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.383251	-0.394285	-4.777536	24168.567428
HLA A*0219	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.437836	-0.340176	-4.778013	27405.421991
HLA B*1503	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.438520	-0.339553	-4.778073	27448.599715
HLA B*4403	1:77-85	9	TGEAETPAG	0.744525	-0.853468	-4.669157	-0.108943	-4.778100	46682.852921
HLA B*4402	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.401732	-0.376448	-4.778180	25219.237856
HLA A*8001	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.438978	-0.339553	-4.778531	27477.571301
HLA B*4001	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.367634	-0.410971	-4.778605	23314.917439
HLA A*0202	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.533364	-0.245356	-4.778720	34147.916003
HLA A*2603	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.649831	-0.129168	-4.778999	44650.931708
HLA A*1101	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.439852	-0.339553	-4.779405	27532.925010
HLA A*3301	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.623885	-0.155719	-4.779604	42061.539338
HLA A*3301	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.638675	-0.141893	-4.780568	43518.625565
HLA A*0301	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.347668	-0.432915	-4.780583	22267.320411
HLA B*3801	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.544964	-0.236114	-4.781078	35072.248687
HLA B*4801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.404831	-0.376448	-4.781279	25399.836933
HLA B*1503	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.441138	-0.340176	-4.781314	27614.521370
HLA A*2301	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.545612	-0.236114	-4.781726	35124.655207
HLA A*2602	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.545807	-0.236114	-4.781921	35140.430450
HLA A*0201	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.393478	-0.388552	-4.782030	24744.473464
HLA B*1502	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.594171	-0.188668	-4.782839	39279.977090
HLA B*1517	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.443081	-0.340176	-4.783257	27738.344926
HLA A*6901	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.351284	-0.432915	-4.784199	22453.488023
HLA B*1509	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.524709	-0.259643	-4.784352	33474.084008
HLA A*2603	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.395879	-0.388552	-4.784431	24881.662252
HLA B*1517	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.444899	-0.339553	-4.784452	27854.735936
HLA B*5701	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.408132	-0.376448	-4.784580	25593.633990
HLA B*3501	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.373787	-0.410971	-4.784758	23647.606123
HLA B*1501	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.418397	-0.366558	-4.784955	26205.765766
HLA A*3301	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.639641	-0.145362	-4.785003	43615.495335
HLA B*5701	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.396495	-0.388552	-4.785047	24916.954301
HLA B*4801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.352285	-0.432915	-4.785200	22505.294292
HLA A*6802	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.374628	-0.410971	-4.785599	23693.449775
HLA A*6801	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.640672	-0.145362	-4.786034	43719.202678
HLA B*4501	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.641147	-0.145362	-4.786509	43767.005033
HLA A*2402	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.598020	-0.188668	-4.786687	39629.599400
HLA B*0803	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.410683	-0.376448	-4.787132	25744.442740
HLA A*2501	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.447686	-0.339553	-4.787238	28034.030074
HLA B*5301	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.551147	-0.236114	-4.787262	35575.208694
HLA B*4002	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.207589	-0.579820	-4.787409	16128.326737
HLA B*1801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.411165	-0.376448	-4.787613	25773.009867
HLA B*4001	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.399124	-0.388552	-4.787676	25068.250705
HLA A*2902	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.411431	-0.376448	-4.787879	25788.770175
HLA A*0250	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.599413	-0.188668	-4.788081	39756.937848
HLA A*3201	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.617741	-0.170363	-4.788104	41470.689812
HLA A*0201	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.394044	-0.394285	-4.788329	24776.755935
HLA B*0801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.394261	-0.394285	-4.788545	24789.090639
HLA A*2403	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.422259	-0.366558	-4.788818	26439.875646
HLA A*6802	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.422558	-0.366558	-4.789116	26458.047561
HLA A*0101	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.356432	-0.432915	-4.789347	22721.214277
HLA A*2902	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.449297	-0.340176	-4.789474	28138.262810
HLA B*4002	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.644457	-0.145362	-4.789819	44101.895243

HLA B*1502	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.619644	-0.170363	-4.790007	41652.813540
HLA A*3301	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.636969	-0.153340	-4.790309	43348.037921
HLA A*0203	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.357435	-0.432915	-4.790350	22773.761466
HLA A*2601	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.397550	-0.394285	-4.791835	24977.552152
HLA A*2601	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.390539	-0.401420	-4.791959	24577.573933
HLA B*0802	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.452554	-0.339553	-4.792106	28350.039467
HLA B*0802	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.425600	-0.366558	-4.792159	26644.058337
HLA A*3002	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.603555	-0.188668	-4.792223	40137.939029
HLA A*0201	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.390927	-0.401420	-4.792346	24599.522449
HLA A*2301	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.547264	-0.245356	-4.792620	35258.493956
HLA B*5701	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.426296	-0.366558	-4.792854	26686.758372
HLA B*4002	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.651111	-0.141893	-4.793004	44782.774316
HLA A*2602	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.605345	-0.188668	-4.794013	40303.742595
HLA A*8001	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.454873	-0.340176	-4.795049	28501.821083
HLA A*6801	1:610-618	9	AGTGVNRDG	0.608058	-0.737226	-4.666606	-0.129168	-4.795774	46409.388749
HLA B*4002	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.643750	-0.153340	-4.797090	44030.139186
HLA B*4403	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.217556	-0.579820	-4.797376	16502.731298
