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      1:63-71 9       LSGGPASVY       1.785456        1.238638        -0.894815       3.024094        2.129279        7.849020
HLA B*1517      1:284-292       9       VTVDAAETF       1.414591        1.171836        -0.532107       2.586427        2.054321        3.404918
HLA B*1503      1:32-40 9       RRVREARVF       1.516847        1.396018        -0.871753       2.912865        2.041112        7.443084
HLA B*1517      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -0.957829       2.963921        2.006093        9.074624
HLA A*2902      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -1.124120       2.963921        1.839801        13.308236
HLA B*1517      1:464-472       9       RTYGHPIVL       1.770618        0.581401        -0.557429       2.352019        1.794589        3.609353
HLA A*3201      1:464-472       9       RTYGHPIVL       1.770618        0.581401        -0.811813       2.352019        1.540206        6.483550
HLA A*0219      1:82-90 9       LLDLGVPVL       1.833552        0.417767        -0.820736       2.251319        1.430583        6.618144
HLA A*2602      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -1.557746       2.963921        1.406175        36.119867
HLA A*0250      1:82-90 9       LLDLGVPVL       1.833552        0.417767        -0.852539       2.251319        1.398780        7.120965
HLA A*0216      1:82-90 9       LLDLGVPVL       1.833552        0.417767        -0.964360       2.251319        1.286959        9.212133
HLA B*1501      1:63-71 9       LSGGPASVY       1.785456        1.238638        -1.812444       3.024094        1.211650        64.929853
HLA A*0211      1:82-90 9       LLDLGVPVL       1.833552        0.417767        -1.051662       2.251319        1.199656        11.263215
HLA A*6801      1:46-54 9       HTASIEEIR       1.076887        0.539178        -0.424059       1.616065        1.192006        2.654963
HLA B*1517      1:384-392       9       RAVGRELGL       1.384772        0.599348        -0.842835       1.984120        1.141285        6.963626
HLA B*1517      1:355-363       9       KSHHNVGGL       1.450340        0.496960        -0.828123       1.947300        1.119177        6.731672
HLA A*2902      1:331-339       9       EFLVQGTLY       1.312322        1.328885        -1.557051       2.641207        1.084156        36.062074
HLA B*1517      1:107-115       9       VAHTGTREY       1.258906        1.336295        -1.514055       2.595201        1.081146        32.662929
HLA B*2705      1:32-40 9       RRVREARVF       1.516847        1.396018        -1.834633       2.912865        1.078232        68.333388
HLA B*1501      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -1.901640       2.963921        1.062281        79.733397
HLA B*3501      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -1.902636       2.963921        1.061285        79.916499
HLA B*1503      1:367-375       9       LKFTLVEPL       1.359064        0.428202        -0.751003       1.787266        1.036263        5.636422
HLA B*3501      1:482-490       9       TADWTRVPY       1.136050        1.222581        -1.354215       2.358631        1.004416        22.605544
HLA A*2602      1:284-292       9       VTVDAAETF       1.414591        1.171836        -1.599168       2.586427        0.987260        39.734483
HLA A*0250      1:62-70 9       VLSGGPASV       1.079564        0.190032        -0.287084       1.269596        0.982512        1.936795
HLA A*2601      1:18-26 9       LVVDFGAQY       1.578161        1.385760        -1.989831       2.963921        0.974091        97.685597
HLA A*3101      1:307-315       9       KIIGRQFIR       1.192172        0.833564        -1.069368       2.025736        0.956368        11.731893
HLA A*0202      1:275-283       9       FVAATGANL       1.478982        0.382621        -0.924151       1.861603        0.937452        8.397522
HLA B*3901      1:55-63 9       ARQPVALVL       1.819352        0.612094        -1.509300       2.431446        0.922146        32.307233
HLA A*0211      1:449-457       9       VLLADVRSV       1.028902        0.199167        -0.330328       1.228069        0.897741        2.139578
HLA B*4001      1:431-439       9       REELTAAGL       1.365493        0.421291        -0.897325       1.786784        0.889459        7.894501
HLA A*0211      1:62-70 9       VLSGGPASV       1.079564        0.190032        -0.382294       1.269596        0.887301        2.411538
HLA A*0219      1:62-70 9       VLSGGPASV       1.079564        0.190032        -0.382820       1.269596        0.886775        2.414462
HLA A*6801      1:239-247       9       AVAAALVQR       1.496975        0.797447        -1.412299       2.294422        0.882123        25.840382
HLA A*2403      1:194-202       9       RFLHDFAGL       1.457268        0.626845        -1.205356       2.084113        0.878757        16.045612
HLA A*0212      1:82-90 9       LLDLGVPVL       1.833552        0.417767        -1.375938       2.251319        0.875380        23.765026
HLA B*4001      1:330-338       9       AEFLVQGTL       1.554668        0.473057        -1.191391       2.027725        0.836334        15.537851
HLA A*0250      1:449-457       9       VLLADVRSV       1.028902        0.199167        -0.410380       1.228069        0.817689        2.572645
HLA B*1517      1:369-377       9       FTLVEPLRL       1.354455        0.417802        -0.961724       1.772257        0.810533        9.156386
HLA B*3501      1:161-169       9       APVAAFEAF       1.105718        1.050873        -1.366479       2.156591        0.790111        23.253015
HLA A*0250      1:248-256       9       AIGDRLTCV       1.133412        0.240495        -0.599979       1.373907        0.773929        3.980875
HLA A*0219      1:449-457       9       VLLADVRSV       1.028902        0.199167        -0.458385       1.228069        0.769685        2.873323
HLA B*5801      1:284-292       9       VTVDAAETF       1.414591        1.171836        -1.819582       2.586427        0.766845        66.005808
HLA A*0211      1:126-134       9       KLHSDLPEV       0.948868        0.190064        -0.379221       1.138932        0.759711        2.394534
HLA A*0203      1:62-70 9       VLSGGPASV       1.079564        0.190032        -0.513409       1.269596        0.756186        3.261441
HLA A*0250      1:126-134       9       KLHSDLPEV       0.948868        0.190064        -0.385222       1.138932        0.753711        2.427848
HLA A*0211      1:464-472       9       RTYGHPIVL       1.770618        0.581401        -1.613232       2.352019        0.738787        41.042290
HLA A*6801      1:491-499       9       EVLERISTR       1.036599        0.600822        -0.903072       1.637421        0.734349        7.999660
HLA A*3002      1:63-71 9       LSGGPASVY       1.785456        1.238638        -2.311658       3.024094        0.712436        204.954894
HLA A*0250      1:480-488       9       AMTADWTRV       0.947260        0.174566        -0.411677       1.121826        0.710150        2.580339
HLA B*1801      1:394-402       9       EEIVARQPF       0.860370        0.918985        -1.078160       1.779355        0.701195        11.971812
HLA A*3201      1:284-292       9       VTVDAAETF       1.414591        1.171836        -1.919266       2.586427        0.667161        83.035940
HLA A*3101      1:24-32 9       AQYAQLIAR       1.102364        0.807456        -1.245166       1.909820        0.664654        17.585955
HLA B*3501      1:107-115       9       VAHTGTREY       1.258906        1.336295        -1.933509       2.595201        0.661693        85.804227
HLA A*6801      1:479-487       9       DAMTADWTR       1.140857        0.484835        -0.979176       1.625692        0.646516        9.531825
HLA A*0211      1:81-89 9       ALLDLGVPV       0.769820        0.151628        -0.279701       0.921448        0.641746        1.904151
HLA A*0250      1:77-85 9       KLDPALLDL       1.284905        0.332102        -0.986243       1.617007        0.630763        9.688205
HLA A*0203      1:98-106        9       AMAQALGGI       0.985073        0.332445        -0.697275       1.317518        0.620242        4.980529
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HLA A*0250	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.306265	0.921448	0.615183	2.024253
HLA A*0203	1:275-283	9	FVAATGANL	1.478982	0.382621	-1.250307	1.861603	0.611297	17.795354
HLA B*1503	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-1.711059	2.306412	0.595352	51.411401
HLA A*3101	1:239-247	9	AVAAALVQR	1.496975	0.797447	-1.708381	2.294422	0.586041	51.095309
HLA B*0702	1:161-169	9	APVAAFEAF	1.105718	1.050873	-1.580414	2.156591	0.576177	38.055197
HLA B*3901	1:207-215	9	TPANIANAL	1.335334	0.257961	-1.017402	1.593295	0.575893	10.408837
HLA A*6802	1:42-50	9	EVIPHTASI	1.080334	0.256013	-0.769757	1.336347	0.566590	5.885144
HLA A*0250	1:499-507	9	RITNEVAEV	0.947033	0.285622	-0.674941	1.232655	0.557714	4.730873
HLA B*1503	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-1.840657	2.396811	0.556154	69.287842
HLA A*0212	1:62-70	9	VLSGGPASV	1.079564	0.190032	-0.717556	1.269596	0.552039	5.218626
HLA A*3301	1:491-499	9	EVLERISTR	1.036599	0.600822	-1.092858	1.637421	0.544563	12.383923
HLA A*0212	1:449-457	9	VLLADVRSV	1.028902	0.199167	-0.683977	1.228069	0.544092	4.830336
HLA A*3001	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-1.810175	2.352019	0.541844	64.591418
HLA B*1517	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-1.798550	2.334336	0.535786	62.885362
HLA A*0216	1:77-85	9	KLDPALLDL	1.284905	0.332102	-1.091575	1.617007	0.525431	12.347398
HLA A*3002	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-2.438615	2.963921	0.525306	274.545965
HLA A*0250	1:275-283	9	FVAATGANL	1.478982	0.382621	-1.345339	1.861603	0.516265	22.148209
HLA B*1503	1:53-61	9	IRARQPVAL	1.567292	0.450462	-1.506537	2.017754	0.511217	32.102346
HLA A*6901	1:42-50	9	EVIPHTASI	1.080334	0.256013	-0.829965	1.336347	0.506382	6.760285
HLA B*5801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-1.848124	2.352019	0.503895	70.489381
HLA A*0216	1:62-70	9	VLSGGPASV	1.079564	0.190032	-0.769809	1.269596	0.499787	5.885844
HLA B*4002	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-1.530097	2.027725	0.497628	33.892016
HLA B*1501	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-1.837062	2.334336	0.497274	68.716704
HLA A*6802	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-0.860635	1.353717	0.493082	7.254962
HLA A*2602	1:42-50	9	EVIPHTASI	1.080334	0.256013	-0.845819	1.336347	0.490528	7.011635
HLA A*3101	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-1.617254	2.097879	0.480625	41.424178
HLA B*1517	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-1.574099	2.050505	0.476406	37.505811
HLA B*1502	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-2.515340	2.963921	0.448581	327.596948
HLA A*0211	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-1.195535	1.639403	0.443868	15.686839
HLA B*1502	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-2.380559	2.817549	0.436989	240.192416
HLA A*6802	1:275-283	9	FVAATGANL	1.478982	0.382621	-1.428294	1.861603	0.433309	26.809840
HLA A*0203	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.707294	1.138932	0.431639	5.096754
HLA A*3201	1:88-96	9	PVLGICYGF	1.280744	0.979414	-1.835112	2.260158	0.425046	68.408844
HLA A*0212	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.498401	0.921448	0.423047	3.150656
HLA A*0216	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.719116	1.138932	0.419816	5.237406
HLA A*0212	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.735060	1.138932	0.403872	5.433252
HLA A*0206	1:275-283	9	FVAATGANL	1.478982	0.382621	-1.473390	1.861603	0.388213	29.743374
HLA B*5801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-2.254791	2.639184	0.384392	179.800692
HLA A*0211	1:480-488	9	AMTADWTRV	0.947260	0.174566	-0.739247	1.121826	0.382580	5.485885
HLA A*0216	1:449-457	9	VLLADVRSV	1.028902	0.199167	-0.852539	1.228069	0.375530	7.120965
HLA A*0201	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-1.877802	2.251319	0.373516	75.474873
HLA A*0219	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.765824	1.138932	0.373108	5.832088
HLA A*3101	1:30-38	9	IARRVREAR	0.966536	0.718626	-1.312084	1.685162	0.373078	20.515589
HLA A*3002	1:107-115	9	VAHTGTREY	1.258906	1.336295	-2.236226	2.595201	0.358976	172.276376
HLA A*2902	1:63-71	9	LSGGPASVY	1.785456	1.238638	-2.666435	3.024094	0.357659	463.911596
HLA B*1503	1:161-169	9	APVAAFEAF	1.105718	1.050873	-1.804005	2.156591	0.352585	63.680295
HLA A*2602	1:63-71	9	LSGGPASVY	1.785456	1.238638	-2.678483	3.024094	0.345611	476.961569
HLA A*2902	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-2.472786	2.817549	0.344763	297.020192
HLA B*2705	1:55-63	9	ARQPVALVL	1.819352	0.612094	-2.087494	2.431446	0.343952	122.319002
HLA A*0219	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.577574	0.921448	0.343874	3.780715
HLA B*1517	1:514-522	9	ITSKPPATI	1.110493	0.169612	-0.950456	1.280105	0.329649	8.921871
HLA A*2403	1:70-78	9	VYADGAPKL	1.519604	0.588887	-1.790110	2.108491	0.318381	61.675150
HLA A*0206	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-1.242408	1.553110	0.310702	17.474617
HLA B*1501	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.279165	2.586427	0.307262	190.180032
HLA B*1503	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-2.033155	2.334336	0.301181	107.933197
HLA A*0216	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.620278	0.921448	0.301169	4.171364
HLA B*4001	1:388-396	9	RELGLPEEI	1.155087	0.273281	-1.135328	1.428368	0.293040	13.656127
HLA B*5301	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-1.428393	1.718496	0.290103	26.815932
HLA B*1503	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-2.112727	2.394415	0.281688	129.636530
HLA A*3301	1:479-487	9	DAMTADWTR	1.140857	0.484835	-1.344324	1.625692	0.281368	22.096507
HLA A*6801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-1.324001	1.604651	0.280650	21.086310
HLA A*6801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-1.389720	1.667650	0.277930	24.531290
HLA A*3101	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-1.327985	1.604651	0.276665	21.280671
HLA A*0216	1:480-488	9	AMTADWTRV	0.947260	0.174566	-0.846007	1.121826	0.275819	7.014670
HLA B*4001	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-1.482657	1.756081	0.273425	30.384816

HLA B*4801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-1.895456	2.164911	0.269455	78.606131
HLA A*6802	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-0.911887	1.159455	0.247568	8.163696
HLA B*1503	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-2.160850	2.407496	0.246647	144.827005
HLA A*6801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-1.479922	1.721649	0.241727	30.194080
HLA B*5701	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.345543	2.586427	0.240885	221.586127
HLA A*3101	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-1.442198	1.678625	0.236426	27.682064
HLA A*0202	1:62-70	9	VLSGGPASV	1.079564	0.190032	-1.035653	1.269596	0.233943	10.855579
HLA A*6801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-2.731873	2.963921	0.232048	539.352982
HLA A*0206	1:77-85	9	KLDPALLDL	1.284905	0.332102	-1.388001	1.617007	0.229006	24.434337
HLA A*1101	1:239-247	9	AVAAALVQR	1.496975	0.797447	-2.065667	2.294422	0.228755	116.323434
HLA A*0203	1:480-488	9	AMTADWTRV	0.947260	0.174566	-0.901855	1.121826	0.219972	7.977274
HLA A*0211	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-0.698290	0.900138	0.201847	4.992182
HLA A*0206	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.721677	0.921448	0.199770	5.268381
HLA A*0212	1:77-85	9	KLDPALLDL	1.284905	0.332102	-1.423374	1.617007	0.193632	26.507844
HLA A*0201	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.947275	1.138932	0.191658	8.856758
HLA A*0203	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-1.105879	1.295300	0.189421	12.760835
HLA A*2902	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-2.422305	2.610483	0.188178	264.426478
HLA B*1517	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-1.679529	1.858036	0.178506	47.811168
HLA A*3002	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-2.649843	2.817549	0.167706	446.522312
HLA A*3001	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-1.785923	1.947300	0.161376	61.083432
HLA B*1503	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.427385	2.586427	0.159043	267.537415
HLA A*0203	1:449-457	9	VLLADVRSV	1.028902	0.199167	-1.069641	1.228069	0.158428	11.739258
HLA A*0206	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-0.984336	1.138932	0.154597	9.645740
HLA A*0211	1:98-106	9	AMAQALGGI	0.985073	0.332445	-1.170922	1.317518	0.146596	14.822527
HLA A*0250	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-1.493774	1.639403	0.145629	31.172696
HLA A*0211	1:499-507	9	RITNEVAEV	0.947033	0.285622	-1.090203	1.232655	0.142452	12.308449
HLA B*4801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.211490	2.352019	0.140528	162.738516
HLA B*2705	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-2.256384	2.396811	0.140427	180.461395
HLA B*1503	1:63-71	9	LSGGPASVY	1.785456	1.238638	-2.887747	3.024094	0.136347	772.231152
HLA A*6802	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-1.293354	1.426359	0.133005	19.649609
HLA B*1503	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-2.831181	2.963921	0.132740	677.924167
HLA A*6801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-1.508130	1.638021	0.129891	32.220311
HLA A*0211	1:278-286	9	ATGANLVTV	1.225117	0.184937	-1.283862	1.410054	0.126192	19.224807
HLA B*1501	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-2.694512	2.817549	0.123037	494.893299
HLA B*3901	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-1.430686	1.553110	0.122424	26.957896
HLA B*1503	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-1.791102	1.909820	0.118718	61.816114
HLA A*0250	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-0.790578	0.900138	0.109559	6.174165
HLA B*1502	1:63-71	9	LSGGPASVY	1.785456	1.238638	-2.918901	3.024094	0.105193	829.662553
HLA A*0250	1:278-286	9	ATGANLVTV	1.225117	0.184937	-1.326298	1.410054	0.083756	21.198170
HLA A*2902	1:86-94	9	GVPVLGICY	1.484470	1.266426	-2.676016	2.750896	0.074879	474.259924
HLA A*0202	1:98-106	9	AMAQALGGI	0.985073	0.332445	-1.243206	1.317518	0.074311	17.506789
HLA B*3901	1:53-61	9	IRARQPVAL	1.567292	0.450462	-1.944067	2.017754	0.073686	87.915868
HLA A*3101	1:109-117	9	HTGTREYGR	1.076414	0.591236	-1.596705	1.667650	0.070945	39.509843
HLA B*0702	1:207-215	9	TPANIANAL	1.335334	0.257961	-1.528777	1.593295	0.064518	33.789129
HLA A*6801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-1.439111	1.503120	0.064009	27.485982
HLA A*3001	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-1.167257	1.228391	0.061134	14.697959
HLA A*0250	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-1.234236	1.295300	0.061064	17.148896
HLA A*0250	1:98-106	9	AMAQALGGI	0.985073	0.332445	-1.264582	1.317518	0.052936	18.390016
HLA A*6901	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-1.301187	1.353717	0.052530	20.007236
HLA B*3501	1:207-215	9	TPANIANAL	1.335334	0.257961	-1.543236	1.593295	0.050059	34.932988
HLA B*1503	1:107-115	9	VAHTGTREY	1.258906	1.336295	-2.550089	2.595201	0.045113	354.885888
HLA A*0201	1:77-85	9	KLDPALLDL	1.284905	0.332102	-1.572379	1.617007	0.044628	37.357580
HLA B*5301	1:161-169	9	APVAAFEAF	1.105718	1.050873	-2.118902	2.156591	0.037689	131.492761
HLA A*0203	1:499-507	9	RITNEVAEV	0.947033	0.285622	-1.200366	1.232655	0.032289	15.862294
HLA A*3201	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-2.180350	2.204297	0.023946	151.478249
HLA B*3501	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.003765	3.024094	0.020330	1008.706656
HLA A*6901	1:275-283	9	FVAATGANL	1.478982	0.382621	-1.846902	1.861603	0.014701	70.291363
HLA A*3301	1:30-38	9	IARRVREAR	0.966536	0.718626	-1.670691	1.685162	0.014471	46.847950
HLA A*0250	1:492-500	9	VLERISTRI	1.151890	0.131612	-1.276062	1.283502	0.007440	18.882596
HLA B*1517	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-2.304394	2.306412	0.002018	201.555051
HLA A*3101	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-1.727327	1.725080	-0.002247	53.373696
HLA A*0101	1:482-490	9	TADWTRVPY	1.136050	1.222581	-2.363027	2.358631	-0.004397	230.689291
HLA A*0202	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-1.145148	1.138932	-0.006216	13.968455
HLA B*1503	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-1.735245	1.728396	-0.006849	54.355694
HLA A*0203	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-1.646843	1.639403	-0.007440	44.344863