HLA B*4002	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.644913	-0.152648	-4.797561	44148.205295
HLA B*4402	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.431025	-0.366558	-4.797584	26978.968232
HLA A*2603	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.642007	-0.155719	-4.797726	43853.750403
HLA A*0212	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.409828	-0.388552	-4.798380	25693.796675
HLA A*6801	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.646062	-0.153340	-4.799402	44265.151155
HLA B*4601	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.405519	-0.394285	-4.799804	25440.130077
HLA A*3201	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.611640	-0.188551	-4.800190	40892.121904
HLA A*1101	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.460168	-0.340176	-4.800345	28851.496779
HLA A*0203	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.434087	-0.366558	-4.800645	27169.817152
HLA B*4501	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.647660	-0.153340	-4.800999	44428.290344
HLA A*0212	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.434465	-0.366558	-4.801023	27193.492159
HLA B*1502	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.412580	-0.388552	-4.801132	25857.083030
HLA A*2603	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.659487	-0.141893	-4.801379	45654.848806
HLA A*2602	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.462485	-0.339553	-4.802038	29005.806199
HLA A*6802	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.425636	-0.376448	-4.802084	26646.220546
HLA B*4403	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.657751	-0.145362	-4.803113	45472.689288
HLA B*1503	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.392155	-0.410971	-4.803126	24669.222206
HLA B*4402	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.409323	-0.394285	-4.803608	25663.928921
HLA B*0801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.370768	-0.432915	-4.803683	23483.784959
HLA A*3301	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.633739	-0.170363	-4.804102	43026.785626
HLA B*4601	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.371485	-0.432915	-4.804400	23522.565570
HLA A*3101	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.410496	-0.394285	-4.804780	25733.303184
HLA B*4501	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.663084	-0.141893	-4.804977	46034.557234
HLA A*2603	1:590-598	9	GADVDAGGS	0.918910	-1.064272	-4.659651	-0.145362	-4.805013	45672.141217
HLA A*2603	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.652596	-0.153340	-4.805936	44936.150909
HLA B*4801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.439545	-0.366558	-4.806103	27513.419463
HLA B*5301	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.466136	-0.340176	-4.806312	29250.684977
HLA A*3201	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.617802	-0.188668	-4.806470	41476.523370
HLA A*0250	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.570996	-0.236114	-4.807110	37238.819560
HLA A*2501	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.467283	-0.340176	-4.807459	29328.009568
HLA A*3301	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.619177	-0.188551	-4.807728	41607.995586
HLA B*4001	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.406924	-0.401420	-4.808344	25522.565062
HLA A*8001	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.407202	-0.401420	-4.808621	25538.863025
HLA B*1502	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.549113	-0.259643	-4.808756	35408.929931
HLA B*4403	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.653063	-0.155719	-4.808783	44984.553778
HLA A*6801	1:229-237	9	VREDPIPPS	0.776949	-0.932668	-4.653395	-0.155719	-4.809114	45018.880833
HLA B*4801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.420732	-0.388552	-4.809284	26347.065005
HLA A*2403	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.415046	-0.394285	-4.809331	26004.379133
HLA A*8001	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.443447	-0.366558	-4.810005	27761.764380
HLA B*0802	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.433600	-0.376448	-4.810048	27139.408142
HLA B*0802	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.470424	-0.340176	-4.810600	29540.908724
HLA B*5701	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.399829	-0.410971	-4.810800	25108.968676
HLA A*2602	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.640731	-0.170363	-4.811094	43725.115979
HLA A*2603	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.658493	-0.152648	-4.811141	45550.492470
HLA B*4501	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.659792	-0.152648	-4.812440	45686.968496
HLA B*5401	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.552954	-0.259643	-4.812598	35723.517129
HLA B*0802	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.411687	-0.401420	-4.813106	25803.981728
HLA B*4801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.402432	-0.410971	-4.813403	25259.927764

HLA B*4403	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.671610	-0.141893	-4.813503	46947.260111
HLA A*2902	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.412237	-0.401420	-4.813656	25836.668036
HLA A*0206	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.473840	-0.340176	-4.814016	29774.193189
HLA B*5701	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.412711	-0.401420	-4.814131	25864.917718
HLA A*0219	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.437815	-0.376448	-4.814263	27404.087681
HLA B*4403	1:189-197	9	RGDSVDARS	0.842174	-0.995514	-4.661110	-0.153340	-4.814450	45825.836683
HLA A*8001	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.403574	-0.410971	-4.814545	25326.428705
HLA A*2603	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.578641	-0.236114	-4.814755	37900.167553
HLA A*3001	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.308497	-0.506277	-4.814775	20346.857542
HLA A*8001	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.439009	-0.376448	-4.815457	27479.503827
HLA A*6802	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.421183	-0.394285	-4.815468	26374.445885
HLA B*1501	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.421536	-0.394285	-4.815821	26395.856996
HLA B*5701	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.421611	-0.394285	-4.815896	26400.426948
HLA A*2902	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.449368	-0.366558	-4.815926	28142.829927
HLA B*1503	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.414790	-0.401420	-4.816210	25989.049445
HLA A*0201	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.383437	-0.432915	-4.816352	24178.898828
HLA B*4501	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.556749	-0.259643	-4.816392	36036.999912
HLA B*4001	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.422252	-0.394285	-4.816537	26439.446539
HLA B*4402	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.429017	-0.388552	-4.817569	26854.466384
HLA A*0212	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.416292	-0.401420	-4.817711	26079.046956
HLA B*0702	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.416621	-0.401420	-4.818040	26098.806303
HLA B*3901	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.454269	-0.366558	-4.820827	28462.221353
HLA B*3901	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.481300	-0.339553	-4.820852	30290.023957
HLA A*0211	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.480698	-0.340176	-4.820875	30248.103380
HLA A*3301	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.632355	-0.188668	-4.821023	42889.902213
HLA A*0203	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.426759	-0.394285	-4.821043	26715.214896
HLA A*2402	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.585121	-0.236114	-4.821235	38469.895766
HLA A*2402	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.576306	-0.245356	-4.821662	37696.909057
HLA A*0212	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.427419	-0.394285	-4.821704	26755.857685
HLA B*4002	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.651583	-0.170363	-4.821946	44831.497040
HLA A*0250	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.563304	-0.259643	-4.822947	36585.053281
HLA B*4002	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.447225	-0.376448	-4.823673	28004.320273
HLA B*2705	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.422906	-0.401420	-4.824325	26479.240039
HLA B*7301	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.588298	-0.236114	-4.824412	38752.302655
HLA A*2403	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.413872	-0.410971	-4.824843	25934.133777
HLA B*4403	1:234-242	9	IPPSARHEG	0.644382	-0.797030	-4.672769	-0.152648	-4.825416	47072.639115
HLA A*2403	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.437376	-0.388552	-4.825928	27376.378374
HLA A*6801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.487253	-0.339553	-4.826806	30708.118781
HLA A*6801	1:311-319	9	PLPRQDLDD	0.913385	-1.055278	-4.684955	-0.141893	-4.826848	48412.256575
HLA B*1517	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.394044	-0.432915	-4.826960	24776.755935
HLA A*0219	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.460439	-0.366558	-4.826997	28869.451954
HLA B*4801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.433227	-0.394285	-4.827512	27116.073611
HLA B*4002	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.638903	-0.188668	-4.827571	43541.468360
HLA B*4801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.427318	-0.401420	-4.828738	26749.634322
HLA B*1517	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.452843	-0.376448	-4.829291	28368.910325
HLA B*0802	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.440872	-0.388552	-4.829424	27597.645290
HLA B*4501	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.640762	-0.188668	-4.829429	43728.191212
HLA B*4402	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.419137	-0.410971	-4.830108	26250.461479
HLA B*4501	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.660307	-0.170363	-4.830670	45741.128928
HLA B*2705	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.398445	-0.432915	-4.831360	25029.088172
HLA A*1101	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.455075	-0.376448	-4.831523	28515.084654
HLA A*2601	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.398703	-0.432915	-4.831619	25043.987109
HLA A*0212	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.400024	-0.432915	-4.832939	25120.245656
HLA A*3002	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.492927	-0.340176	-4.833104	31111.948991
HLA B*3901	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.422360	-0.410971	-4.833331	26446.026943
HLA B*5101	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.467113	-0.366558	-4.833672	29316.588180
HLA A*0250	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.588793	-0.245356	-4.834149	38796.563146
HLA A*0216	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.467602	-0.366558	-4.834160	29349.595442
HLA B*4002	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.589531	-0.245356	-4.834887	38862.523077
HLA A*0211	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.424026	-0.410971	-4.834997	26547.658411
HLA B*3901	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.458726	-0.376448	-4.835174	28755.820562
HLA A*0216	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.459412	-0.376448	-4.835860	28801.281674
HLA A*0219	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.434613	-0.401420	-4.836033	27202.761906
HLA B*5301	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.591051	-0.245356	-4.836407	38998.787951
HLA B*4402	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.403506	-0.432915	-4.836421	25322.455635

HLA A*2602	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.591472	-0.245356	-4.836828	39036.571504
HLA A*2403	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.435435	-0.401420	-4.836855	27254.318075
HLA A*2301	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.460502	-0.376448	-4.836950	28873.669137
HLA A*2501	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.460537	-0.376448	-4.836985	28876.012282
HLA B*4403	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.666857	-0.170363	-4.837220	46436.260978
HLA B*3501	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.437118	-0.401420	-4.838537	27360.091872
HLA A*8001	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.406036	-0.432915	-4.838951	25470.426325
HLA A*2603	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.668676	-0.170363	-4.839039	46631.109061
HLA B*3501	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.406135	-0.432915	-4.839050	25476.214254
HLA A*2501	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.472498	-0.366558	-4.839057	29682.361225
HLA A*0216	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.450977	-0.388552	-4.839529	28247.314375
HLA B*0702	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.334086	-0.506277	-4.840363	21581.696735
HLA A*0219	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.451971	-0.388552	-4.840523	28312.029069
HLA A*2603	1:193-201	9	VDARSDVYS	0.863963	-1.052514	-4.652077	-0.188551	-4.840627	44882.458002
HLA A*6802	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.408466	-0.432915	-4.841381	25613.302682
HLA A*2603	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.430551	-0.410971	-4.841522	26949.501784
HLA B*1801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.409055	-0.432915	-4.841970	25648.106154
HLA B*4501	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.606182	-0.236114	-4.842296	40381.439195
HLA B*2705	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.431589	-0.410971	-4.842560	27014.019757
HLA A*0219	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.448487	-0.394285	-4.842772	28085.794205
HLA B*3801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.503834	-0.340176	-4.844010	31903.147184
HLA B*4403	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.655591	-0.188668	-4.844259	45247.174318