HLA B*5801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.044073	3.024094	-0.019978	1106.808922
HLA A*0206	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-2.185970	2.164911	-0.021059	153.451184
HLA A*0201	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.946800	0.921448	-0.025353	8.847084
HLA B*5101	1:488-496	9	VPYEVLERI	1.256779	0.264787	-1.553550	1.521566	-0.031984	35.772556
HLA B*4403	1:394-402	9	EEIVARQPF	0.860370	0.918985	-1.816410	1.779355	-0.037055	65.525501
HLA A*0203	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-0.959520	0.921448	-0.038073	9.110040
HLA B*3501	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-1.130342	1.091915	-0.038427	13.500254
HLA A*0250	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-0.850725	0.809432	-0.041293	7.091286
HLA A*3001	1:54-62	9	RARQPVALV	0.737262	0.289291	-1.068339	1.026553	-0.041786	11.704127
HLA A*0211	1:77-85	9	KLDPALLDL	1.284905	0.332102	-1.659831	1.617007	-0.042825	45.691064
HLA A*0206	1:480-488	9	AMTADWTRV	0.947260	0.174566	-1.165876	1.121826	-0.044049	14.651279
HLA A*3101	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-2.074722	2.004292	-0.070430	118.774204
HLA A*6802	1:496-504	9	ISTRITNEV	1.144524	0.204306	-1.424159	1.348830	-0.075329	26.555784
HLA B*3501	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-2.415971	2.334336	-0.081635	260.597790
HLA A*0250	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-1.119450	1.036964	-0.082486	13.165875
HLA A*2603	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.112532	3.024094	-0.088437	1295.782008
HLA A*0203	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-0.899735	0.809432	-0.090303	7.938442
HLA A*0206	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.677807	2.586427	-0.091379	476.219018
HLA A*0212	1:278-286	9	ATGANLVTV	1.225117	0.184937	-1.502284	1.410054	-0.092230	31.789537
HLA A*1101	1:69-77	9	SVYADGAPK	0.472549	0.433678	-1.000054	0.906227	-0.093826	10.001234
HLA A*3301	1:109-117	9	HTGTREYGR	1.076414	0.591236	-1.769407	1.667650	-0.101757	58.803957
HLA B*4002	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-1.862784	1.756081	-0.106703	72.909561
HLA B*0702	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-1.201372	1.091915	-0.109457	15.899064
HLA A*0212	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-1.018431	0.900138	-0.118294	10.433530
HLA A*2403	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-2.451321	2.324609	-0.126712	282.696922
HLA A*3101	1:27-35	9	AQLIARRVR	1.168509	0.724756	-2.020036	1.893265	-0.126771	104.721418
HLA B*1517	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-2.738095	2.610483	-0.127611	547.135029
HLA A*0203	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-1.514788	1.373907	-0.140881	32.718107
HLA A*0206	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-2.393637	2.251319	-0.142318	247.534949
HLA B*1502	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-2.784558	2.641207	-0.143351	608.916771
HLA A*0201	1:62-70	9	VLSGGPASV	1.079564	0.190032	-1.414249	1.269596	-0.144653	25.956672
HLA A*2602	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-2.446016	2.297367	-0.148649	279.264636
HLA A*0206	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-1.461784	1.311116	-0.150668	28.959015
HLA B*1501	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-2.458750	2.306412	-0.152338	287.574353
HLA A*0216	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-1.532611	1.373907	-0.158704	34.088772
HLA A*3001	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-1.180189	1.012736	-0.167452	15.142187
HLA A*3301	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-1.892919	1.725080	-0.167838	78.148200
HLA A*0216	1:98-106	9	AMAQALGGI	0.985073	0.332445	-1.489151	1.317518	-0.171633	30.842572
HLA A*0202	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-1.095316	0.921448	-0.173868	12.454199
HLA A*2602	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-2.516378	2.334336	-0.182042	328.381226
HLA A*0206	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-1.667989	1.477798	-0.190191	46.557396
HLA A*0250	1:228-236	9	AICGLSGGV	0.815527	0.247463	-1.259319	1.062990	-0.196329	18.168508
HLA A*1101	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-2.111835	1.909820	-0.202015	129.370303
HLA A*0250	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-2.598845	2.394415	-0.204430	397.050039
HLA B*0702	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.069661	1.861603	-0.208058	117.398173
HLA A*2902	1:88-96	9	PVLGICYGF	1.280744	0.979414	-2.483697	2.260158	-0.223539	304.576915
HLA B*1503	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.578574	2.352019	-0.226555	378.942998
HLA A*0250	1:422-430	9	TLRHADSIV	1.051790	0.095468	-1.374204	1.147258	-0.226946	23.670334
HLA A*0202	1:480-488	9	AMTADWTRV	0.947260	0.174566	-1.350127	1.121826	-0.228301	22.393752
HLA B*4002	1:388-396	9	RELGLPEEI	1.155087	0.273281	-1.658976	1.428368	-0.230608	45.601178
HLA A*0201	1:449-457	9	VLLADVRSV	1.028902	0.199167	-1.459369	1.228069	-0.231299	28.798410
HLA A*2501	1:42-50	9	EVIPHTASI	1.080334	0.256013	-1.576124	1.336347	-0.239777	37.681121
HLA B*2705	1:53-61	9	IRARQPVAL	1.567292	0.450462	-2.260139	2.017754	-0.242385	182.028247
HLA A*0211	1:211-219	9	IANALIEQV	1.224006	0.188649	-1.657096	1.412655	-0.244442	45.404246
HLA A*0211	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-2.358413	2.111966	-0.246447	228.251187
HLA A*8001	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.211643	2.963921	-0.247721	1627.955842
HLA A*0206	1:499-507	9	RITNEVAEV	0.947033	0.285622	-1.481952	1.232655	-0.249297	30.335542
HLA A*2301	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.842167	2.586427	-0.255740	695.292121
HLA B*1503	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.042576	1.779355	-0.263221	110.300245
HLA A*6802	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-1.896063	1.632644	-0.263418	78.715923
HLA A*1101	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.233333	2.963921	-0.269412	1711.327251
HLA A*0206	1:98-106	9	AMAQALGGI	0.985073	0.332445	-1.589920	1.317518	-0.272402	38.897348
HLA A*2603	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.248581	2.963921	-0.284660	1772.479512
HLA A*2402	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-2.610485	2.324609	-0.285876	407.835092
HLA A*3001	1:33-41	9	RVREARVFS	1.063374	-0.731690	-0.622341	0.331684	-0.290657	4.191225

HLA A*1101	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-2.319839	2.025736	-0.294103	208.852270
HLA B*3501	1:284-292	9	VTVDAAETF	1.414591	1.171836	-2.880868	2.586427	-0.294441	760.095261
HLA A*0216	1:499-507	9	RITNEVAEV	0.947033	0.285622	-1.528020	1.232655	-0.295365	33.730320
HLA B*1503	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-3.019055	2.713718	-0.305337	1044.853339
HLA A*2601	1:42-50	9	EVIPHTASI	1.080334	0.256013	-1.642610	1.336347	-0.306262	43.914662
HLA B*4403	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-2.334495	2.027725	-0.306770	216.020660
HLA B*3901	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.669579	2.352019	-0.317560	467.281771
HLA B*1503	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-2.487099	2.164911	-0.322188	306.972194
HLA A*8001	1:107-115	9	VAHTGTREY	1.258906	1.336295	-2.923652	2.595201	-0.328451	838.787881
HLA A*2902	1:107-115	9	VAHTGTREY	1.258906	1.336295	-2.924380	2.595201	-0.329179	840.195763
HLA A*0250	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-0.998301	0.656026	-0.342275	9.960953
HLA B*1517	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-2.662516	2.320077	-0.342439	459.744230
HLA B*1517	1:482-490	9	TADWTRVPY	1.136050	1.222581	-2.703731	2.358631	-0.345100	505.511399
HLA B*1501	1:107-115	9	VAHTGTREY	1.258906	1.336295	-2.944863	2.595201	-0.349662	880.771590
HLA A*3301	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-1.954480	1.604651	-0.349830	90.049268
HLA A*0211	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-1.645443	1.295300	-0.350143	44.202112
HLA B*4002	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.136711	1.779355	-0.357356	136.996964
HLA A*6802	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-2.343912	1.982154	-0.361758	220.755750
HLA A*2301	1:88-96	9	PVLGICYGF	1.280744	0.979414	-2.622937	2.260158	-0.362779	419.697964
HLA A*0202	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-2.765071	2.394415	-0.370656	582.198802
HLA A*0206	1:278-286	9	ATGANLVTV	1.225117	0.184937	-1.791308	1.410054	-0.381254	61.845549
HLA A*3101	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-2.027065	1.638021	-0.389044	106.430273
HLA B*1503	1:55-63	9	ARQPVALVL	1.819352	0.612094	-2.824617	2.431446	-0.393171	667.754241
HLA A*0250	1:211-219	9	IANALIEQV	1.224006	0.188649	-1.811481	1.412655	-0.398826	64.785995
HLA B*3501	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-2.117544	1.718496	-0.399048	131.082237
HLA A*6802	1:211-219	9	IANALIEQV	1.224006	0.188649	-1.827030	1.412655	-0.414375	67.147527
HLA A*0250	1:70-78	9	VYADGAPKL	1.519604	0.588887	-2.523779	2.108491	-0.415288	334.025173
HLA B*4001	1:35-43	9	REARVFSEV	0.807139	0.210046	-1.432768	1.017185	-0.415583	27.087420
HLA A*0211	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.278328	1.861603	-0.416725	189.814113
HLA B*1502	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.015728	2.595201	-0.420527	1036.879920
HLA B*5701	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.445651	3.024094	-0.421557	2790.302748
HLA A*6802	1:206-214	9	WTPANIANA	1.064045	-0.280364	-1.208636	0.783681	-0.424956	16.167251
HLA A*3001	1:497-505	9	STRITNEVA	1.301822	-0.192924	-1.534265	1.108898	-0.425367	34.218849
HLA A*0201	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.287435	1.861603	-0.425832	193.836296
HLA A*0211	1:228-236	9	AICGLSGGV	0.815527	0.247463	-1.489094	1.062990	-0.426104	30.838568
HLA A*0203	1:422-430	9	TLRHADSIV	1.051790	0.095468	-1.579437	1.147258	-0.432179	37.969650
HLA A*0206	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-1.809757	1.373907	-0.435849	64.529249
HLA A*0202	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-2.688018	2.251319	-0.436699	487.548245
HLA A*3101	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-2.159651	1.721649	-0.438002	144.427972
HLA A*0216	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-1.341251	0.900138	-0.441113	21.940701
HLA B*4501	1:35-43	9	REARVFSEV	0.807139	0.210046	-1.460571	1.017185	-0.443387	28.878288
HLA A*0250	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-2.556945	2.111966	-0.444979	360.532589
HLA A*0206	1:285-293	9	TVDAAETFL	1.547755	0.411166	-2.408546	1.958921	-0.449625	256.180669
HLA A*0206	1:449-457	9	VLLADVRSV	1.028902	0.199167	-1.679652	1.228069	-0.451582	47.824620
HLA B*4402	1:477-485	9	SEDAMTADW	0.981632	0.294154	-1.729691	1.275786	-0.453905	53.664966
HLA B*0702	1:301-309	9	APEGKRKII	1.207147	0.122555	-1.785759	1.329702	-0.456057	61.060305
HLA B*5801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.421019	2.963921	-0.457098	2636.448705
HLA A*0211	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-1.834121	1.373907	-0.460213	68.252846
HLA B*4403	1:477-485	9	SEDAMTADW	0.981632	0.294154	-1.736730	1.275786	-0.460944	54.541856
HLA A*0201	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-2.666501	2.204297	-0.462204	463.981873
HLA A*2301	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-2.786936	2.324609	-0.462327	612.259616
HLA A*2301	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-2.857251	2.394415	-0.462836	719.864906
HLA A*2602	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.816262	2.352019	-0.464243	655.031049
HLA A*0202	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-1.274055	0.809432	-0.464623	18.795558
HLA A*6801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-2.493461	2.025736	-0.467725	311.502433
HLA A*3101	1:46-54	9	HTASIEEIR	1.076887	0.539178	-2.092132	1.616065	-0.476067	123.632261
HLA A*3101	1:25-33	9	QYAQLIARR	0.855428	0.838712	-2.174815	1.694140	-0.480675	149.559805
HLA A*0206	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-1.862789	1.372792	-0.489998	72.910350
HLA B*1503	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-1.567995	1.077535	-0.490459	36.982358
HLA A*0202	1:285-293	9	TVDAAETFL	1.547755	0.411166	-2.450926	1.958921	-0.492005	282.440107
HLA B*3901	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-2.288577	1.787266	-0.501311	194.346603
HLA A*0206	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-1.409700	0.905240	-0.504460	25.686232
HLA B*1517	1:54-62	9	RARQPVALV	0.737262	0.289291	-1.531070	1.026553	-0.504517	33.968009
HLA A*6801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-2.199132	1.694140	-0.504992	158.172893
HLA A*1101	1:482-490	9	TADWTRVPY	1.136050	1.222581	-2.865211	2.358631	-0.506580	733.180755