HLA A*0216	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.442951	-0.401420	-4.844371	27730.092778
HLA A*2403	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.411600	-0.432915	-4.844515	25798.817168
HLA A*2902	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.451001	-0.394285	-4.845285	28248.842564
HLA B*1801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.505892	-0.339553	-4.845444	32054.697023
HLA A*1101	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.451499	-0.394285	-4.845784	28281.259649
HLA B*3501	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.451557	-0.394285	-4.845842	28285.084870
HLA B*5101	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.506364	-0.339553	-4.845917	32089.571865
HLA A*8001	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.451912	-0.394285	-4.846197	28308.200205
HLA A*0206	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.479690	-0.366558	-4.846249	30177.983698
HLA A*2603	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.657997	-0.188668	-4.846665	45498.526858
HLA B*0702	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.452866	-0.394285	-4.847151	28370.445093
HLA A*1101	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.480785	-0.366558	-4.847343	30254.158625
HLA B*1509	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.507969	-0.340176	-4.848145	32208.360690
HLA A*0216	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.455162	-0.394285	-4.849446	28520.792973
HLA A*0219	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.439206	-0.410971	-4.850177	27491.994194
HLA A*6801	1:395-403	9	PPDHVIGTD	1.031472	-1.201835	-4.680334	-0.170363	-4.850697	47899.820870
HLA B*0801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.344534	-0.506277	-4.850811	22107.200260
HLA B*1517	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.484873	-0.366558	-4.851432	30540.291889
HLA B*0803	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.450113	-0.401420	-4.851532	28191.134455
HLA A*6801	1:491-499	9	GPATKDIPD	0.779646	-0.968314	-4.664094	-0.188668	-4.852762	46141.769884
HLA B*1801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.486598	-0.366558	-4.853156	30661.804165
HLA B*4402	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.452135	-0.401420	-4.853555	28322.752646
HLA B*0803	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.514423	-0.339553	-4.853975	32690.582291
HLA B*1801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.466164	-0.388552	-4.854716	29252.583955
HLA B*7301	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.609464	-0.245356	-4.854820	40687.782726
HLA B*4501	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.479458	-0.376448	-4.855906	30161.825330
HLA B*5301	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.596615	-0.259643	-4.856258	39501.600298
HLA A*0219	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.424484	-0.432915	-4.857399	26575.679066
HLA B*0803	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.490958	-0.366558	-4.857517	30971.222603
HLA B*3901	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.469089	-0.388552	-4.857641	29450.274239
HLA B*0803	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.517569	-0.340176	-4.857745	32928.247455
HLA A*0202	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.456513	-0.401420	-4.857932	28609.650344
HLA B*5801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.352036	-0.506277	-4.858313	22492.392370
HLA B*1509	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.482056	-0.376448	-4.858504	30342.834688
HLA B*1502	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.613456	-0.245356	-4.858812	41063.484447
HLA B*0702	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.426176	-0.432915	-4.859091	26679.396395
HLA A*0206	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.482834	-0.376448	-4.859282	30397.217468
HLA A*0206	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.465887	-0.394285	-4.860172	29233.916032
HLA B*1503	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.472059	-0.388552	-4.860611	29652.348270
HLA B*0802	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.467311	-0.394285	-4.861596	29329.913565
HLA B*5101	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.460326	-0.401420	-4.861746	28861.956262
HLA B*7301	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.602152	-0.259643	-4.861796	40008.514488
HLA A*3301	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.616475	-0.245356	-4.861831	41349.940307

HLA A*2603	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.602279	-0.259643	-4.861923	40020.204043
HLA B*4001	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.429172	-0.432915	-4.862087	26864.056555
HLA A*0216	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.429390	-0.432915	-4.862305	26877.575791
HLA B*3801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.487460	-0.376448	-4.863908	30722.741483
HLA A*0206	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.476556	-0.388552	-4.865108	29960.979442
HLA B*4501	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.620791	-0.245356	-4.866147	41762.923329
HLA B*2705	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.499809	-0.366558	-4.866367	31608.861947
HLA A*3301	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.478125	-0.388552	-4.866678	30069.448483
HLA A*0202	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.491069	-0.376448	-4.867517	30979.098496
HLA B*4002	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.631451	-0.236114	-4.867565	42800.663776
HLA B*4002	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.608435	-0.259643	-4.868078	40591.485880
HLA A*2301	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.528825	-0.339553	-4.868378	33792.863919
HLA A*2501	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.467156	-0.401420	-4.868575	29319.443110
HLA A*1101	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.467832	-0.401420	-4.869252	29365.159817
HLA B*2705	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.480841	-0.388552	-4.869394	30258.087000
HLA A*6801	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.624926	-0.245356	-4.870282	42162.464108
HLA A*0202	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.438358	-0.432915	-4.871273	27438.355549
HLA B*5401	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.470450	-0.401420	-4.871869	29542.666720
HLA B*1801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.461454	-0.410971	-4.872424	28937.000848
HLA B*4403	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.613799	-0.259643	-4.873442	41095.930999
HLA B*1509	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.534266	-0.339553	-4.873819	34218.928531
HLA A*0301	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.368057	-0.506277	-4.874334	23337.632098
HLA B*0802	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.463711	-0.410971	-4.874682	29087.833264
HLA A*3002	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.473391	-0.401420	-4.874811	29743.443737
HLA B*3801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.508511	-0.366558	-4.875070	32248.636136
HLA A*2301	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.535822	-0.340176	-4.875998	34341.698084
HLA B*3801	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.536651	-0.339553	-4.876204	34407.342771
HLA A*2902	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.444342	-0.432915	-4.877257	27819.045046
HLA A*2602	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.618390	-0.259643	-4.878033	41532.657169
HLA B*5101	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.489643	-0.388552	-4.878195	30877.536095
HLA B*0803	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.489744	-0.388552	-4.878296	30884.719825
HLA A*6901	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.373014	-0.506277	-4.879291	23605.554282
HLA A*3301	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.620079	-0.259643	-4.879722	41694.521772
HLA A*3002	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.513405	-0.366558	-4.879964	32614.094811
HLA A*3201	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.493829	-0.388552	-4.882381	31176.648053
HLA B*5101	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.490881	-0.394285	-4.885166	30965.693918
HLA B*3901	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.492683	-0.394285	-4.886968	31094.449446
HLA A*2501	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.493378	-0.394285	-4.887663	31144.281722
HLA A*6801	1:519-527	9	KFSQASVDS	0.595252	-0.854895	-4.628857	-0.259643	-4.888500	42545.797911
HLA B*1509	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.499952	-0.388552	-4.888504	31619.294695
HLA B*1509	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.487357	-0.401420	-4.888776	30715.429262
HLA A*3001	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.308974	-0.579820	-4.888794	20369.214888
HLA A*0212	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.382591	-0.506277	-4.888868	24131.854795
HLA B*4001	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.382765	-0.506277	-4.889042	24141.517477
HLA A*0211	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.512733	-0.376448	-4.889181	32563.672378
HLA B*5301	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.522871	-0.366558	-4.889430	33332.769909
HLA A*3201	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.513932	-0.376448	-4.890380	32653.641022
HLA B*1517	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.496231	-0.394285	-4.890515	31349.498228
HLA B*5101	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.514857	-0.376448	-4.891305	32723.316368
HLA B*5401	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.552099	-0.339553	-4.891652	35653.239610
HLA B*4403	1:454-462	9	QANSPSTPE	0.410677	-0.646791	-4.655808	-0.236114	-4.891922	45269.699886
HLA A*2402	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.554888	-0.339553	-4.894440	35882.924935
HLA A*0211	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.463220	-0.432915	-4.896135	29054.963201
HLA A*3201	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.485876	-0.410971	-4.896847	30610.922203
HLA B*1502	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.558149	-0.339553	-4.897702	36153.381315
HLA A*2601	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.391695	-0.506277	-4.897972	24643.078349
HLA B*2705	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.504602	-0.394285	-4.898887	31959.634877
HLA A*3301	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.523219	-0.376448	-4.899667	33359.468931
HLA B*3901	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.499170	-0.401420	-4.900590	31562.384031
HLA B*1503	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.534121	-0.366558	-4.900679	34207.452978
HLA B*1801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.499830	-0.401420	-4.901250	31610.400988
HLA A*0206	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.500502	-0.401420	-4.901922	31659.347351
HLA A*0201	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.395936	-0.506277	-4.902213	24884.893031
HLA A*2603	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.657466	-0.245356	-4.902823	45442.932761
HLA A*0101	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.397430	-0.506277	-4.903707	24970.661688

HLA B*5101	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.494372	-0.410971	-4.905343	31215.633379
HLA B*0803	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.494555	-0.410971	-4.905526	31228.808261
HLA B*1509	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.539038	-0.366558	-4.905597	34596.981613
HLA A*0206	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.473647	-0.432915	-4.906562	29760.987961
HLA B*5401	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.497579	-0.410971	-4.908550	31446.998388
HLA A*3002	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.475663	-0.432915	-4.908578	29899.450189
HLA B*0803	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.514773	-0.394285	-4.909058	32716.943926
HLA A*2301	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.543909	-0.366558	-4.910467	34987.160167
HLA A*0211	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.509089	-0.401420	-4.910509	32291.582248
HLA A*3201	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.570921	-0.340176	-4.911097	37232.373466
HLA B*0802	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.479669	-0.432915	-4.912584	30176.514398
HLA B*4403	1:43-51	9	RADLARDPS	0.657590	-0.902946	-4.667254	-0.245356	-4.912610	46478.735731
HLA A*3201	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.573186	-0.339553	-4.912738	37427.052448
HLA A*0211	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.524269	-0.388552	-4.912821	33440.237099
HLA B*3901	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.480068	-0.432915	-4.912984	30204.279935
HLA B*5401	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.541179	-0.376448	-4.917627	34767.910546
HLA B*1509	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.507830	-0.410971	-4.918801	32198.081955
HLA A*0202	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.530324	-0.388552	-4.918876	33909.701819
HLA B*4601	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.413024	-0.506277	-4.919301	25883.534617
HLA A*0211	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.552780	-0.366558	-4.919339	35709.218731
HLA A*2501	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.486588	-0.432915	-4.919503	30661.140664
HLA B*1503	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.525667	-0.394285	-4.919952	33548.050772
HLA A*0202	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.581005	-0.340176	-4.921181	38106.995778
HLA B*1502	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.554719	-0.366558	-4.921277	35868.950826
HLA A*2301	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.532866	-0.388552	-4.921418	34108.774328
HLA B*5401	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.533211	-0.388552	-4.921764	34135.910245
HLA A*3101	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.417553	-0.506277	-4.923831	26154.919624