HLA A*0250	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-2.711047	2.204297	-0.506751	514.099580
HLA A*0202	1:77-85	9	KLDPALLDL	1.284905	0.332102	-2.126820	1.617007	-0.509813	133.912035
HLA B*3901	1:112-120	9	TREYGRTEL	1.503201	0.420922	-2.439315	1.924123	-0.515192	274.988930
HLA A*0250	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-1.995497	1.477798	-0.517700	98.968615
HLA A*0203	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.872748	2.352019	-0.520729	746.016108
HLA A*0202	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.164144	1.639403	-0.524740	145.929646
HLA B*3501	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.170061	2.641207	-0.528855	1479.317637
HLA A*0101	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.554865	3.024094	-0.530770	3588.102060
HLA A*0202	1:211-219	9	IANALIEQV	1.224006	0.188649	-1.945087	1.412655	-0.532432	88.122527
HLA A*0202	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-1.908454	1.373907	-0.534546	80.994173
HLA A*6801	1:30-38	9	IARRVREAR	0.966536	0.718626	-2.219718	1.685162	-0.534557	165.851058
HLA A*0206	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-2.594409	2.050505	-0.543904	393.015262
HLA A*6802	1:237-245	9	DSAVAAALV	0.764846	0.042930	-1.353031	0.807776	-0.545254	22.543992
HLA A*0201	1:480-488	9	AMTADWTRV	0.947260	0.174566	-1.683895	1.121826	-0.562068	48.294169
HLA A*0301	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-2.600852	2.025736	-0.575115	398.888673
HLA B*5701	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.545495	2.963921	-0.581574	3511.519153
HLA A*0211	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-2.785874	2.204297	-0.581577	610.764305
HLA A*3002	1:482-490	9	TADWTRVPY	1.136050	1.222581	-2.940789	2.358631	-0.582159	872.547926
HLA A*0212	1:499-507	9	RITNEVAEV	0.947033	0.285622	-1.815038	1.232655	-0.582383	65.318808
HLA B*3901	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-2.301913	1.718496	-0.583417	200.406881
HLA A*1101	1:509-517	9	RVVLDITSK	0.817327	0.463904	-1.865674	1.281231	-0.584443	73.396331
HLA A*0219	1:77-85	9	KLDPALLDL	1.284905	0.332102	-2.205758	1.617007	-0.588751	160.604462
HLA A*3301	1:25-33	9	QYAQLIARR	0.855428	0.838712	-2.288887	1.694140	-0.594747	194.485436
HLA A*0211	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-2.370687	1.772257	-0.598430	234.793870
HLA A*2501	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.564338	2.963921	-0.600417	3667.227994
HLA A*0202	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-2.652099	2.050505	-0.601594	448.847355
HLA A*0211	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-1.638723	1.036964	-0.601760	43.523469
HLA B*1503	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-2.813884	2.204297	-0.609588	651.454679
HLA A*0203	1:429-437	9	IVREELTAA	1.079993	-0.117018	-1.576222	0.962975	-0.613248	37.689684
HLA B*1502	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-2.955323	2.334336	-0.620987	902.242343
HLA A*0216	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-1.431912	0.809432	-0.622480	27.034132
HLA A*2602	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.441718	2.817549	-0.624170	2765.147413
HLA B*0702	1:382-390	9	EVRAVGREL	1.480172	0.348600	-2.453271	1.828772	-0.624499	283.969144
HLA A*0219	1:480-488	9	AMTADWTRV	0.947260	0.174566	-1.750568	1.121826	-0.628742	56.307777
HLA B*5701	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-2.982549	2.352019	-0.630530	960.614277
HLA A*2403	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-2.536457	1.901679	-0.634778	343.919673
HLA A*0216	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.496817	1.861603	-0.635213	313.918209
HLA A*0206	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-1.413713	0.778023	-0.635690	25.924675
HLA A*0219	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.500510	1.861603	-0.638907	316.599262
HLA A*2301	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-2.724717	2.084113	-0.640603	530.538070
HLA B*4501	1:51-59	9	EEIRARQPV	0.859860	0.021658	-1.527865	0.881518	-0.646348	33.718279
HLA B*5301	1:488-496	9	VPYEVLERI	1.256779	0.264787	-2.168983	1.521566	-0.647417	147.565036
HLA A*0301	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-2.558209	1.909820	-0.648389	361.583455
HLA A*6901	1:421-429	9	DTLRHADSI	0.987060	0.113427	-1.749361	1.100487	-0.648874	56.151420
HLA A*0250	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-1.839487	1.190433	-0.649054	69.101423
HLA B*1502	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.046248	2.394415	-0.651833	1112.367456
HLA B*1517	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.514165	1.861603	-0.652562	326.712014
HLA A*3201	1:388-396	9	RELGLPEEI	1.155087	0.273281	-2.085539	1.428368	-0.657172	121.769678
HLA B*1503	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-2.517088	1.858036	-0.659052	328.918169
HLA B*4402	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.439658	1.779355	-0.660303	275.206214
HLA B*0702	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-1.786901	1.126421	-0.660480	61.221056
HLA B*1503	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-2.821459	2.155890	-0.665569	662.916681
HLA B*1517	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-2.652160	1.982154	-0.670005	448.910493
HLA B*1801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-3.389104	2.713718	-0.675386	2449.649345
HLA A*0250	1:1-9	9	VVQPADIDV	0.757996	0.154834	-1.590301	0.912830	-0.677471	38.931453
HLA B*1517	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-2.985824	2.297367	-0.688458	967.886025
HLA A*0212	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.328734	1.639403	-0.689331	213.174057
HLA A*0211	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-1.508416	0.809432	-0.698984	32.241583
HLA B*4501	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.481037	1.779355	-0.701682	302.717387
HLA A*0216	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.113475	1.410054	-0.703420	129.859742
HLA B*1503	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-2.006855	1.301147	-0.705708	101.590923
HLA B*1517	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.523870	2.817549	-0.706322	3340.953119
HLA A*1101	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-2.433681	1.721649	-0.712032	271.444563
HLA A*2602	1:161-169	9	APVAAFEAF	1.105718	1.050873	-2.870681	2.156591	-0.714090	742.472988
HLA B*1502	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.021494	2.306412	-0.715082	1050.737181

HLA A*0216	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-1.752401	1.036964	-0.715437	56.545882
HLA A*0212	1:98-106	9	AMAQALGGI	0.985073	0.332445	-2.033042	1.317518	-0.715524	107.905173
HLA A*0219	1:98-106	9	AMAQALGGI	0.985073	0.332445	-2.036360	1.317518	-0.718842	108.732591
HLA A*3001	1:69-77	9	SVYADGAPK	0.472549	0.433678	-1.629434	0.906227	-0.723206	42.602358
HLA A*3002	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.122874	2.394415	-0.728459	1327.010558
HLA A*2603	1:382-390	9	EVRAVGREL	1.480172	0.348600	-2.564350	1.828772	-0.735578	366.733096
HLA A*0203	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-2.987088	2.251319	-0.735769	970.707180
HLA B*3901	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.599682	1.861603	-0.738078	397.815463
HLA A*0206	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.702502	2.963921	-0.738580	5040.826227
HLA A*0206	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.378074	1.639403	-0.738670	238.821563
HLA A*2603	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.383949	2.641207	-0.742742	2420.745603
HLA A*8001	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.385425	2.641207	-0.744218	2428.983856
HLA B*3501	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.359327	2.610483	-0.748843	2287.318006
HLA A*6802	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-1.348797	0.595350	-0.753447	22.325287
HLA A*0203	1:228-236	9	AICGLSGGV	0.815527	0.247463	-1.820621	1.062990	-0.757630	66.163828
HLA A*6901	1:291-299	9	TFLEALSGV	0.900311	0.134202	-1.794485	1.034513	-0.759972	62.299557
HLA B*2705	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-3.167848	2.407496	-0.760352	1471.798040
HLA B*1501	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.162369	2.394415	-0.767954	1453.346674
HLA A*2602	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-2.822324	2.050505	-0.771819	664.237756
HLA A*0301	1:239-247	9	AVAAALVQR	1.496975	0.797447	-3.067239	2.294422	-0.772816	1167.450763
HLA A*3201	1:514-522	9	ITSKPPATI	1.110493	0.169612	-2.053144	1.280105	-0.773040	113.017178
HLA A*6801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-2.474581	1.695841	-0.778740	298.250363
HLA B*1801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.747649	2.963921	-0.783728	5593.059379
HLA B*1501	1:91-99	9	GICYGFQAM	1.154925	0.134428	-2.078636	1.289353	-0.789283	119.849540
HLA A*1101	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-2.168321	1.377330	-0.790990	147.340084
HLA B*1503	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-2.707984	1.914570	-0.793414	510.485629
HLA A*3201	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.191855	2.394415	-0.797440	1555.447144
HLA A*0203	1:211-219	9	IANALIEQV	1.224006	0.188649	-2.212994	1.412655	-0.800339	163.302946
HLA A*0219	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-2.177080	1.373907	-0.803172	150.341816
HLA A*6802	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-2.758850	1.954913	-0.803937	573.918033
HLA B*0702	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-2.525151	1.718496	-0.806655	335.082153
HLA A*0202	1:492-500	9	VLERISTRI	1.151890	0.131612	-2.091107	1.283502	-0.807605	123.340992
HLA A*0212	1:480-488	9	AMTADWTRV	0.947260	0.174566	-1.937893	1.121826	-0.816066	86.674795
HLA B*1501	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.169700	2.352019	-0.817681	1478.085697
HLA A*0301	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.181362	2.352019	-0.829344	1518.317011
HLA B*5301	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.796303	2.963921	-0.832381	6256.083916
HLA A*0202	1:499-507	9	RITNEVAEV	0.947033	0.285622	-2.070643	1.232655	-0.837988	117.663950
HLA B*2705	1:423-431	9	LRHADSIVR	1.231621	0.752419	-2.822427	1.984040	-0.838387	664.395887
HLA A*8001	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.863315	3.024094	-0.839220	7299.860766
HLA A*0202	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-2.627138	1.787266	-0.839871	423.777351
HLA B*1503	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-3.479272	2.639184	-0.840089	3014.896844
HLA A*0301	1:69-77	9	SVYADGAPK	0.472549	0.433678	-1.750197	0.906227	-0.843970	56.259668
HLA B*3901	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.051694	2.204297	-0.847398	1126.404510
HLA A*0212	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.712852	1.861603	-0.851248	516.240002
HLA A*6901	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-2.627532	1.772257	-0.855276	424.162681
HLA B*4601	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.443119	2.586427	-0.856691	2774.077450
HLA A*2902	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-2.861781	2.004292	-0.857489	727.412582
HLA A*0206	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-2.944807	2.084113	-0.860694	880.657240
HLA A*8001	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.612004	2.750896	-0.861109	4092.646770
HLA B*4001	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.640788	1.779355	-0.861433	437.308833
HLA B*4001	1:10-18	9	PETPARPVL	1.635476	0.153516	-2.651887	1.788992	-0.862895	448.628869
HLA A*0206	1:62-70	9	VLSGGPASV	1.079564	0.190032	-2.132867	1.269596	-0.863272	135.789811
HLA A*0212	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-2.240173	1.373907	-0.866266	173.849267
HLA B*3501	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.071538	2.204297	-0.867242	1179.066040
HLA A*0201	1:499-507	9	RITNEVAEV	0.947033	0.285622	-2.101304	1.232655	-0.868649	126.271169
HLA A*0206	1:211-219	9	IANALIEQV	1.224006	0.188649	-2.282445	1.412655	-0.869790	191.621748
HLA A*0101	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.836211	2.963921	-0.872290	6858.212188
HLA A*2402	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.463568	2.586427	-0.877141	2907.826563
HLA A*2902	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.237924	2.358631	-0.879293	1729.513514
HLA A*0301	1:63-71	9	LSGGPASVY	1.785456	1.238638	-3.903984	3.024094	-0.879890	8016.488282
HLA B*5801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.494267	2.610483	-0.883784	3120.806706
HLA A*2403	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.499205	2.610483	-0.888722	3156.497778
HLA A*0201	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-2.263785	1.373907	-0.889878	183.563017
HLA A*0219	1:499-507	9	RITNEVAEV	0.947033	0.285622	-2.126007	1.232655	-0.893352	133.661610
HLA A*2402	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.290139	2.394415	-0.895724	1950.468382

HLA A*0301	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-2.276214	1.377330	-0.898883	188.892173
HLA A*6801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-2.624760	1.725080	-0.899680	421.463591
HLA A*1101	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.651800	2.750896	-0.900904	4485.386173
HLA A*3301	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-2.906618	2.004292	-0.902327	806.526016
HLA A*6802	1:285-293	9	TVDAAETFL	1.547755	0.411166	-2.861522	1.958921	-0.902601	726.979837
HLA A*3101	1:491-499	9	EVLERISTR	1.036599	0.600822	-2.543383	1.637421	-0.905962	349.448596
HLA A*2301	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.518673	2.610483	-0.908190	3301.211282
HLA A*0201	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.265996	2.352019	-0.913977	1844.996755
HLA A*6801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-1.820931	0.906227	-0.914703	66.211093
HLA A*2402	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.024760	2.108491	-0.916269	1058.668240
HLA B*1501	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.074334	2.156591	-0.917743	1186.681080
HLA B*2705	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-3.633159	2.713718	-0.919441	4296.937392
HLA A*3301	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-2.560239	1.638021	-0.922218	363.277505
HLA A*0219	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.132080	2.204297	-0.927783	1355.438011
HLA B*1501	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-3.568619	2.639184	-0.929435	3703.553928
HLA A*0206	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.283213	2.352019	-0.931194	1919.608361
HLA B*3501	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-3.573214	2.639184	-0.934031	3742.952068
HLA B*4402	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-2.961883	2.027725	-0.934158	915.973622
HLA A*3201	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.046685	2.111966	-0.934720	1113.487327
HLA A*0202	1:288-296	9	AAETFLEAL	1.587358	0.379068	-2.902103	1.966426	-0.935676	798.183362
HLA A*0206	1:288-296	9	AAETFLEAL	1.587358	0.379068	-2.902107	1.966426	-0.935681	798.191998
HLA B*1517	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.047738	2.111966	-0.935772	1116.189282
HLA A*0211	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-1.718061	0.781791	-0.936270	52.246946
HLA B*4601	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.901682	2.963921	-0.937760	7974.099800
HLA A*2902	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.527597	2.586427	-0.941169	3369.742107
HLA A*6801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.302272	2.358631	-0.943641	2005.726235
HLA B*4501	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-2.972390	2.027725	-0.944665	938.404029
HLA A*0301	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.910098	2.963921	-0.946176	8130.130601
HLA A*0250	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.912113	2.963921	-0.948192	8167.955824
HLA B*4601	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.545016	2.595201	-0.949814	3507.645917
HLA A*6901	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-2.111200	1.159455	-0.951745	129.181473
HLA A*3201	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.249314	2.297367	-0.951948	1775.473780
HLA A*0202	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-3.916808	2.963921	-0.952886	8256.721789
HLA B*4801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.158305	2.204297	-0.954008	1439.808099
HLA B*1501	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.705030	2.750896	-0.954134	5070.254651
HLA A*0250	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-1.737162	0.781791	-0.955372	54.596175
HLA A*2603	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.773494	2.817549	-0.955945	5935.998261
HLA A*0250	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-1.964870	1.005151	-0.959719	92.229448
HLA B*0702	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.312309	2.352019	-0.960290	2052.620467
HLA A*0201	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-2.733626	1.772257	-0.961369	541.534089
HLA A*6901	1:237-245	9	DSAVAAALV	0.764846	0.042930	-1.769454	0.807776	-0.961677	58.810320
HLA B*0702	1:9-17	9	VPETPARPV	0.601332	-0.092772	-1.470265	0.508560	-0.961706	29.530134
HLA A*3002	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.712872	2.750896	-0.961977	5162.646075
HLA B*4501	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-2.336704	1.374504	-0.962200	217.121986
HLA B*1501	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.577199	2.610483	-0.966716	3777.452327
HLA B*3901	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-2.724082	1.756081	-0.968001	529.763694
HLA A*0202	1:449-457	9	VLLADVRSV	1.028902	0.199167	-2.197877	1.228069	-0.969808	157.716610
HLA B*5401	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-1.721632	0.748391	-0.973241	52.678345
HLA B*3501	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.792637	2.817549	-0.975089	6203.508318
HLA B*5301	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-2.089233	1.113445	-0.975788	122.809666
HLA A*2603	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.728614	2.750896	-0.977718	5353.205341
HLA B*1502	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.840391	1.861603	-0.978788	692.454270
HLA B*4501	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-1.874086	0.892605	-0.981480	74.831682
HLA B*3901	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-3.234052	2.251319	-0.982733	1714.162573
HLA B*4002	1:35-43	9	REARVFSEV	0.807139	0.210046	-2.000530	1.017185	-0.983345	100.122133
HLA A*3301	1:46-54	9	HTASIEEIR	1.076887	0.539178	-2.606505	1.616065	-0.990440	404.114622
HLA B*1501	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-2.905477	1.914570	-0.990907	804.408278
HLA A*3201	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.403208	1.410054	-0.993154	253.051156
HLA B*1501	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.162435	2.164911	-0.997524	1453.566839
HLA A*0203	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-1.650833	0.644580	-1.006252	44.754091
HLA B*1503	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.617032	2.610483	-1.006549	4140.303339
HLA A*0203	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-1.678528	0.666703	-1.011826	47.701109
HLA A*2902	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.408191	2.394415	-1.013776	2559.712198
HLA B*5301	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.372695	2.358631	-1.014064	2358.821722
HLA B*1501	1:394-402	9	EEIVARQPF	0.860370	0.918985	-2.793815	1.779355	-1.014460	622.035122