HLA B*1501	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.417864	-0.506277	-4.924141	26173.603663
HLA A*3301	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.514510	-0.410971	-4.925481	32697.126486
HLA A*2403	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.419391	-0.506277	-4.925668	26265.803266
HLA B*3901	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.419858	-0.506277	-4.926136	26294.095414
HLA B*1801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.532110	-0.394285	-4.926394	34049.409100
HLA B*4501	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.346780	-0.579820	-4.926600	22221.831646
HLA A*2301	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.525498	-0.401420	-4.926918	33534.985947
HLA A*2402	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.587593	-0.340176	-4.927769	38689.459966
HLA A*0211	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.533787	-0.394285	-4.928072	34181.184758
HLA B*4001	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.348427	-0.579820	-4.928247	22306.264213
HLA A*0250	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.588824	-0.340176	-4.929000	38799.291748
HLA B*5701	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.423787	-0.506277	-4.930064	26533.013223
HLA A*2602	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.553751	-0.376448	-4.930199	35789.092472
HLA B*5801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.351594	-0.579820	-4.931414	22469.527905
HLA B*7301	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.591711	-0.340176	-4.931888	39058.118168
HLA A*0250	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.521612	-0.410971	-4.932583	33236.254857
HLA A*2301	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.541806	-0.394285	-4.936091	34818.167008
HLA B*5101	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.504322	-0.432915	-4.937237	31939.066627
HLA B*7301	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.536019	-0.401420	-4.937439	34357.307552
HLA B*0803	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.504860	-0.432915	-4.937775	31978.659326
HLA B*4402	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.431942	-0.506277	-4.938219	27035.950081
HLA B*4801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.432501	-0.506277	-4.938778	27070.782736
HLA B*1509	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.544987	-0.394285	-4.939272	35074.146108
HLA A*3301	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.601382	-0.339553	-4.940934	39937.584583
HLA A*2402	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.530148	-0.410971	-4.941119	33895.946031
HLA B*1502	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.539971	-0.401420	-4.941391	34671.366300
HLA A*2301	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.531332	-0.410971	-4.942303	33988.492289
HLA B*5401	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.510024	-0.432915	-4.942940	32361.185317
HLA B*7301	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.605183	-0.339553	-4.944736	40288.700727
HLA B*1502	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.533959	-0.410971	-4.944930	34194.686322
HLA B*5401	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.550887	-0.394285	-4.945171	35553.852276
HLA B*3801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.551439	-0.394285	-4.945724	35599.081484
HLA B*5301	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.606257	-0.339553	-4.945810	40388.430492
HLA A*6802	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.440773	-0.506277	-4.947051	27591.375393
HLA A*0250	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.570726	-0.376448	-4.947174	37215.659109
HLA A*0301	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.367751	-0.579820	-4.947572	23321.224848
HLA B*1502	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.610441	-0.340176	-4.950618	40779.454261
HLA B*3801	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.562308	-0.388552	-4.950860	36501.230914

HLA A*2602	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.612107	-0.340176	-4.952284	40936.168757
HLA A*0203	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.448280	-0.506277	-4.954557	28072.426576
HLA B*3801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.553473	-0.401420	-4.954893	35766.253190
HLA B*7301	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.570526	-0.388552	-4.959078	37198.549773
HLA A*2402	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.570632	-0.388552	-4.959184	37207.606676
HLA B*3801	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.548619	-0.410971	-4.959590	35368.725512
HLA A*0250	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.571797	-0.388552	-4.960349	37307.580104
HLA A*0250	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.594293	-0.366558	-4.960852	39291.028661
HLA A*2403	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.381256	-0.579820	-4.961076	24057.815832
HLA A*2603	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.585130	-0.376448	-4.961578	38470.728246
HLA A*3301	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.560186	-0.401420	-4.961606	36323.352493
HLA A*3002	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.568139	-0.394285	-4.962424	36994.650775
HLA B*4002	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.622400	-0.340176	-4.962577	41917.974402
HLA A*8001	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.457152	-0.506277	-4.963429	28651.780143
HLA A*0250	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.563191	-0.401420	-4.964611	36575.554302
HLA A*2402	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.599068	-0.366558	-4.965626	39725.333564
HLA A*0202	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.571997	-0.394285	-4.966282	37324.739588
HLA B*5101	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.460131	-0.506277	-4.966408	28848.999552
HLA B*4501	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.627799	-0.339553	-4.967352	42442.348261
HLA A*0202	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.601558	-0.366558	-4.968116	39953.792214
HLA B*1501	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.389017	-0.579820	-4.968837	24491.565433
HLA A*6901	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.389214	-0.579820	-4.969034	24502.697681
HLA A*2602	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.603236	-0.366558	-4.969794	40108.418605
HLA A*2301	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.537311	-0.432915	-4.970226	34459.687863
HLA A*0201	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.390699	-0.579820	-4.970519	24586.617008
HLA B*7301	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.594430	-0.376448	-4.970878	39303.359082
HLA A*0203	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.391072	-0.579820	-4.970893	24607.774836
HLA A*2601	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.393817	-0.579820	-4.973637	24763.757514
HLA A*1101	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.468403	-0.506277	-4.974681	29403.788731