HLA A*2403	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.410705	2.394415	-1.016290	2574.572268
HLA B*1503	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.878011	1.861603	-1.016408	755.111442
HLA A*2301	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.125388	2.108491	-1.016897	1334.714342
HLA A*3301	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-3.044590	2.025736	-1.018853	1108.127003
HLA B*5701	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.325419	2.306412	-1.019007	2115.528017
HLA A*0202	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-2.110350	1.087303	-1.023047	128.928734
HLA B*1503	1:27-35	9	AQLIARRVR	1.168509	0.724756	-2.917337	1.893265	-1.024072	826.678669
HLA A*0203	1:77-85	9	KLDPALLDL	1.284905	0.332102	-2.642203	1.617007	-1.025196	438.735362
HLA A*0101	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.636387	2.610483	-1.025904	4328.996337
HLA B*3501	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-2.146377	1.113445	-1.032932	140.080190
HLA A*6801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.059774	3.024094	-1.035679	11475.558034
HLA B*4601	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.062542	3.024094	-1.038447	11548.923563
HLA A*0202	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-2.079224	1.036964	-1.042260	120.011743
HLA A*1101	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.068096	3.024094	-1.044001	11697.570990
HLA A*6901	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-1.967708	0.921448	-1.046260	92.834154
HLA A*0211	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-1.703555	0.656026	-1.047529	50.530685
HLA A*2602	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.643614	2.595201	-1.048413	4401.637106
HLA A*0201	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.688910	1.639403	-1.049507	488.551557
HLA A*6802	1:514-522	9	ITSKPPATI	1.110493	0.169612	-2.329613	1.280105	-1.049508	213.605808
HLA A*0202	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.401782	2.352019	-1.049763	2522.212902
HLA A*2603	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.646889	2.595201	-1.051688	4434.957029
HLA A*0206	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-2.350589	1.295300	-1.055290	224.176075
HLA A*0206	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.450994	2.394415	-1.056579	2824.841311
HLA B*3501	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.364016	2.306412	-1.057604	2312.150615
HLA A*0203	1:29-37	9	LIARRVREA	1.156929	-0.187736	-2.027145	0.969193	-1.057952	106.449851
HLA B*3901	1:32-40	9	RRVREARVF	1.516847	1.396018	-3.971964	2.912865	-1.059099	9374.846406
HLA A*0202	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-2.354973	1.295300	-1.059674	226.450560
HLA A*3201	1:32-40	9	RRVREARVF	1.516847	1.396018	-3.973581	2.912865	-1.060715	9409.804636
HLA B*3501	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.362757	2.297367	-1.065390	2305.455782
HLA A*6802	1:276-284	9	VAATGANLV	0.993882	0.146839	-2.212219	1.140721	-1.071497	163.011668
HLA A*2402	1:32-40	9	RRVREARVF	1.516847	1.396018	-3.985596	2.912865	-1.072731	9673.772574
HLA B*5801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-2.865361	1.791215	-1.074146	733.434651
HLA A*2602	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.058762	1.982154	-1.076607	1144.884384
HLA A*0211	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.242665	2.164911	-1.077754	1748.498325
HLA A*3002	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.719738	2.641207	-1.078531	5244.904057
HLA B*1503	1:423-431	9	LRHADSIVR	1.231621	0.752419	-3.064711	1.984040	-1.080671	1160.674726
HLA A*0216	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-1.864415	0.781791	-1.082624	73.183812
HLA A*6802	1:207-215	9	TPANIANAL	1.335334	0.257961	-2.677365	1.593295	-1.084070	475.734922
HLA A*0203	1:42-50	9	EVIPHTASI	1.080334	0.256013	-2.420491	1.336347	-1.084144	263.324421
HLA A*0250	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.436681	2.352019	-1.084662	2733.260298
HLA A*0201	1:98-106	9	AMAQALGGI	0.985073	0.332445	-2.403330	1.317518	-1.085813	253.122353
HLA B*3901	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-2.723110	1.635727	-1.087383	528.578513
HLA A*6901	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.052166	2.963921	-1.088245	11276.288566
HLA A*3201	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.909416	2.817549	-1.091867	8117.385501
HLA A*6802	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-2.148097	1.055834	-1.092262	140.636013
HLA A*0301	1:509-517	9	RVVLDITSK	0.817327	0.463904	-2.374042	1.281231	-1.092811	236.614753
HLA B*0801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-3.060331	1.965836	-1.094495	1149.029258
HLA A*3001	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.059562	2.963921	-1.095641	11469.972059
HLA A*2602	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.359378	2.260158	-1.099220	2287.590254
HLA A*6802	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-2.225860	1.125828	-1.100032	168.213095
HLA B*3501	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.853315	2.750896	-1.102419	7133.705370
HLA A*6801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-2.779741	1.675016	-1.104725	602.201027
HLA A*0211	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.500413	2.394415	-1.105998	3165.287213
HLA A*2403	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.694100	2.586427	-1.107673	4944.244828
HLA A*2602	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.860378	2.750896	-1.109482	7250.663004
HLA A*0201	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-2.014726	0.905240	-1.109485	103.448853
HLA A*3201	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.445548	2.334336	-1.111212	2789.638637
HLA B*1501	1:275-283	9	FVAATGANL	1.478982	0.382621	-2.975604	1.861603	-1.114001	945.374665
HLA B*1502	1:86-94	9	GVPVLGICY	1.484470	1.266426	-3.869766	2.750896	-1.118871	7409.113752
HLA B*1501	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.032675	2.912865	-1.119810	10781.392417
HLA A*0202	1:496-504	9	ISTRITNEV	1.144524	0.204306	-2.469257	1.348830	-1.120427	294.616488
HLA A*0206	1:42-50	9	EVIPHTASI	1.080334	0.256013	-2.460545	1.336347	-1.124198	288.765402
HLA B*4001	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-2.679860	1.553110	-1.126751	478.476029
HLA A*0203	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.070798	0.943730	-1.127069	117.705970
HLA A*3001	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.722308	2.595201	-1.127106	5276.037635

HLA A*6901	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.088478	1.958921	-1.129557	1225.964566
HLA A*2501	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.111996	1.982154	-1.129842	1294.184704
HLA B*2705	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.042259	1.909820	-1.132439	1102.196046
HLA A*3101	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-2.829489	1.695841	-1.133648	675.288707
HLA B*1503	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-2.691706	1.553110	-1.138597	491.706884
HLA B*1801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.170033	2.027725	-1.142308	1479.221605
HLA A*0211	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.106533	2.963921	-1.142612	12780.070928
HLA A*6801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-2.867551	1.720897	-1.146654	737.141979
HLA A*0202	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.264036	2.111966	-1.152070	1836.691162
HLA B*3801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.069350	2.912865	-1.156485	11731.412737
HLA A*6901	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.509482	2.352019	-1.157463	3232.080250
HLA B*1503	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-3.975611	2.817549	-1.158062	9453.890372
HLA A*0216	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.510690	2.352019	-1.158671	3241.080147
HLA B*1517	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-2.951042	1.791215	-1.159827	893.392790
HLA A*2602	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.799769	1.639403	-1.160365	630.621106
HLA A*0211	1:492-500	9	VLERISTRI	1.151890	0.131612	-2.444024	1.283502	-1.160521	277.986419
HLA B*2705	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-1.883718	0.718317	-1.165402	76.510034
HLA B*0702	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.248172	2.082473	-1.165700	1770.811825
HLA B*1801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.191448	3.024094	-1.167354	15539.904699
HLA A*0206	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-2.940117	1.772257	-1.167861	871.198939
HLA A*0203	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.578005	1.410054	-1.167951	378.447213
HLA A*0206	1:451-459	9	LADVRSVGV	1.034616	0.104608	-2.307838	1.139224	-1.168614	203.159919
HLA A*0203	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.223775	2.050505	-1.173270	1674.076736
HLA A*3001	1:30-38	9	IARRVREAR	0.966536	0.718626	-2.860211	1.685162	-1.175050	724.788599
HLA A*6801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-2.851194	1.675762	-1.175432	709.894856
HLA A*2402	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.263637	2.084113	-1.179524	1835.002768
HLA B*5801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-2.460644	1.280105	-1.180539	288.831022
HLA A*3101	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.144576	2.963921	-1.180655	13950.061598
HLA A*3301	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-2.861203	1.678625	-1.182578	726.445162
HLA A*0206	1:276-284	9	VAATGANLV	0.993882	0.146839	-2.323782	1.140721	-1.183060	210.756820
HLA A*0202	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-1.839891	0.656026	-1.183865	69.165752
HLA B*1501	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.197128	2.013049	-1.184079	1574.445030
HLA A*6802	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-2.114579	0.929716	-1.184863	130.190349
HLA B*1501	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.181701	1.995235	-1.186465	1519.500278
HLA A*2902	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.507062	2.320077	-1.186985	3214.120582
HLA A*0216	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.149217	1.958921	-1.190296	1409.992505
HLA B*5301	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.215117	3.024094	-1.191023	16410.320497
HLA A*3101	1:487-495	9	RVPYEVLER	0.866973	0.808043	-2.866423	1.675016	-1.191407	735.230291
HLA A*0216	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.396782	2.204297	-1.192485	2493.343068
HLA A*6901	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.602774	1.410054	-1.192720	400.657782
HLA A*0202	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.397689	2.204297	-1.193392	2498.555150
HLA A*0216	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-1.840737	0.644580	-1.196156	69.300588
HLA A*3001	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.221132	3.024094	-1.197037	16639.173284
HLA B*5301	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.807538	2.610483	-1.197055	6420.041017
HLA B*1517	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.211389	2.013049	-1.198340	1627.004958
HLA A*0206	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-2.576375	1.374504	-1.201871	377.029011
HLA A*0216	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.236550	1.034513	-1.202037	172.405040
HLA A*6901	1:207-215	9	TPANIANAL	1.335334	0.257961	-2.797475	1.593295	-1.204181	627.300169
HLA A*0219	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-2.395060	1.190433	-1.204627	248.347797
HLA A*0206	1:429-437	9	IVREELTAA	1.079993	-0.117018	-2.167818	0.962975	-1.204844	147.169605
HLA B*1501	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-2.580890	1.374504	-1.206387	380.969738
HLA B*5801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.601394	2.394415	-1.206979	3993.870590
HLA B*1503	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.509825	2.297367	-1.212458	3234.634097
HLA A*0206	1:35-43	9	REARVFSEV	0.807139	0.210046	-2.229957	1.017185	-1.212773	169.807670
HLA B*1502	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-3.926516	2.713718	-1.212798	8443.368099
HLA A*2603	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.800630	2.586427	-1.214203	6318.737544
HLA B*5801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.548639	2.334336	-1.214303	3537.029259
HLA A*2403	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.131959	2.912865	-1.219094	13550.626998
HLA B*5701	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.815376	2.595201	-1.220174	6536.957851
HLA A*0211	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.257188	1.034513	-1.222675	180.795590
HLA B*5801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-2.995264	1.772257	-1.223008	989.155226
HLA A*0203	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.187807	2.963921	-1.223885	15410.142308
HLA A*3201	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.190203	2.963921	-1.226282	15495.411859
HLA A*0216	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.335066	2.108491	-1.226574	2163.046057
HLA A*6801	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.813872	2.586427	-1.227445	6514.363888

HLA A*8001	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.624941	2.394415	-1.230525	4216.387599
HLA A*6801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-2.903108	1.672339	-1.230769	800.033643
HLA A*6801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-3.238436	2.004292	-1.234145	1731.554429
HLA A*2301	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.148613	2.912865	-1.235747	14080.320502
HLA A*6901	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.877245	1.639403	-1.237842	753.780884
HLA B*1503	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.879907	2.641207	-1.238700	7584.145213
HLA A*0206	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.273578	1.034513	-1.239065	187.749090
HLA B*3501	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.559686	2.320077	-1.239609	3628.155822
HLA A*0250	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-1.884362	0.644580	-1.239782	76.623530
HLA B*5801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.224593	1.984120	-1.240473	1677.231391
HLA A*2601	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.060075	2.817549	-1.242526	11483.507218
HLA A*2403	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.503134	2.260158	-1.242976	3185.178876
HLA A*0211	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-2.729885	1.477798	-1.252088	536.890130
HLA A*3201	1:42-50	9	EVIPHTASI	1.080334	0.256013	-2.591651	1.336347	-1.255304	390.527050
HLA B*1517	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.169330	2.912865	-1.256465	14768.292972
HLA A*6802	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.224144	2.963921	-1.260222	16754.975008
HLA A*0203	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.654962	2.394415	-1.260547	4518.166662
HLA A*2601	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.286532	3.024094	-1.262438	19343.364211
HLA B*5701	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-3.054025	1.791215	-1.262810	1132.465733
HLA A*0212	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-2.074919	0.809432	-1.265487	118.828191
HLA A*3101	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.618813	2.352019	-1.266794	4157.316323
HLA A*0216	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-2.907483	1.639403	-1.268080	808.133279
HLA A*2501	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.855256	2.586427	-1.268829	7165.654150
HLA A*1101	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.088607	2.817549	-1.271058	12263.281389
HLA A*2403	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-2.114781	0.843518	-1.271263	130.250935
HLA A*6901	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-1.909666	0.635184	-1.274482	81.220584
HLA B*3901	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.431207	2.156591	-1.274616	2699.023669
HLA A*1101	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-2.915217	1.638021	-1.277197	822.654534
HLA A*1101	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-1.989502	0.712255	-1.277247	97.611640
HLA A*2601	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.921666	2.641207	-1.280460	8349.613761
HLA B*5701	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.676404	2.394415	-1.281989	4746.829655
HLA B*4501	1:388-396	9	RELGLPEEI	1.155087	0.273281	-2.711635	1.428368	-1.283267	514.795356
HLA A*0211	1:488-496	9	VPYEVLERI	1.256779	0.264787	-2.805417	1.521566	-1.283850	638.876132
HLA A*3201	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.308453	3.024094	-1.284358	20344.766239
HLA A*3001	1:509-517	9	RVVLDITSK	0.817327	0.463904	-2.565929	1.281231	-1.284698	368.068760
HLA A*0206	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.269595	1.984120	-1.285475	1860.351538
HLA A*3101	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-2.957851	1.672339	-1.285512	907.509648
HLA B*1502	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.584980	2.297367	-1.287614	3845.745021
HLA A*2403	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-2.911374	1.622722	-1.288652	815.405691
HLA A*6801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.931107	2.641207	-1.289900	8533.095712
HLA B*0702	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.276061	1.984120	-1.291940	1888.255683
HLA A*2603	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.644061	2.352019	-1.292042	4406.163782
HLA A*0206	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.202245	1.909820	-1.292425	1593.106027
HLA B*1801	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.879004	2.586427	-1.292577	7568.406283
HLA A*8001	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.903895	2.610483	-1.293412	8014.840456
HLA B*4402	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.317573	3.024094	-1.293479	20776.548636
HLA A*2402	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.907588	2.610483	-1.297105	8083.292086
HLA A*0212	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-2.850297	1.553110	-1.297187	708.429318
HLA A*2601	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-2.656746	1.353717	-1.303029	453.676153
HLA A*0203	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-2.856325	1.553110	-1.303216	718.332151
HLA B*5801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.251753	1.947300	-1.304453	1785.471937
HLA B*1503	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.253839	1.947300	-1.306540	1794.069947
HLA A*0206	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.307215	1.995235	-1.311980	2028.686651
HLA A*2501	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.336224	3.024094	-1.312129	21688.205365
HLA B*0702	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.646889	2.334336	-1.312553	4434.957029
HLA B*1501	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-2.865930	1.553110	-1.312820	734.395487
HLA B*4002	1:490-498	9	YEVLERIST	1.211490	-0.403834	-2.121491	0.807656	-1.313835	132.279023
HLA A*0219	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-2.214126	0.900138	-1.313989	163.729325
HLA A*3301	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.957449	2.641207	-1.316242	9066.695758
HLA B*0801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.229322	2.912865	-1.316457	16955.946957
HLA B*0801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.623056	2.306412	-1.316645	4198.133456
HLA B*1503	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-3.642120	2.324609	-1.317511	4386.518463
HLA A*6901	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.342758	3.024094	-1.318663	22016.969191
HLA A*0219	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.283146	2.963921	-1.319225	19193.156354
HLA A*1101	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-2.549234	1.228391	-1.320842	354.187735

HLA B*7301	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.234789	2.912865	-1.321924	17170.751416
HLA B*3901	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-2.635154	1.311116	-1.324038	431.672303
HLA B*1503	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.075257	2.750896	-1.324361	11892.055292
HLA A*0301	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.076497	2.750896	-1.325602	11926.072575
HLA B*5701	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.239075	2.912865	-1.326209	17341.024889
HLA A*8001	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.144430	2.817549	-1.326882	13945.383349
HLA A*2403	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.351058	3.024094	-1.326964	22441.829846
HLA A*3101	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.352576	3.024094	-1.328482	22520.396499
HLA A*3001	1:239-247	9	AVAAALVQR	1.496975	0.797447	-3.623230	2.294422	-1.328808	4199.814438
HLA A*2501	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.148951	2.817549	-1.331402	14091.293684
HLA B*1801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.690068	2.358631	-1.331438	4898.557967
HLA A*3001	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-2.470535	1.138932	-1.331603	295.484816
HLA A*2402	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.685679	2.352019	-1.333661	4849.304033
HLA A*0219	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.445971	2.111966	-1.334005	2792.356455
HLA A*3201	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.384612	2.050505	-1.334107	2424.441484
HLA A*6802	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-2.814998	1.477798	-1.337200	653.127340
HLA B*5701	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.155041	2.817549	-1.337492	14290.279775
HLA A*2603	1:491-499	9	EVLERISTR	1.036599	0.600822	-2.975623	1.637421	-1.338202	945.415581
HLA A*3001	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.253670	2.912865	-1.340804	17933.694298
HLA A*6801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-3.020089	1.678625	-1.341464	1047.343420
HLA B*1503	1:115-123	9	YGRTELKVL	1.725445	0.240391	-3.307906	1.965836	-1.342070	2031.915860
HLA A*6901	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.550166	2.204297	-1.345869	3549.488862
HLA A*2603	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.059741	2.713718	-1.346023	11474.688926
HLA B*4801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.371882	3.024094	-1.347787	23544.081410
HLA B*1801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-3.989651	2.641207	-1.348444	9764.524158
HLA A*0250	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-1.956707	0.607629	-1.349079	90.512278
HLA A*2601	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.100392	2.750896	-1.349496	12600.614072
HLA A*0212	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.313420	2.963921	-1.349498	20578.774843
HLA A*3001	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-2.637320	1.287816	-1.349504	433.830828
HLA B*1502	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.463399	2.111966	-1.351434	2906.694150
HLA B*4601	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.686817	2.334336	-1.352481	4862.018023
HLA B*1517	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-3.992165	2.639184	-1.352981	9821.210810
HLA A*2603	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.614706	2.260158	-1.354548	4118.188018
HLA B*0702	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.379647	3.024094	-1.355552	23968.827989
HLA B*4601	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.662142	2.306412	-1.355731	4593.484686
HLA A*6802	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.215538	1.858036	-1.357502	1642.623633
HLA B*1509	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.382859	3.024094	-1.358764	24146.742160
HLA B*4001	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.383523	3.024094	-1.359429	24183.739103
HLA B*4402	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.324970	2.963921	-1.361048	21133.410247
HLA A*2602	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.002954	2.641207	-1.361747	10068.247161
HLA A*0201	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-2.398824	1.036964	-1.361861	250.509493
HLA A*0206	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.659718	2.297367	-1.362351	4567.910692
HLA B*4402	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.275713	2.912865	-1.362847	18867.424930
HLA A*3301	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.328050	2.963921	-1.364128	21283.828880
HLA B*0801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.388638	3.024094	-1.364544	24470.242759
HLA B*2705	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.389691	3.024094	-1.365596	24529.621509
HLA B*1503	1:516-524	9	SKPPATIEW	1.492290	0.425272	-3.284016	1.917562	-1.366454	1923.163273
HLA B*4002	1:224-232	9	GDGHAICGL	1.646336	0.138147	-3.152877	1.784483	-1.368394	1421.927003
HLA A*0201	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.392924	3.024094	-1.368829	24712.901517
HLA A*0216	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.333280	2.963921	-1.369358	21541.687044
HLA A*0211	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-2.723579	1.353717	-1.369862	529.150733
HLA A*2602	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.282817	2.912865	-1.369952	19178.625259
HLA A*6802	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.313749	0.943730	-1.370020	205.944091
HLA A*0212	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.723022	2.352019	-1.371003	5284.721779
HLA B*0802	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.395785	3.024094	-1.371691	24876.278553
HLA A*0219	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.396453	3.024094	-1.372358	24914.528055
HLA A*2602	1:394-402	9	EEIVARQPF	0.860370	0.918985	-3.152924	1.779355	-1.373569	1422.080861
HLA B*5101	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.397994	3.024094	-1.373899	25003.103987
HLA B*4801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.290294	1.914570	-1.375724	1951.164926
HLA B*5801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.289093	2.912865	-1.376228	19457.764724
HLA B*2705	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.341447	2.963921	-1.377525	21950.606383
HLA B*5101	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.343733	2.963921	-1.379811	22066.455106
HLA B*1503	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.375228	1.995235	-1.379993	2372.618232
HLA B*4801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.293052	2.912865	-1.380187	19635.946041
HLA B*4801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.344487	2.963921	-1.380565	22104.808440

HLA A*0101	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.132674	2.750896	-1.381778	13572.930780
HLA A*3201	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-3.993528	2.610483	-1.383045	9852.075572
HLA A*0212	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.407845	3.024094	-1.383751	25576.747599
HLA A*0203	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.408503	3.024094	-1.384409	25615.519820
HLA A*2902	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.100857	2.713718	-1.387139	12614.118553
HLA B*4002	1:426-434	9	ADSIVREEL	1.526192	0.333690	-3.247092	1.859882	-1.387209	1766.410552
HLA A*0219	1:211-219	9	IANALIEQV	1.224006	0.188649	-2.800375	1.412655	-1.387720	631.501911
HLA A*6802	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.412401	3.024094	-1.388307	25846.454034
HLA A*3001	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.206208	2.817549	-1.388659	16077.103804
HLA A*0250	1:276-284	9	VAATGANLV	0.993882	0.146839	-2.530217	1.140721	-1.389495	339.013339
HLA A*2601	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.977664	2.586427	-1.391237	9498.696507
HLA B*5401	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.357923	2.963921	-1.394002	22799.402223
HLA A*6802	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.804106	1.410054	-1.394052	636.950453
HLA A*6801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-2.821896	1.424271	-1.397625	663.584070
HLA B*5301	1:107-115	9	VAHTGTREY	1.258906	1.336295	-3.993951	2.595201	-1.398749	9861.673999
HLA B*2705	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.394254	1.995235	-1.399019	2478.871378
HLA A*1101	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.751644	2.352019	-1.399625	5644.734953
HLA A*6802	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-2.687543	1.287816	-1.399727	487.015744
HLA A*0301	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-3.038312	1.638021	-1.400291	1092.223997
HLA A*0201	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.365353	2.963921	-1.401431	23192.765237
HLA B*7301	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.117219	2.713718	-1.403501	13098.414269
HLA B*2705	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.221202	2.817549	-1.403653	16641.873985
HLA B*0702	1:75-83	9	APKLDPALL	1.420023	0.333020	-3.158112	1.753043	-1.405069	1439.169526
HLA B*3801	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.429381	3.024094	-1.405286	26876.994179
HLA B*4001	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.319385	2.912865	-1.406520	20863.389111
HLA B*3801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.371318	2.963921	-1.407397	23513.532238
HLA B*1801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.714024	2.306412	-1.407612	5176.349608
HLA A*0206	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.519994	2.111966	-1.408028	3311.263419
HLA A*0216	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-2.065700	0.656026	-1.409674	116.332244
HLA A*0206	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-2.711982	1.301147	-1.410836	515.207699
HLA B*2705	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-2.520011	1.109115	-1.410896	331.139222
HLA B*1509	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.324436	2.912865	-1.411571	21107.473401
HLA B*1502	1:284-292	9	VTVDAAETF	1.414591	1.171836	-3.998767	2.586427	-1.412340	9971.651366
HLA B*2705	1:27-35	9	AQLIARRVR	1.168509	0.724756	-3.306228	1.893265	-1.412964	2024.082397
HLA B*3501	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.325956	2.912865	-1.413091	21181.483192
HLA A*6802	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.617403	2.204297	-1.413107	4143.843828
HLA A*2602	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.808337	2.394415	-1.413922	6431.860666
HLA B*2705	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-3.569840	2.155890	-1.413951	3713.987221
HLA A*0216	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.439082	3.024094	-1.414987	27484.112706
HLA A*6901	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-2.010497	0.595350	-1.415147	102.446378
HLA A*8001	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.328191	2.912865	-1.415325	21290.738591
HLA B*0801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.810141	2.394415	-1.415726	6458.639319
HLA B*3901	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.440069	3.024094	-1.415974	27546.631827
HLA B*4001	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.581160	2.164911	-1.416249	3812.064356
HLA A*2403	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.384538	2.963921	-1.420617	24240.324341
HLA A*6801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-3.085790	1.663852	-1.421938	1218.400608
HLA A*0202	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.832295	1.410054	-1.422241	679.664790
HLA B*4001	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.387734	2.963921	-1.423812	24419.328998
HLA A*6802	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.474536	2.050505	-1.424031	2982.194023
HLA A*6801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-3.229179	1.804702	-1.424477	1695.036977
HLA B*0702	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.390445	2.963921	-1.426524	24572.256030
HLA B*0802	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.391058	2.963921	-1.427137	24606.976097
HLA B*0702	1:54-62	9	RARQPVALV	0.737262	0.289291	-2.453948	1.026553	-1.427395	284.411927
HLA B*5701	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.069877	2.639184	-1.430693	11745.637658
HLA A*0250	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.465517	1.034513	-1.431003	292.089986
HLA B*0803	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.455307	3.024094	-1.431213	28530.360826
HLA B*0702	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.739652	2.306412	-1.433240	5491.004291
HLA B*4403	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.346204	2.912865	-1.433339	22192.397833
HLA B*0801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-2.292026	0.857166	-1.434860	195.896193
HLA B*1503	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.794127	2.358631	-1.435496	6224.822074
HLA B*1517	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.518725	2.082473	-1.436252	3301.604208
HLA A*2603	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.771403	2.334336	-1.437067	5907.486304
HLA A*0301	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.254689	2.817549	-1.437141	17975.850142
HLA B*4601	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.351888	2.912865	-1.439022	22484.727751
HLA B*0801	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.403482	2.963921	-1.439561	25321.085755

HLA A*3201	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-3.847817	2.407496	-1.440321	7043.967988
HLA A*0202	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.436272	1.995235	-1.441037	2730.688634
HLA B*1801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.258860	2.817549	-1.441311	18149.295627
HLA A*0216	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.214274	1.772257	-1.442017	1637.849694
HLA B*0803	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.407178	2.963921	-1.443257	25537.481438
HLA B*1502	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.458136	2.013049	-1.445088	2871.682953
HLA A*0301	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.040865	2.595201	-1.445664	10986.646682
HLA A*3201	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.393747	1.947300	-1.446447	2475.976419
HLA B*1503	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-3.222201	1.775111	-1.447090	1668.019818
HLA B*5801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.744487	2.297367	-1.447120	5552.480260
HLA A*0211	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.471310	3.024094	-1.447215	29601.219723
HLA B*1509	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.414283	2.963921	-1.450362	25958.698041
HLA A*3002	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.559395	2.108491	-1.450903	3625.722776
HLA A*2301	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.656828	2.204297	-1.452531	4537.615972
HLA B*3501	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.166473	2.713718	-1.452755	14671.459716
HLA A*0301	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.366064	2.912865	-1.453199	23230.813910
HLA A*2402	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.478541	3.024094	-1.454447	30098.255285
HLA A*1101	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-3.175747	1.720897	-1.454850	1498.812094
HLA A*2602	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.093445	1.637421	-1.456024	1240.065797
HLA B*4403	1:388-396	9	RELGLPEEI	1.155087	0.273281	-2.884580	1.428368	-1.456213	766.620117
HLA B*0702	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.369990	2.912865	-1.457125	23441.770801
HLA A*6901	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-2.387199	0.929716	-1.457483	243.892775
HLA B*1501	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.569742	2.111966	-1.457776	3713.143442
HLA B*1509	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.276265	2.817549	-1.458716	18891.426793
HLA A*0202	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.543366	2.084113	-1.459253	3494.350045
HLA B*4403	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.483797	3.024094	-1.459703	30464.714984
HLA A*0212	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.664858	2.204297	-1.460562	4622.301581
HLA B*1501	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.759190	2.297367	-1.461823	5743.678208
HLA B*4601	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.102022	2.639184	-1.462839	12648.011533
HLA A*0203	1:492-500	9	VLERISTRI	1.151890	0.131612	-2.750251	1.283502	-1.466749	562.666107
HLA B*0702	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.284732	2.817549	-1.467184	19263.371650
HLA A*3001	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.552534	2.084113	-1.468421	3568.897693
HLA A*6901	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.381369	2.912865	-1.468504	24064.063849
HLA B*4601	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.287284	2.817549	-1.469735	19376.879759
HLA A*0212	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.865265	2.394415	-1.470850	7332.712360
HLA A*0202	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.426268	1.954913	-1.471355	2668.505336
HLA A*0206	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.082174	2.610483	-1.471691	12082.972961
HLA B*4801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.259671	1.787266	-1.472404	1818.321999
HLA A*0202	1:228-236	9	AICGLSGGV	0.815527	0.247463	-2.535484	1.062990	-1.472494	343.150260
HLA B*1502	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.385488	2.912865	-1.472622	24293.361816
HLA B*5301	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-3.264882	1.791215	-1.473667	1840.271714
HLA A*3101	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.386761	2.912865	-1.473896	24364.698372
HLA A*1101	1:487-495	9	RVPYEVLER	0.866973	0.808043	-3.149391	1.675016	-1.474374	1410.557083
HLA A*0206	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.498486	3.024094	-1.474392	31512.735164
HLA A*0101	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.388718	2.912865	-1.475853	24474.744137
HLA A*2403	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-3.884648	2.407496	-1.477151	7667.396116
HLA A*0201	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.390339	2.912865	-1.477474	24566.274765
HLA A*0250	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.107072	1.629570	-1.477502	1279.592666
HLA A*0250	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-1.776765	0.299099	-1.477666	59.808807
HLA A*2601	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.390555	2.912865	-1.477690	24578.504684
HLA A*0202	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.586761	2.108491	-1.478270	3861.547631
HLA A*0250	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.422366	0.943730	-1.478636	264.463674
HLA A*2301	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.635396	2.156591	-1.478805	4319.124627
HLA A*3001	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.230140	2.750896	-1.479244	16987.898993
HLA B*0802	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.393135	2.912865	-1.480270	24724.936912
HLA A*0219	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-2.290706	0.809432	-1.481273	195.301503
HLA B*1503	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.566481	2.084113	-1.482368	3685.366141
HLA A*3001	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.094236	2.610483	-1.483753	12423.273879
HLA A*6802	1:99-107	9	MAQALGGIV	1.150311	0.231441	-2.866968	1.381752	-1.485217	736.153654
HLA A*0201	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.444293	1.958921	-1.485372	2781.591333
HLA B*1502	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.641984	2.156591	-1.485393	4385.142306
HLA A*3001	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.199742	2.713718	-1.486024	15839.520603
HLA A*0206	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-2.617030	1.130410	-1.486620	414.028519
HLA A*0101	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.304188	2.817549	-1.486640	20145.979556
HLA B*1801	1:10-18	9	PETPARPVL	1.635476	0.153516	-3.277616	1.788992	-1.488624	1895.030305

HLA B*3901	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.453663	2.963921	-1.489741	28422.522879
HLA B*4002	1:51-59	9	EEIRARQPV	0.859860	0.021658	-2.372270	0.881518	-1.490752	235.651554
HLA B*1501	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.133219	2.641207	-1.492012	13589.976783
HLA A*0301	1:113-121	9	REYGRTELK	0.904130	0.335113	-2.734213	1.239243	-1.494970	542.266994
HLA B*1517	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.246617	2.750896	-1.495721	17644.794650
HLA A*2602	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.443307	1.947300	-1.496007	2775.278306
HLA B*5701	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.107778	2.610483	-1.497295	12816.767058
HLA B*5401	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.521957	3.024094	-1.497863	33262.696624
HLA A*0203	1:276-284	9	VAATGANLV	0.993882	0.146839	-2.638725	1.140721	-1.498004	435.236593
HLA B*5101	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-2.624878	1.126421	-1.498457	421.577610
HLA A*0203	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.411811	2.912865	-1.498946	25811.381413
HLA B*0803	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.413674	2.912865	-1.500809	25922.351188
HLA B*5801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.318610	2.817549	-1.501061	20826.175693
HLA A*2902	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.414400	2.912865	-1.501535	25965.720674
HLA A*0203	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-2.159252	0.656026	-1.503226	144.295205
HLA A*2301	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.855679	2.352019	-1.503660	7172.635320
HLA B*5801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.100387	2.595201	-1.505186	12600.477737
HLA B*1509	1:55-63	9	ARQPVALVL	1.819352	0.612094	-3.937455	2.431446	-1.506009	8658.744513
HLA A*0212	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.617991	2.111966	-1.506025	4149.452053
HLA A*0201	1:278-286	9	ATGANLVTV	1.225117	0.184937	-2.916416	1.410054	-1.506362	824.927408
HLA B*1501	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-2.880018	1.372792	-1.507226	758.608163
HLA A*3001	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-2.829903	1.322138	-1.507765	675.931983
HLA A*3001	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-3.533926	2.025736	-1.508190	3419.213168
HLA A*2301	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.533336	3.024094	-1.509242	34145.699238
HLA A*3201	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.149402	2.639184	-1.510218	14105.937897
HLA A*0212	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.423831	2.912865	-1.510966	26535.740636
HLA A*0216	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-2.422963	0.911989	-1.510973	264.827326
HLA A*3201	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.223318	0.712255	-1.511063	167.231335
HLA B*3901	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.541318	2.027725	-1.513593	3477.904537
HLA A*0206	1:228-236	9	AICGLSGGV	0.815527	0.247463	-2.577305	1.062990	-1.514315	377.837592
HLA A*3002	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.101073	2.586427	-1.514646	12620.398286
HLA B*4402	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.332894	2.817549	-1.515346	21522.583265
HLA B*5801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.837029	2.320077	-1.516951	6871.135904
HLA A*0219	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.430062	2.912865	-1.517197	26919.193725
HLA B*1502	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.070796	1.553110	-1.517686	1177.052120
HLA B*1801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.430950	2.912865	-1.518085	26974.298133
HLA A*6901	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.040102	1.521566	-1.518536	1096.735804
HLA A*3002	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.431643	2.912865	-1.518778	27017.381251
HLA A*6802	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.871853	2.352019	-1.519834	7444.792629
HLA B*2705	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-3.248337	1.728396	-1.519941	1771.482545
HLA A*0206	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.433685	2.912865	-1.520820	27144.694220
HLA B*1501	1:482-490	9	TADWTRVPY	1.136050	1.222581	-3.881119	2.358631	-1.522488	7605.345952
HLA A*2301	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.486473	2.963921	-1.522552	30653.013946
HLA B*3801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.340434	2.817549	-1.522885	21899.484605
HLA A*0250	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.483304	1.958921	-1.524383	3043.015563
HLA B*1503	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.844857	2.320077	-1.524780	6996.116335
HLA A*0211	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-2.735148	1.210159	-1.524989	543.435827
HLA B*4403	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.489119	2.963921	-1.525197	30840.307733
HLA A*0202	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.550297	3.024094	-1.526202	35505.607097
HLA A*6802	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.440468	2.912865	-1.527603	27571.977599
HLA A*2301	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.167460	2.639184	-1.528277	14704.833424
HLA A*0206	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.472128	0.943730	-1.528399	296.570616
HLA A*2402	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.492826	2.963921	-1.528905	31104.712408
HLA B*3501	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.391477	1.861603	-1.529874	2463.070834
HLA A*0250	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.554042	3.024094	-1.529948	35813.108790
HLA B*5101	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-3.250625	1.718496	-1.532129	1780.841533
HLA A*3101	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.142927	2.610483	-1.532444	13897.183333
HLA B*1801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.289744	1.756081	-1.533663	1948.696482
HLA B*1801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.690435	2.156591	-1.533844	4902.693814
HLA B*1501	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.392755	1.858036	-1.534719	2470.330279
HLA B*4801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.519853	1.984120	-1.535732	3310.188779
HLA A*0250	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-2.559313	1.020890	-1.538423	362.504005
HLA A*1101	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.451614	2.912865	-1.538749	28288.757568
HLA A*3002	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.253066	2.713718	-1.539348	17908.777663
HLA A*2403	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-2.590505	1.050933	-1.539571	389.497408