HLA A*0219	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.468549	-0.506277	-4.974826	29413.652802
HLA B*4601	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.396248	-0.579820	-4.976068	24902.804534
HLA A*2902	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.470208	-0.506277	-4.976485	29526.209582
HLA A*0101	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.396697	-0.579820	-4.976517	24928.549622
HLA B*0802	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.470607	-0.506277	-4.976884	29553.376772
HLA B*5301	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.588373	-0.388552	-4.976925	38759.011897
HLA B*4501	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.637599	-0.340176	-4.977776	43410.931668
HLA B*5301	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.585105	-0.394285	-4.979389	38468.438968
HLA B*7301	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.613592	-0.366558	-4.980150	41076.371105
HLA A*3301	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.642174	-0.340176	-4.982350	43870.597958
HLA B*4002	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.588471	-0.394285	-4.982756	38767.819540
HLA B*4002	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.643414	-0.339553	-4.982967	43996.090019
HLA A*0216	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.478020	-0.506277	-4.984297	30062.129117
HLA B*4002	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.573599	-0.410971	-4.984570	37462.705230
HLA B*2705	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.479787	-0.506277	-4.986064	30184.678082
HLA A*0250	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.592094	-0.394285	-4.986379	39092.575273
HLA B*1517	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.480254	-0.506277	-4.986531	30217.191437
HLA B*7301	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.576071	-0.410971	-4.987042	37676.520962
HLA B*5301	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.610695	-0.376448	-4.987143	40803.287354
HLA A*2603	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.648858	-0.339553	-4.988410	44551.039185
HLA A*3201	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.622273	-0.366558	-4.988832	41905.730524
HLA A*2402	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.588359	-0.401420	-4.989778	38757.753825
HLA B*7301	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.597392	-0.394285	-4.991677	39572.398128
HLA A*8001	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.412716	-0.579820	-4.992536	25865.197572
HLA B*4403	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.652927	-0.340176	-4.993104	44970.441029
HLA A*2402	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.598943	-0.394285	-4.993228	39713.944985
HLA B*5301	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.592221	-0.401420	-4.993641	39103.997212
HLA B*4501	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.583345	-0.410971	-4.994316	38312.879961
HLA B*4403	1:158-166	9	GIARAIADS	0.697391	-1.036944	-4.654844	-0.339553	-4.994397	45169.400498
HLA A*2501	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.488278	-0.506277	-4.994555	30780.635869
HLA B*4801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.414889	-0.579820	-4.994709	25994.955227
HLA A*2602	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.597437	-0.401420	-4.998857	39576.465900
HLA B*3801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.566250	-0.432915	-4.999165	36834.090096
HLA A*6801	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.622971	-0.376448	-4.999419	41973.116136
HLA B*1509	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.567044	-0.432915	-4.999959	36901.504413
HLA B*5701	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.421115	-0.579820	-5.000935	26370.308408

HLA B*1801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.494974	-0.506277	-5.001251	31258.894846
HLA B*0803	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.495606	-0.506277	-5.001883	31304.417787
HLA B*4501	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.635649	-0.366558	-5.002207	43216.444527
HLA A*2602	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.609964	-0.394285	-5.004249	40734.694541
HLA A*3301	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.637714	-0.366558	-5.004273	43422.440762
HLA A*6802	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.424677	-0.579820	-5.004497	26587.470943
HLA A*2603	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.638139	-0.366558	-5.004698	43464.980402
HLA B*4002	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.573914	-0.432915	-5.006829	37489.872733
HLA A*2402	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.573954	-0.432915	-5.006869	37493.320765
HLA B*7301	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.574673	-0.432915	-5.007588	37555.439588
HLA A*3101	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.427830	-0.579820	-5.007650	26781.200269
HLA A*0212	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.429320	-0.579820	-5.009140	26873.214004
HLA A*2603	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.608315	-0.401420	-5.009735	40580.288057
HLA A*2603	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.669585	-0.340176	-5.009761	46728.839485
HLA B*5301	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.599039	-0.410971	-5.010010	39722.754732
HLA B*4403	1:451-459	9	RFKQANSPS	0.434936	-0.811384	-4.633781	-0.376448	-5.010229	43030.975692
HLA B*4002	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.644286	-0.366558	-5.010844	44084.481877
HLA A*6801	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.610747	-0.401420	-5.012167	40808.143951
HLA A*0250	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.579776	-0.432915	-5.012691	37999.329296
HLA A*2902	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.434827	-0.579820	-5.014647	27216.157120
HLA A*3201	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.621223	-0.394285	-5.015508	41804.515659
HLA B*1502	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.622215	-0.394285	-5.016499	41900.063274
HLA A*6801	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.652354	-0.366558	-5.018912	44911.118626
HLA A*6801	1:389-397	9	KPDSTIPPD	0.632059	-0.972235	-4.678884	-0.340176	-5.019061	47740.202525
HLA B*5301	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.513032	-0.506277	-5.019309	32586.053129
HLA B*4501	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.586876	-0.432915	-5.019791	38625.674369
HLA B*4002	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.632026	-0.388552	-5.020578	42857.430365
HLA B*0702	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.441403	-0.579820	-5.021223	27631.407771
HLA A*0206	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.441499	-0.579820	-5.021320	27637.537247
HLA A*3201	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.621698	-0.401420	-5.023118	41850.224505
HLA B*4501	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.635144	-0.388552	-5.023696	43166.207571
HLA B*1502	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.592158	-0.432915	-5.025073	39098.285825