HLA B*0702	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.151126	2.610483	-1.540643	14162.061939
HLA B*3901	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.623479	2.082473	-1.541007	4202.223505
HLA A*0202	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-3.865805	2.324609	-1.541196	7341.841945
HLA B*1517	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-3.935651	2.394415	-1.541235	8622.843837
HLA A*3301	1:239-247	9	AVAAALVQR	1.496975	0.797447	-3.836601	2.294422	-1.542179	6864.373914
HLA A*2403	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.361831	2.817549	-1.544282	23005.445826
HLA A*0206	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.653383	2.108491	-1.544892	4501.770934
HLA A*2402	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.806311	2.260158	-1.546153	6401.936640
HLA B*1801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.141409	2.595201	-1.546208	13848.700386
HLA A*0202	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.133176	2.586427	-1.546749	13588.653482
HLA A*2602	1:421-429	9	DTLRHADSI	0.987060	0.113427	-2.647475	1.100487	-1.546988	444.093978
HLA B*4801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.365381	2.817549	-1.547832	23194.270929
HLA A*0212	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.365484	2.817549	-1.547935	23199.792637
HLA B*2705	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.712957	2.164911	-1.548046	5163.651629
HLA A*0211	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-2.553369	1.005151	-1.548218	357.576206
HLA A*0211	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.135418	2.586427	-1.548991	13658.966276
HLA A*2403	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.901193	2.352019	-1.549174	7965.131936
HLA A*0216	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.716411	2.164911	-1.551499	5204.879476
HLA B*4002	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.464515	2.912865	-1.551650	29141.700869
HLA A*3201	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.717581	2.164911	-1.552669	5218.920977
HLA A*6901	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.140587	2.586427	-1.554159	13822.503219
HLA A*6901	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.372171	2.817549	-1.554622	23559.753241
HLA B*4001	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.372941	2.817549	-1.555393	23601.595808
HLA A*0203	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-2.460639	0.905240	-1.555399	288.827897
HLA A*3301	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-3.277517	1.721649	-1.555868	1894.599774
HLA A*0202	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.328252	1.772257	-1.555996	2129.375536
HLA A*1101	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.151540	2.595201	-1.556339	14175.552633
HLA A*2301	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.569681	2.013049	-1.556632	3712.621199
HLA A*2402	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.196096	2.639184	-1.556912	15707.086391
HLA B*1501	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-2.938576	1.381432	-1.557144	868.112632
HLA A*1101	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-2.913756	1.356576	-1.557180	819.890994
HLA A*2403	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.539499	1.982154	-1.557345	3463.372114
HLA A*2403	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.891692	2.334336	-1.557356	7792.766378
HLA A*3301	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.582008	3.024094	-1.557913	38195.125553
HLA B*2705	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.308831	2.750896	-1.557935	20362.494090
HLA B*5301	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.154940	1.593295	-1.561645	1428.697055
HLA B*1501	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.275461	2.713718	-1.561743	18856.506528
HLA B*1501	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-3.813435	2.251319	-1.562116	6507.812176
HLA B*1509	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.914952	2.352019	-1.562933	8221.509408
HLA B*1509	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.277160	2.713718	-1.563442	18930.405349
HLA B*7301	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-2.755777	1.190075	-1.565702	569.871246
HLA B*0801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.616760	2.050505	-1.566255	4137.705919
HLA A*2403	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.207509	2.641207	-1.566303	16125.360426
HLA A*0211	1:514-522	9	ITSKPPATI	1.110493	0.169612	-2.846777	1.280105	-1.566672	702.711398
HLA B*5701	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.886791	2.320077	-1.566713	7705.319136
HLA B*7301	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.590901	3.024094	-1.566806	38985.287624
HLA A*6802	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.206939	1.639403	-1.567536	1610.419244
HLA A*0216	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.481163	2.912865	-1.568298	30280.521239
HLA A*3101	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.323128	2.750896	-1.572232	21043.965809
HLA A*3101	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.214638	2.641207	-1.573431	16392.219772
HLA A*0211	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.624222	2.050505	-1.573717	4209.413455
HLA A*0250	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-2.480732	0.905240	-1.575492	302.504565
HLA A*0211	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-2.766049	1.190433	-1.575616	583.510524
HLA A*2602	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.437259	1.861603	-1.575656	2736.900232
HLA A*0202	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.490583	1.914570	-1.576013	3094.445784
HLA A*0201	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.393814	2.817549	-1.576265	24763.623546
HLA B*5101	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.489354	2.912865	-1.576488	30856.996512
HLA A*3002	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.188277	2.610483	-1.577793	15426.824764
HLA A*6901	1:211-219	9	IANALIEQV	1.224006	0.188649	-2.991801	1.412655	-1.579146	981.298893
HLA A*6801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-2.974904	1.394918	-1.579986	943.851810
HLA A*0216	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.398013	2.817549	-1.580464	25004.186123
HLA B*5301	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.399251	2.817549	-1.581702	25075.575064
HLA A*0301	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-3.277842	1.695841	-1.582000	1896.014743
HLA B*2705	1:263-271	9	LRAGERAQV	0.865849	0.254971	-2.703618	1.120820	-1.582798	505.380147
HLA B*0802	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.400506	2.817549	-1.582957	25148.120148

HLA A*2501	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.495859	2.912865	-1.582994	31322.713302
HLA A*3101	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.667151	2.084113	-1.583038	4646.772119
HLA A*0211	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.691882	2.108491	-1.583391	4919.059254
HLA A*6802	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.169857	2.586427	-1.583429	14786.200262
HLA A*6801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.178794	2.595201	-1.583593	15093.641303
HLA B*4001	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.936966	2.352019	-1.584948	8649.006680
HLA A*0203	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.403635	2.817549	-1.586086	25329.991298
HLA A*6901	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-2.713491	1.126421	-1.587070	517.000203
HLA A*3101	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.405829	2.817549	-1.588281	25458.303499
HLA A*0219	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.406396	2.817549	-1.588847	25491.517257
HLA A*0201	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-2.900185	1.311116	-1.589069	794.667571
HLA B*4601	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.340650	2.750896	-1.589754	21910.386906
HLA B*5801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.340652	2.750896	-1.589757	21910.505440
HLA B*4402	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.342222	2.750896	-1.591326	21989.828998
HLA A*0250	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.363729	1.772257	-1.591473	2310.625084
HLA A*0216	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-2.782147	1.190433	-1.591714	605.546313
HLA A*0202	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-2.807315	1.215498	-1.591817	641.674894
HLA A*2902	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.703850	2.111966	-1.591885	5056.503715
HLA B*2705	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.944174	2.352019	-1.592156	8793.756839
HLA B*0803	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.203041	2.610483	-1.592558	15960.287494
HLA B*4501	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.616832	3.024094	-1.592738	41383.956477
HLA B*1801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.203341	2.610483	-1.592858	15971.343275
HLA A*3201	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-3.619020	2.025736	-1.593283	4159.295969
HLA A*2602	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.307661	2.713718	-1.593943	20307.708822
HLA A*0206	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.798253	2.204297	-1.593956	6284.238196
HLA A*2501	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.231698	1.637421	-1.594277	1704.895736
HLA A*0301	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.235875	2.641207	-1.594668	17213.721132
HLA B*0801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.413256	2.817549	-1.595707	25897.401009
HLA B*4501	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.382873	1.786784	-1.596090	2414.755076
HLA B*0702	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.027567	2.431446	-1.596121	10655.334138
HLA A*0202	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-2.512915	0.915104	-1.597811	325.773069
HLA B*4002	1:63-71	9	LSGGPASVY	1.785456	1.238638	-4.623244	3.024094	-1.599149	41999.464512
HLA A*0203	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.554625	1.954913	-1.599712	3586.122661
HLA B*1801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.350711	2.750896	-1.599815	22423.868681
HLA A*6901	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-2.381725	0.781170	-1.600555	240.837791
HLA A*0202	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-2.249092	0.644580	-1.604511	177.456335
HLA A*2601	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.199775	2.595201	-1.604573	15840.720309
HLA A*2501	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.355487	2.750896	-1.604591	22671.854431
HLA A*2902	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.713333	2.108491	-1.604841	5168.123130
HLA A*0203	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-2.915974	1.311116	-1.604858	824.088835
HLA A*0250	1:451-459	9	LADVRSVGV	1.034616	0.104608	-2.744119	1.139224	-1.604894	554.777195
HLA A*0203	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.554104	1.947300	-1.606804	3581.818329
HLA B*3501	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-1.709283	0.101982	-1.607301	51.201565
HLA A*0212	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-2.645027	1.036964	-1.608063	441.597616
HLA A*2601	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.321821	2.713718	-1.608103	20980.762800
HLA B*0803	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.426378	2.817549	-1.608829	26691.811884
HLA A*3201	1:421-429	9	DTLRHADSI	0.987060	0.113427	-2.710765	1.100487	-1.610278	513.765942
HLA B*5101	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.767000	2.156591	-1.610409	5847.897994
HLA B*4402	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.324378	2.713718	-1.610660	21104.618866
HLA A*3001	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.253033	2.641207	-1.611826	17907.421332
HLA B*4402	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.253106	2.641207	-1.611899	17910.424776
HLA A*0216	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.363102	2.750896	-1.612206	23072.875643
HLA A*0206	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.363318	2.750896	-1.612422	23084.362097
HLA B*3501	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.725611	2.111966	-1.613646	5316.321795
HLA A*0101	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.254335	2.639184	-1.615151	17961.171788
HLA A*0211	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.528214	2.912865	-1.615349	33745.365263
HLA B*1503	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-2.334862	0.718317	-1.616545	216.203046
HLA B*7301	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.048637	2.431446	-1.617191	11185.032612
HLA B*0801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.257340	2.639184	-1.618156	18085.880541
HLA B*0801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-3.970658	2.352019	-1.618639	9346.690188
HLA A*0211	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.436504	2.817549	-1.618956	27321.487201
HLA A*2602	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.447780	1.828772	-1.619008	2804.012596
HLA B*3901	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.437223	2.817549	-1.619675	27366.753361
HLA A*6901	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-2.829992	1.210159	-1.619833	676.070953
HLA B*1509	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.648727	2.027725	-1.621002	4453.759006

HLA A*0206	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.535857	1.914570	-1.621288	3434.452023
HLA A*0101	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.216602	2.595201	-1.621400	16466.524229
HLA A*8001	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.335608	2.713718	-1.621890	21657.486474
HLA A*6801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-3.479949	1.857234	-1.622715	3019.597860
HLA B*4501	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-2.995650	1.372792	-1.622858	990.033216
HLA B*1501	1:98-106	9	AMAQALGGI	0.985073	0.332445	-2.940409	1.317518	-1.622891	871.783558
HLA B*5701	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.608085	1.984120	-1.623965	4055.882099
HLA A*0216	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.674712	2.050505	-1.624207	4728.376145
HLA B*3501	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.019292	2.394415	-1.624877	10454.233283
HLA A*3001	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-3.004489	1.377330	-1.627158	1010.388810
HLA B*1517	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.341021	2.713718	-1.627303	21929.123090
HLA A*2403	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.378799	2.750896	-1.627903	23922.063267
HLA A*2402	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.269324	2.641207	-1.628118	18591.925950
HLA A*6802	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.456896	1.828772	-1.628124	2863.491920
HLA A*0101	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.269832	2.641207	-1.628625	18613.663984
HLA A*2601	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.239366	2.610483	-1.628883	17352.661606
HLA A*2603	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.542743	2.912865	-1.629878	34893.404788
HLA A*3201	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.658158	2.027725	-1.630433	4551.531433
HLA B*4002	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.418468	1.786784	-1.631684	2621.004613
HLA B*1517	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-3.582222	1.949733	-1.632489	3821.397288
HLA B*3501	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.892697	2.260158	-1.632539	7810.830908
HLA A*3001	1:429-437	9	IVREELTAA	1.079993	-0.117018	-2.595890	0.962975	-1.632915	394.357034
HLA A*0212	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.717393	2.084113	-1.633280	5216.662763
HLA B*3901	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.420253	1.786784	-1.633470	2631.803099
HLA B*0702	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.228777	2.595201	-1.633576	16934.678995
HLA A*6802	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.451534	2.817549	-1.633985	28283.554719
HLA B*5801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.349411	2.713718	-1.635693	22356.884143
HLA A*3001	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.275614	2.639184	-1.636430	18863.138448
HLA B*5701	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.388013	2.750896	-1.637118	24435.054657
HLA A*0201	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.388697	2.750896	-1.637801	24473.552515
HLA B*1502	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-2.933285	1.295300	-1.637985	857.600520
HLA A*0219	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.673803	1.034513	-1.639290	471.849189
HLA A*3201	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-2.695437	1.055834	-1.639603	495.949288
HLA B*4001	1:51-59	9	EEIRARQPV	0.859860	0.021658	-2.521199	0.881518	-1.639682	332.046925
HLA B*7301	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.603980	2.963921	-1.640059	40177.260943
HLA B*4801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.391237	2.750896	-1.640341	24617.095374
HLA B*0801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.250930	2.610483	-1.640447	17820.925838
HLA B*5301	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.227325	2.586427	-1.640898	16878.155628
HLA B*4403	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.282841	2.641207	-1.641634	19179.662829
HLA A*6901	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.392663	2.750896	-1.641767	24698.065931
HLA A*1101	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.252688	2.610483	-1.642205	17893.186050
HLA B*1517	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.053175	1.410054	-1.643121	1130.250105
HLA B*0802	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.357552	2.713718	-1.643834	22779.922476
HLA B*4001	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.395948	2.750896	-1.645052	24885.566162
HLA A*0216	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.058010	1.412655	-1.645355	1142.904115
HLA B*5301	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.558405	2.912865	-1.645540	36174.706452
HLA A*0301	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.359855	2.713718	-1.646137	22901.015309
HLA B*4002	1:10-18	9	PETPARPVL	1.635476	0.153516	-3.436103	1.788992	-1.647111	2729.625205
HLA A*0203	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.398149	2.750896	-1.647253	25012.033006
HLA B*1517	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.852216	2.204297	-1.647919	7115.666899
HLA A*6801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.398859	2.750896	-1.647963	25052.930729
HLA B*3501	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.661686	2.013049	-1.648638	4588.666268
HLA A*0250	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-2.578405	0.929716	-1.648689	378.795424
HLA B*0702	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.363142	2.713718	-1.649424	23074.997709
HLA A*6801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-2.431534	0.781170	-1.650364	270.105680
HLA A*0301	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.261623	2.610483	-1.651140	18265.130064
HLA A*0301	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.365194	0.712255	-1.652939	231.842824
HLA B*5401	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.566161	2.912865	-1.653295	36826.518677
HLA A*8001	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.295479	2.639184	-1.656295	19745.987057
HLA B*0801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.407505	2.750896	-1.656609	25556.692198
HLA B*5801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.015862	2.358631	-1.657231	10371.986407
HLA B*4402	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.444472	1.786784	-1.657688	2782.735224
HLA B*0802	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.409476	2.750896	-1.658580	25672.955044
HLA A*0101	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.372382	2.713718	-1.658664	23571.227043
HLA B*1502	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-3.979069	2.320077	-1.658992	9529.475631

HLA A*2403	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-3.956570	2.297367	-1.659204	9048.369672
HLA A*3001	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-2.952433	1.293038	-1.659395	896.258605
HLA B*4601	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.373200	2.713718	-1.659482	23615.645010
HLA B*1509	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.642139	1.982154	-1.659984	4386.708312
HLA B*1517	1:115-123	9	YGRTELKVL	1.725445	0.240391	-3.626280	1.965836	-1.660444	4229.409474
HLA B*0702	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.334366	1.673173	-1.661193	2159.561718
HLA B*5101	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.478863	2.817549	-1.661314	30120.571020
HLA B*0802	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.300509	2.639184	-1.661326	19976.026036
HLA A*0206	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-3.995948	2.334336	-1.661612	9907.126402
HLA A*0212	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.412756	2.750896	-1.661860	25867.576455
HLA A*3001	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.249098	2.586427	-1.662670	17745.885073
HLA A*0206	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-3.987574	2.324609	-1.662965	9717.938348
HLA A*0202	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.274030	2.610483	-1.663547	18794.483684
HLA A*3101	1:260-268	9	HGLLRAGER	1.105522	0.436138	-3.205393	1.541660	-1.663733	1604.696815
HLA A*0216	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.775726	2.111966	-1.663760	5966.584229
HLA A*6901	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.378282	2.713718	-1.664564	23893.608747
HLA A*3201	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-3.762719	2.097879	-1.664840	5790.539478
HLA B*1502	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.304212	2.639184	-1.665028	20147.069461
HLA A*0216	1:228-236	9	AICGLSGGV	0.815527	0.247463	-2.728405	1.062990	-1.665415	535.063399
HLA A*2602	1:239-247	9	AVAAALVQR	1.496975	0.797447	-3.960499	2.294422	-1.666076	9130.586482
HLA B*5301	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.417469	2.750896	-1.666573	26149.826292
HLA A*2301	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.778597	2.111966	-1.666631	6006.159297
HLA A*6801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.277301	2.610483	-1.666818	18936.551030
HLA B*2705	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-2.951033	1.284024	-1.667009	893.373457
HLA A*3001	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-3.973623	2.306412	-1.667211	9410.720989
HLA B*4403	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.253799	2.586427	-1.667372	17939.031153
HLA A*0202	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.581639	2.912865	-1.668774	38162.698197
HLA B*2705	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.456172	1.787266	-1.668906	2858.724612
HLA A*6801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-3.445064	1.775111	-1.669953	2786.531492
HLA A*0211	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-2.575740	0.905240	-1.670500	376.478698
HLA A*2403	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.310295	2.639184	-1.671111	20431.238827
HLA B*4801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.384870	2.713718	-1.671152	24258.821778
HLA A*0250	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.488813	2.817549	-1.671265	30818.625814
HLA A*0211	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.224518	1.553110	-1.671408	1676.941059
HLA B*4002	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.635736	2.963921	-1.671815	43225.095851
HLA A*3201	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.422985	2.750896	-1.672090	26484.110978
HLA A*0206	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-2.888349	1.215498	-1.672851	773.301380
HLA A*6801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-3.771074	2.097879	-1.673195	5903.013759
HLA B*2705	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.284016	2.610483	-1.673533	19231.612983
HLA B*4501	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-2.865545	1.191820	-1.673725	733.744204
HLA A*6901	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-3.393060	1.718496	-1.674564	2472.068237
HLA B*5801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.316862	2.641207	-1.675655	20742.519689
HLA B*5101	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.426554	2.750896	-1.675659	26702.644062
HLA B*3501	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.027732	2.352019	-1.675713	10659.369995
HLA A*0203	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-3.840680	2.164911	-1.675768	6929.144819
HLA B*0803	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.426909	2.750896	-1.676013	26724.466184
HLA A*6901	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-3.927864	2.251319	-1.676546	8469.627841
HLA A*3101	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.391171	2.713718	-1.677453	24613.366735
HLA A*0206	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-2.607806	0.929716	-1.678090	405.327602
HLA A*2301	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.000571	2.320077	-1.680494	10013.167718
HLA A*0203	1:206-214	9	WTPANIANA	1.064045	-0.280364	-2.464427	0.783681	-1.680746	291.357705
HLA A*0203	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.062530	1.381752	-1.680778	1154.862303
HLA A*6801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-2.962151	1.281231	-1.680920	916.538702
HLA B*4501	1:18-26	9	LVVDFGAQY	1.578161	1.385760	-4.645571	2.963921	-1.681650	44215.130301
HLA A*0250	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.595043	2.912865	-1.682178	39358.893879
HLA A*2402	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.089852	2.407496	-1.682355	12298.493633
HLA B*0801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.396267	2.713718	-1.682549	24903.882329
HLA A*2501	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.323788	2.641207	-1.682581	21075.980729
HLA B*5301	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.321812	2.639184	-1.682628	20980.308791
HLA A*3101	1:69-77	9	SVYADGAPK	0.472549	0.433678	-2.588888	0.906227	-1.682661	388.050392
HLA B*5701	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.396749	2.713718	-1.683031	24931.516734
HLA A*2403	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.114540	2.431446	-1.683095	13017.881354
HLA B*1503	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.696637	2.013049	-1.683589	4973.217025
HLA B*1503	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.711505	2.027725	-1.683780	5146.416760
HLA A*6901	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.042853	2.358631	-1.684222	11037.045238

HLA B*4402	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.279676	2.595201	-1.684475	19040.406317
HLA A*0202	1:276-284	9	VAATGANLV	0.993882	0.146839	-2.825204	1.140721	-1.684483	668.657971
HLA B*1509	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.435501	2.750896	-1.684605	27258.446787
HLA B*3901	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-2.777058	1.091915	-1.685144	598.492042
HLA B*1503	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.651715	1.966426	-1.685289	4484.512702
HLA A*0250	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-2.587474	0.902116	-1.685358	386.788663
HLA A*3201	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.668016	1.982154	-1.685862	4656.032310
HLA A*0201	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.399643	2.713718	-1.685925	25098.239866
HLA A*8001	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.272557	2.586427	-1.686130	18730.840786
HLA B*4001	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.272602	2.586427	-1.686175	18732.766188
HLA B*0801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-2.655520	0.969193	-1.686326	452.396796
HLA A*6801	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.504292	2.817549	-1.686743	31936.820478
HLA A*0211	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-2.331728	0.644580	-1.687147	214.648370
HLA A*0206	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.506585	2.817549	-1.689036	32105.894511
HLA B*3901	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.440123	2.750896	-1.689227	27550.059598
HLA A*2501	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.740169	2.050505	-1.689664	5497.543441
HLA A*2403	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.009800	2.320077	-1.689723	10228.224872
HLA A*6802	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.440743	2.750896	-1.689847	27589.435000
HLA B*0702	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.440985	2.750896	-1.690089	27604.812630
HLA A*2902	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.330129	2.639184	-1.690945	21385.974902
HLA A*8001	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.049666	2.358631	-1.691036	11211.567324
HLA B*4001	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.405714	2.713718	-1.691996	25451.555790
HLA B*3501	1:394-402	9	EEIVARQPF	0.860370	0.918985	-3.471646	1.779355	-1.692291	2962.415892
HLA A*3101	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.287991	2.595201	-1.692790	19408.458322
HLA A*3101	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.332923	2.639184	-1.693739	21523.980528
HLA B*4501	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.606985	2.912865	-1.694120	40456.221370
HLA B*0802	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.305925	2.610483	-1.695442	20226.682545
HLA B*1503	1:112-120	9	TREYGRTEL	1.503201	0.420922	-3.621012	1.924123	-1.696889	4178.420932
HLA A*0250	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-2.983141	1.286148	-1.696993	961.924768
HLA A*0219	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.448322	2.750896	-1.697427	28075.160346
HLA B*1502	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.307980	2.610483	-1.697497	20322.655614
HLA B*1509	1:53-61	9	IRARQPVAL	1.567292	0.450462	-3.715753	2.017754	-1.697999	5197.001255
HLA A*2501	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.412516	2.713718	-1.698798	25853.306439
HLA A*3001	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.095660	2.396811	-1.698849	12464.069086
HLA A*2301	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.516413	2.817549	-1.698864	32840.720012
HLA A*3201	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.783333	2.084113	-1.699220	6072.023005
HLA B*4402	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.287126	2.586427	-1.700699	19369.857638
HLA B*4601	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.342079	2.641207	-1.700872	21982.573481
HLA B*5301	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.342706	2.641207	-1.701499	22014.348941
HLA A*0202	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.254821	1.553110	-1.701712	1798.131528
HLA A*0212	1:422-430	9	TLRHADSIV	1.051790	0.095468	-2.849211	1.147258	-1.701953	706.660903
HLA A*0206	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-2.988413	1.286148	-1.702265	973.673503
HLA A*0211	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.786515	2.084113	-1.702401	6116.663809
HLA A*3301	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-3.803187	2.097879	-1.705307	6356.039047
HLA A*6901	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.316441	2.610483	-1.705958	20722.442975
HLA B*3501	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-2.689065	0.982586	-1.706479	488.726027
HLA B*3801	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.457687	2.750896	-1.706792	28687.142621
HLA B*2705	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.348979	2.641207	-1.707772	22334.640734
HLA A*0212	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.294443	2.586427	-1.708015	19698.934000
HLA A*2402	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.525778	2.817549	-1.708229	33556.581944
HLA B*1801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.347635	2.639184	-1.708451	22265.633983
HLA A*2403	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-3.434355	1.725080	-1.709275	2718.660661
HLA A*2402	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.760562	2.050505	-1.710057	5761.853339
HLA A*6901	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.351495	2.641207	-1.710289	22464.423064
HLA A*2603	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.007864	2.297367	-1.710498	10182.731491
HLA A*0212	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-2.493476	0.781791	-1.711685	311.512544
HLA A*0202	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.006478	2.294422	-1.712056	10150.281711
HLA B*4403	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.499370	1.786784	-1.712586	3157.693346
HLA B*3801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.323097	2.610483	-1.712614	21042.485869
HLA B*0803	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.427160	2.713718	-1.713442	26739.940337
HLA B*4801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-3.536356	1.822872	-1.713483	3438.393244
HLA B*3801	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.300580	2.586427	-1.714152	19979.268342
HLA A*6901	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.354465	2.639184	-1.715281	22618.563445
HLA A*0219	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.302062	2.586427	-1.715635	20047.586914
HLA A*0202	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.142314	1.426359	-1.715955	1387.758887

HLA B*3801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.355734	2.639184	-1.716550	22684.736573
HLA B*1517	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.358276	2.641207	-1.717069	22817.911067
HLA A*0216	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.194933	1.477798	-1.717135	1566.509681
HLA A*3001	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-3.445966	1.728396	-1.717571	2792.326242
HLA A*3201	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.702544	1.984120	-1.718424	5041.317117
HLA B*3901	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.684871	1.966426	-1.718445	4840.287862
HLA A*2902	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.015876	2.297367	-1.718509	10372.323080
HLA B*4601	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.329180	2.610483	-1.718697	21339.284859
HLA B*1503	1:35-43	9	REARVFSEV	0.807139	0.210046	-2.736332	1.017185	-1.719148	544.919572
HLA B*2705	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-3.494478	1.775111	-1.719367	3122.326566
HLA A*0301	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.358586	2.639184	-1.719402	22834.211280
HLA B*3801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.151361	2.431446	-1.719916	14169.725530
HLA A*0101	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.307417	2.586427	-1.720989	20296.286341
HLA B*1502	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.635696	1.914570	-1.721127	4322.116508
HLA A*0206	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.010804	1.289353	-1.721451	1025.189014
HLA B*3801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.435424	2.713718	-1.721706	27253.580871
HLA A*0201	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.116589	2.394415	-1.722174	13079.437289
HLA B*1503	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.002365	1.280105	-1.722260	1005.459527
HLA A*2403	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.436486	2.713718	-1.722768	27320.304777
HLA A*6802	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.436556	2.713718	-1.722838	27324.739131
HLA B*1502	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.081906	2.358631	-1.723275	12075.523358
HLA A*3101	1:509-517	9	RVVLDITSK	0.817327	0.463904	-3.005057	1.281231	-1.723826	1011.712471
HLA B*1503	1:88-96	9	PVLGICYGF	1.280744	0.979414	-3.984205	2.260158	-1.724047	9642.840383
HLA B*3801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.319474	2.595201	-1.724273	20867.678559
HLA B*0802	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.320710	2.595201	-1.725509	20927.144228
HLA A*0212	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.721415	1.995235	-1.726180	5265.202520
HLA A*3002	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.365961	2.639184	-1.726777	23225.284819
HLA A*0212	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.441389	2.713718	-1.727671	27630.510888
HLA A*3002	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.675459	1.947300	-1.728159	4736.517583
HLA A*3201	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.012651	1.283502	-1.729148	1029.557576
HLA A*0203	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-2.507671	0.778023	-1.729648	321.863054
HLA B*4801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.757494	2.027725	-1.729769	5721.287503
HLA A*0203	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.316361	2.586427	-1.729934	20718.631717
HLA A*0203	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.443891	2.713718	-1.730173	27790.164442
HLA B*4801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-3.748552	2.017754	-1.730798	5604.690463
HLA A*3301	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.644211	2.912865	-1.731345	44076.850788
HLA B*4001	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.371113	2.639184	-1.731930	23502.467954
HLA B*1501	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.936445	2.204297	-1.732148	8638.625498
HLA A*0206	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.519496	1.787266	-1.732229	3307.467919
HLA A*0203	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.210078	1.477798	-1.732280	1622.100894
HLA A*0206	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.371922	2.639184	-1.732738	23546.246815
HLA A*0211	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.044101	1.311116	-1.732985	1106.880777
HLA A*0219	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.129178	2.394415	-1.734763	13464.108433
HLA A*0202	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.072563	1.336347	-1.736215	1181.850400
HLA A*0250	1:263-271	9	LRAGERAQV	0.865849	0.254971	-2.857552	1.120820	-1.736731	720.363560
HLA B*1501	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.647430	1.909820	-1.737610	4440.478768
HLA B*5401	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.555200	2.817549	-1.737652	35908.752537
HLA A*0219	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.451574	2.713718	-1.737856	28286.156024
HLA A*2603	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-2.897620	1.159455	-1.738165	789.986834
HLA B*4801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.379792	2.641207	-1.738586	23976.868797
HLA A*2603	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.721096	1.982154	-1.738941	5261.330099
HLA B*4001	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.335133	2.595201	-1.739932	21633.832152
HLA B*1517	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.136856	2.396811	-1.740045	13704.264039
HLA A*0211	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.491128	2.750896	-1.740232	30983.288616
HLA B*1509	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.382081	2.641207	-1.740874	24103.541924
HLA A*0202	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-2.174796	0.433361	-1.741435	149.553332
HLA A*3101	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-3.166735	1.424271	-1.742464	1468.028761
HLA A*0206	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.899196	2.156591	-1.742605	7928.589111
HLA B*4801	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.353114	2.610483	-1.742631	22548.313510
HLA A*2402	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.493674	2.750896	-1.742779	31165.518335
HLA B*1503	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.515187	1.772257	-1.742930	3274.814351
HLA A*2601	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.382262	2.639184	-1.743078	24113.584622
HLA B*0702	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.382595	2.639184	-1.743412	24132.115897
HLA B*1503	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-3.117992	1.374504	-1.743488	1312.176176
HLA A*6802	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-2.908996	1.165167	-1.743829	810.953700

HLA A*0216	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.829219	2.084113	-1.745106	6748.680226
HLA B*5801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.758908	2.013049	-1.745860	5739.950699
HLA A*0201	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.385788	2.639184	-1.746605	24310.189964
HLA B*1503	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.829322	2.082473	-1.746850	6750.286840
HLA A*0206	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.774903	2.027725	-1.747178	5955.297422
HLA B*3901	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.462123	2.713718	-1.748405	28981.650860
HLA B*1509	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.387896	2.639184	-1.748712	24428.446004
HLA B*5801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.800001	2.050505	-1.749496	6309.582959
HLA A*0202	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.693877	0.943730	-1.750148	494.170951
HLA A*0202	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.568461	2.817549	-1.750912	37022.079702
HLA B*4403	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.568839	2.817549	-1.751290	37054.339690
HLA A*0216	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.338390	2.586427	-1.751963	21796.654593
HLA A*1101	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.393276	2.641207	-1.752069	24732.963764
HLA B*4402	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.391366	2.639184	-1.752182	24624.421130
HLA B*4801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.747626	1.995235	-1.752391	5592.756809
HLA A*0201	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.363360	2.610483	-1.752877	23086.610116
HLA A*0219	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.392602	2.639184	-1.753418	24694.592217
HLA A*0206	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.014025	2.260158	-1.753866	10328.200058
HLA A*1101	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.393126	2.639184	-1.753942	24724.401881
HLA B*5101	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.340923	2.586427	-1.754495	21924.141022
HLA B*0801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.396923	2.641207	-1.755716	24941.499611
HLA A*0206	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-2.844155	1.087303	-1.756852	698.481604
HLA B*1517	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.723525	1.966426	-1.757099	5290.843530
HLA A*6801	1:32-40	9	RRVREARVF	1.516847	1.396018	-4.671223	2.912865	-1.758357	46905.372196
HLA A*6901	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.353610	2.595201	-1.758408	22574.066804
HLA B*0802	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.153617	2.394415	-1.759202	14243.507335
HLA B*5101	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.472940	2.713718	-1.759222	29712.565299
HLA A*0211	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.084307	2.324609	-1.759698	12142.472708
HLA A*2501	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.370481	2.610483	-1.759998	23468.290623
HLA A*0206	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-2.533069	0.772641	-1.760428	341.247172
HLA B*0802	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.402853	2.641207	-1.761646	25284.400572
HLA B*4801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.400851	2.639184	-1.761667	25168.127238
HLA A*2403	1:25-33	9	QYAQLIARR	0.855428	0.838712	-3.455989	1.694140	-1.761849	2857.518566
HLA A*0201	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.403186	2.641207	-1.761980	25303.831619
HLA A*0216	1:422-430	9	TLRHADSIV	1.051790	0.095468	-2.909489	1.147258	-1.762231	811.875529
HLA B*5401	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.919087	2.156591	-1.762496	8300.163582
HLA A*6901	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.097013	2.334336	-1.762677	12502.968900
HLA B*5101	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.357996	2.595201	-1.762795	22803.226153
HLA B*3801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.115795	2.352019	-1.763776	13055.542835
HLA A*2403	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-3.952355	2.188431	-1.763924	8960.976932
HLA B*0802	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.350555	2.586427	-1.764128	22415.863608
HLA B*3901	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.404011	2.639184	-1.764827	25351.925981
HLA B*4402	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.173052	2.407496	-1.765555	14895.390166
HLA A*0216	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.160031	2.394415	-1.765616	14455.430754
HLA A*6802	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.376466	2.610483	-1.765982	23793.898028
HLA B*1517	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.226186	1.459325	-1.766861	1683.394612
HLA B*3501	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.850430	2.082473	-1.767957	7086.470784
HLA B*0801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.164796	2.396811	-1.767985	14614.898152
HLA B*4001	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.378794	2.610483	-1.768311	23921.804437
HLA B*0801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.925068	2.156591	-1.768478	8415.277476
HLA A*0201	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.355184	2.586427	-1.768757	22656.037815
HLA A*0206	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.127712	2.358631	-1.769081	13418.733320
HLA B*5101	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.410338	2.641207	-1.769131	25723.977515
HLA A*3301	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.587884	2.817549	-1.770335	38715.422579
HLA B*2705	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.410042	2.639184	-1.770859	25706.448843
HLA A*0216	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.484986	2.713718	-1.771268	30548.223459
HLA A*6901	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-2.827544	1.055834	-1.771710	672.270592
HLA B*4001	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.413611	2.641207	-1.772404	25918.565064
HLA A*0212	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.056102	1.283502	-1.772600	1137.894543
HLA A*0203	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.383176	2.610483	-1.772693	24164.383813
HLA B*5701	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.414497	2.641207	-1.773290	25971.480652
HLA A*0301	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.359972	2.586427	-1.773545	22907.210744
HLA A*0216	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.412803	2.639184	-1.773619	25870.375421
HLA A*0203	1:54-62	9	RARQPVALV	0.737262	0.289291	-2.800206	1.026553	-1.773653	631.255981
HLA A*2403	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-3.214800	1.440990	-1.773811	1639.835668