HLA B*0801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.445576	-0.579820	-5.025396	27898.168780
HLA B*4403	1:184-192	9	SPEQARGDS	0.760949	-1.127507	-4.659933	-0.366558	-5.026492	45701.800589
HLA B*5301	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.596537	-0.432915	-5.029452	39494.548851
HLA A*0216	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.450745	-0.579820	-5.030565	28232.189756
HLA B*4002	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.631779	-0.401420	-5.033199	42833.092614
HLA B*4403	1:178-186	9	GTAQYLSPE	0.343313	-0.754284	-4.625807	-0.410971	-5.036778	42248.086276
HLA A*3301	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.642902	-0.394285	-5.037187	43944.233559
HLA B*3501	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.458705	-0.579820	-5.038525	28754.420504
HLA B*4403	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.645016	-0.394285	-5.039301	44158.715369
HLA B*4501	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.646194	-0.394285	-5.040478	44278.563482
HLA A*0219	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.464614	-0.579820	-5.044434	29148.323063
HLA A*0206	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.541242	-0.506277	-5.047519	34772.989362
HLA B*4501	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.647678	-0.401420	-5.049098	44430.213203
HLA A*1101	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.472233	-0.579820	-5.052053	29664.221424
HLA B*3801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.546007	-0.506277	-5.052284	35156.593161
HLA A*2301	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.546199	-0.506277	-5.052477	35172.192469
HLA B*1503	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.473302	-0.579820	-5.053122	29737.329833
HLA B*4403	1:417-425	9	TVNVSTGPE	0.275574	-0.664126	-4.664853	-0.388552	-5.053405	46222.468230
HLA B*1503	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.547151	-0.506277	-5.053428	35249.339406
HLA A*2501	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.474237	-0.579820	-5.054057	29801.427326
HLA A*0211	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.551347	-0.506277	-5.057624	35591.571380
HLA A*2603	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.663528	-0.394285	-5.057813	46081.650216
HLA A*2602	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.624940	-0.432915	-5.057855	42163.832696
HLA B*0802	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.478372	-0.579820	-5.058192	30086.533935
HLA B*4403	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.626512	-0.432915	-5.059427	42316.709186
HLA A*6801	1:317-325	9	LDDTDRDRS	0.850446	-1.244731	-4.666225	-0.394285	-5.060510	46368.733284
HLA B*2705	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.483219	-0.579820	-5.063039	30424.198510
HLA B*1509	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.558628	-0.506277	-5.064906	36193.302840
HLA A*3301	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.633943	-0.432915	-5.066858	43047.041394
HLA A*2603	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.635203	-0.432915	-5.068118	43172.046076
HLA B*1801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.489838	-0.579820	-5.069658	30891.403864
HLA B*4403	1:449-457	9	FGRFKQANS	0.723890	-1.125310	-4.670191	-0.401420	-5.071611	46794.106866
HLA B*1517	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.497502	-0.579820	-5.077322	31441.384771

HLA A*6801	1:557-565	9	KGNQFVMPD	0.442816	-0.875731	-4.649459	-0.432915	-5.082374	44612.782073
HLA B*3901	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.506754	-0.579820	-5.086574	32118.402579
HLA B*5101	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.507882	-0.579820	-5.087702	32201.914320
HLA A*0250	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.598147	-0.506277	-5.104424	39641.178245
HLA A*0211	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.525047	-0.579820	-5.104867	33500.171284
HLA A*2402	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.599805	-0.506277	-5.106083	39792.872542
HLA A*0202	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.601932	-0.506277	-5.108209	39988.174147
HLA B*1502	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.605251	-0.506277	-5.111529	40295.021987
HLA B*0803	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.534454	-0.579820	-5.114275	34233.741385
HLA A*3002	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.535483	-0.579820	-5.115304	34314.955493
HLA B*7301	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.612253	-0.506277	-5.118530	40949.901588
HLA A*2301	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.540457	-0.579820	-5.120277	34710.214675
HLA B*1502	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.542877	-0.579820	-5.122697	34904.166306
HLA A*3002	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.620124	-0.506277	-5.126401	41698.807685
HLA A*3201	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.621322	-0.506277	-5.127599	41814.015366
HLA B*3801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.554672	-0.579820	-5.134492	35865.070095
HLA A*2602	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.630116	-0.506277	-5.136393	42669.347027
HLA B*4501	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.631958	-0.506277	-5.138235	42850.707128
HLA A*3301	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.632280	-0.506277	-5.138557	42882.477908
HLA B*5401	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.559342	-0.579820	-5.139163	36252.875547
HLA A*0202	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.566386	-0.579820	-5.146206	36845.649473
HLA B*4002	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.642827	-0.506277	-5.149104	43936.626747
HLA B*1509	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.571191	-0.579820	-5.151011	37255.544319
HLA A*2402	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.580911	-0.579820	-5.160731	38098.750485
HLA A*0250	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.583888	-0.579820	-5.163708	38360.788899
HLA A*2603	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.664207	-0.506277	-5.170484	46153.753289
HLA B*4403	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.664651	-0.506277	-5.170928	46200.968207
HLA B*7301	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.593551	-0.579820	-5.173371	39223.917048
HLA A*3201	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.599707	-0.579820	-5.179527	39783.832018
HLA A*6801	1:423-431	9	GPEQREIPD	0.551147	-1.057424	-4.678729	-0.506277	-5.185006	47723.159800
HLA B*5301	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.608256	-0.579820	-5.188077	40574.800057
HLA A*2603	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.634740	-0.579820	-5.214560	43126.060056
HLA A*2602	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.635940	-0.579820	-5.215761	43245.444978
HLA A*3301	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.641001	-0.579820	-5.220821	43752.327466
HLA A*6801	1:212-220	9	GEPPFTGDS	0.535836	-1.115656	-4.667649	-0.579820	-5.247469	46520.997661