HLA A*0212	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.546336	1.772257	-1.774080	3518.326643
HLA B*0801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.369626	2.595201	-1.774425	23422.122346
HLA A*3201	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.369730	2.595201	-1.774528	23427.698297
HLA B*4402	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.385286	2.610483	-1.774802	24282.061947
HLA B*0801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-3.979323	2.204297	-1.775026	9535.045026
HLA B*0803	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.416238	2.641207	-1.775031	26075.802208
HLA A*0212	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.414929	2.639184	-1.775745	25997.346044
HLA B*5101	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.386235	2.610483	-1.775752	24335.190743
HLA A*0219	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.128886	2.352019	-1.776868	13455.079385
HLA A*0219	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.416391	1.639403	-1.776987	2608.499997
HLA A*3001	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.208802	2.431446	-1.777356	16173.411905
HLA A*2403	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.372878	2.595201	-1.777676	23598.148645
HLA A*2301	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.680562	1.901679	-1.778883	4792.501255
HLA B*1503	1:30-38	9	IARRVREAR	0.966536	0.718626	-3.464222	1.685162	-1.779060	2912.203076
HLA A*2602	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-3.451426	1.672339	-1.779087	2827.654613
HLA A*0202	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-3.968496	2.188431	-1.780065	9300.286369
HLA B*3901	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.390915	2.610483	-1.780432	24598.857054
HLA B*0803	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.366953	2.586427	-1.780525	23278.368093
HLA A*0216	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.421790	2.641207	-1.780583	26411.283757
HLA A*1101	1:109-117	9	HTGTREYGR	1.076414	0.591236	-3.448927	1.667650	-1.781277	2811.425042
HLA A*3001	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.691177	1.909820	-1.781357	4911.082260
HLA A*0202	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.041528	2.260158	-1.781370	11003.420578
HLA B*4801	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.368047	2.586427	-1.781620	23337.127088
HLA B*4001	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-3.865904	2.084113	-1.781791	7343.510314
HLA A*3101	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.368419	2.586427	-1.781991	23357.083316
HLA B*2705	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.368423	2.586427	-1.781996	23357.336036
HLA A*2301	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.533063	2.750896	-1.782168	34124.277924
HLA A*2301	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.423418	2.641207	-1.782211	26510.486907
HLA B*4001	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.214243	2.431446	-1.782797	16377.328284
HLA A*0219	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.424689	2.641207	-1.783482	26588.190129
HLA A*6802	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.422995	2.639184	-1.783811	26484.684089
HLA A*1101	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.498000	2.713718	-1.784282	31477.465472
HLA B*1509	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.379748	2.595201	-1.784546	23974.404392
HLA A*0202	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.535707	2.750896	-1.784811	34332.595836
HLA A*2403	1:161-169	9	APVAAFEAF	1.105718	1.050873	-3.941520	2.156591	-1.784929	8740.163048
HLA B*1503	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.280713	1.495512	-1.785201	1908.590601
HLA A*0250	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.536402	2.750896	-1.785506	34387.617597
HLA A*2902	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.137824	2.352019	-1.785805	13734.843188
HLA B*4801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.217269	2.431446	-1.785823	16491.842982
HLA A*1101	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-3.458348	1.672339	-1.786009	2873.081487
HLA B*2705	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.381268	2.595201	-1.786066	24058.466592
HLA B*1517	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.037867	2.251319	-1.786548	10911.066821
HLA A*0211	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.746555	1.958921	-1.787633	5578.976988
HLA A*0203	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.427081	2.639184	-1.787897	26735.022346
HLA B*1501	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.108211	2.320077	-1.788134	12829.531471
HLA B*1501	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.735700	1.947300	-1.788400	5441.265901
HLA A*2603	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.428857	1.639403	-1.789454	2684.461675
HLA B*0702	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.430727	2.641207	-1.789520	26960.438538
HLA A*3201	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.148312	2.358631	-1.789681	14070.573737
HLA A*0101	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.184804	2.394415	-1.790389	15303.966540
HLA A*0212	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.432315	2.641207	-1.791109	27059.215663
HLA B*5701	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.149745	2.358631	-1.791114	14117.083786
HLA A*2403	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.903416	2.111966	-1.791450	8006.000018
HLA A*0206	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-2.605076	0.813260	-1.791816	402.787587
HLA B*5101	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.431173	2.639184	-1.791990	26988.164853
HLA B*3501	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-1.723451	-0.069030	-1.792481	52.899385
HLA B*1517	1:77-85	9	KLDPALLDL	1.284905	0.332102	-3.409502	1.617007	-1.792496	2567.450922
HLA B*4801	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.388042	2.595201	-1.792840	24436.641000
HLA A*0201	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.388072	2.595201	-1.792871	24438.359654
HLA B*0801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-3.810653	2.017754	-1.792900	6466.260846
HLA A*3301	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.506759	2.713718	-1.793041	32118.750095
HLA A*2501	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.388923	2.595201	-1.793721	24486.266140
HLA A*0211	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.128097	2.334336	-1.793761	13430.643996
HLA A*6802	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.581842	1.787266	-1.794575	3818.049675
HLA B*7301	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.612293	2.817549	-1.794744	40953.667847

HLA A*2602	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.084841	1.289353	-1.795488	1215.740585
HLA A*1101	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.382351	2.586427	-1.795924	24118.542301
HLA A*0301	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.155365	2.358631	-1.796734	14300.952377
HLA B*3901	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.384000	2.586427	-1.797573	24210.312455
HLA B*0702	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.384104	2.586427	-1.797677	24216.076046
HLA B*0803	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.437329	2.639184	-1.798145	27373.416471
HLA A*0203	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.439836	2.641207	-1.798629	27531.882379
HLA A*0219	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.393885	2.595201	-1.798683	24767.642925
HLA A*6802	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.440155	2.641207	-1.798949	27552.146275
HLA A*0203	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.003631	2.204297	-1.799334	10083.946201
HLA B*4002	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-2.727320	0.927581	-1.799739	533.727748
HLA B*5401	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.550786	2.750896	-1.799890	35545.582515
HLA A*2603	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.658064	1.858036	-1.800028	4550.546608
HLA B*3801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.197205	2.396811	-1.800393	15747.245178
HLA A*0202	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-3.828594	2.027725	-1.800869	6738.975653
HLA A*0101	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-2.892446	1.091476	-1.800970	780.631887
HLA A*0206	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-2.611312	0.809432	-1.801879	408.612465
HLA A*6801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.711843	1.909820	-1.802023	5150.427505
HLA A*0202	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.441748	2.639184	-1.802565	27653.390490
HLA A*2601	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.664323	1.861603	-1.802719	4616.603696
HLA A*0211	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.442188	2.639184	-1.803004	27681.380177
HLA A*3301	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.414400	2.610483	-1.803917	25965.720674
HLA A*3101	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-3.525050	1.720897	-1.804152	3350.038692
HLA B*4402	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.201946	2.396811	-1.805135	15920.102152
HLA A*0212	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.840650	1.034513	-1.806136	692.866463
HLA B*1503	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.789442	1.982154	-1.807288	6158.033814
HLA B*5701	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.141747	2.334336	-1.807411	13859.493060
HLA B*1503	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-2.729087	0.921448	-1.807639	535.903502
HLA A*3002	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.919947	2.111966	-1.807981	8316.614349
HLA A*3101	1:265-273	9	AGERAQVQR	1.125671	0.585693	-3.519453	1.711364	-1.808090	3307.145860
HLA B*4002	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.803807	1.995235	-1.808572	6365.123296
HLA B*4501	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.626211	2.817549	-1.808662	42287.416455
HLA A*0250	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.121920	1.313175	-1.808745	1324.099091
HLA B*3901	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.768146	1.958921	-1.809225	5863.356993
HLA A*3201	1:77-85	9	KLDPALLDL	1.284905	0.332102	-3.426390	1.617007	-1.809384	2669.256130
HLA A*0216	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.420401	2.610483	-1.809918	26326.975275
HLA B*3901	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.168668	2.358631	-1.810037	14745.779808
HLA A*0219	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.164305	1.353717	-1.810588	1459.839790
HLA A*2501	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.449927	2.639184	-1.810743	28179.088667
HLA A*1101	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-3.474794	1.663852	-1.810943	2983.969219
HLA A*0203	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.922912	2.111966	-1.810946	8373.588472
HLA B*3901	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.452239	2.641207	-1.811032	28329.495258
HLA A*2603	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.673044	1.861603	-1.811441	4710.249187
HLA B*1501	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.243602	2.431446	-1.812156	17522.748156
HLA B*0801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.244086	2.431446	-1.812640	17542.287043
HLA A*0212	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.426016	2.610483	-1.815533	26669.583585
HLA B*5401	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-3.076528	1.260962	-1.815566	1192.692359
HLA A*0201	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.929105	2.111966	-1.817139	8493.855253
HLA B*3901	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.799531	1.982154	-1.817376	6302.759822
HLA A*0250	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.428396	2.610483	-1.817913	26816.139922
HLA A*0201	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.868479	2.050505	-1.817974	7387.181077
HLA A*0203	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.413289	2.595201	-1.818088	25899.362512
HLA A*0203	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.099497	1.280105	-1.819392	1257.468175
HLA B*4002	1:458-466	9	GVQGDGRTY	1.559485	1.258064	-4.637399	2.817549	-1.819851	43390.974149
HLA B*1501	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.217030	2.396811	-1.820218	16482.745150
HLA B*1517	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.080680	2.260158	-1.820521	12041.470642
HLA B*0801	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.406967	2.586427	-1.820539	25525.050520
HLA B*1509	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.407056	2.586427	-1.820629	25530.298392
HLA B*1503	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-2.593277	0.772641	-1.820636	391.991784
HLA A*0206	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-2.353592	0.532233	-1.821358	225.731362
HLA A*0250	1:54-62	9	RARQPVALV	0.737262	0.289291	-2.847919	1.026553	-1.821366	704.561402
HLA A*6901	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.871961	2.050505	-1.821456	7446.645533
HLA A*3201	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.609584	1.787266	-1.822318	4069.905200
HLA A*0206	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.254236	2.431446	-1.822790	17957.091197
HLA A*3101	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.147536	2.324609	-1.822928	14045.476466

HLA A*2403	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.836023	2.013049	-1.822974	6855.244657
HLA B*3801	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.464355	2.641207	-1.823148	29130.982411
HLA B*1509	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.434063	2.610483	-1.823580	27168.347335
HLA A*2301	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.538077	2.713718	-1.824359	34520.515414
HLA A*3002	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.085106	2.260158	-1.824948	12164.827668
HLA A*0203	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-2.432577	0.607629	-1.824948	270.755251
HLA A*6801	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.538848	2.713718	-1.825130	34581.824501
HLA A*0211	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.413360	1.587869	-1.825491	2590.359283
HLA A*6802	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.421146	2.595201	-1.825944	26372.163059
HLA B*0803	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.223237	2.396811	-1.826426	16720.023487
HLA B*1509	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-3.982744	2.155890	-1.826854	9610.447229
HLA B*0803	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.423063	2.595201	-1.827861	26488.839512
HLA A*0211	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-2.127365	0.299099	-1.828266	134.080213
HLA A*6802	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.323995	1.495512	-1.828483	2108.603842
HLA A*3301	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.579896	2.750896	-1.829000	38009.814923
HLA A*0219	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.439570	2.610483	-1.829087	27515.056802
HLA A*3001	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.812646	1.982154	-1.830491	6495.993522
HLA B*4801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.155440	2.324609	-1.830831	14303.428321
HLA A*0211	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.117428	1.286148	-1.831280	1310.473587
HLA B*4403	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.582779	2.750896	-1.831883	38262.960818
HLA A*0211	1:451-459	9	LADVRSVGV	1.034616	0.104608	-2.972301	1.139224	-1.833076	938.211136
HLA B*0801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.167479	2.334336	-1.833143	14705.469850
HLA B*4601	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.186749	2.352019	-1.834731	15372.672713
HLA B*1503	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-2.928173	1.091915	-1.836258	847.564106
HLA A*0212	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.431491	2.595201	-1.836289	27007.882454
HLA A*2403	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.001497	2.164911	-1.836586	10034.533510
HLA A*0203	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.831841	1.995235	-1.836606	6789.548197
HLA B*3901	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.431895	2.595201	-1.836693	27033.025010
HLA B*5401	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.550412	2.713718	-1.836694	35515.020333
HLA B*1503	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.948704	2.111966	-1.836739	8885.958070
HLA B*4402	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.171304	2.334336	-1.836968	14835.557347
HLA B*1503	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.781663	0.943730	-1.837934	604.871846
HLA A*6802	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-2.771908	0.933159	-1.838749	591.436753
HLA B*4801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.748928	1.909820	-1.839108	5609.543884
HLA A*1101	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-3.843696	2.004292	-1.839405	6977.444279
HLA B*1509	1:70-78	9	VYADGAPKL	1.519604	0.588887	-3.949000	2.108491	-1.840509	8892.017213
HLA A*0250	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.891123	2.050505	-1.840618	7782.570817
HLA A*0211	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.554575	2.713718	-1.840857	35857.115909
HLA B*5801	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.253525	1.412655	-1.840870	1792.769852
HLA A*2603	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.177599	1.336347	-1.841251	1505.215157
HLA A*2902	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.176947	2.334336	-1.842611	15029.596791
HLA A*0206	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.557200	2.713718	-1.843482	36074.450944
HLA A*0212	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.894060	2.050505	-1.843555	7835.377722
HLA A*2602	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-3.999528	2.155890	-1.843639	9989.145044
HLA A*0211	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.630927	1.787266	-1.843661	4274.910386
HLA B*1502	1:422-430	9	TLRHADSIV	1.051790	0.095468	-2.991369	1.147258	-1.844111	980.322575
HLA B*1509	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.095899	2.251319	-1.844581	12470.948765
HLA A*0206	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.139168	2.294422	-1.844745	13777.410891
HLA B*1503	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.895643	2.050505	-1.845138	7863.999738
HLA A*3201	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.277580	2.431446	-1.846135	18948.745868
HLA B*5701	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.243381	2.396811	-1.846570	17513.839586
HLA B*0702	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.052077	2.204297	-1.847780	11273.970673
HLA A*2603	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.458721	2.610483	-1.848238	28755.509432
HLA B*1801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.108859	2.260158	-1.848701	12848.701930
HLA A*3201	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-2.770644	0.921448	-1.849197	589.717867
HLA B*4001	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.845073	1.995235	-1.849838	6999.599237
HLA B*4403	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.563670	2.713718	-1.849952	36615.942002
HLA B*4601	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.244450	2.394415	-1.850035	17557.002996
HLA A*0203	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.174673	2.324609	-1.850064	14951.095934
HLA A*0203	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-2.623285	0.772641	-1.850644	420.034136
HLA B*0801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-3.934039	2.082473	-1.851566	8590.902185
HLA A*2403	1:516-524	9	SKPPATIEW	1.492290	0.425272	-3.769857	1.917562	-1.852295	5886.494767
HLA A*0212	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.017511	2.164911	-1.852600	10411.451429
HLA A*3101	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.057203	2.204297	-1.852907	11407.841462
HLA A*2603	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.159773	2.306412	-1.853361	14446.831062

HLA A*3101	1:479-487	9	DAMTADWTR	1.140857	0.484835	-3.479221	1.625692	-1.853529	3014.538040
HLA A*3001	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.213092	2.358631	-1.854461	16333.972005
HLA B*1801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.189912	2.334336	-1.855576	15485.020616
HLA A*3201	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.253651	2.396811	-1.856840	17932.918160
HLA A*3001	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.251731	2.394415	-1.857316	17853.831729
HLA A*0211	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.316740	1.459325	-1.857414	2073.670664
HLA A*0216	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.453437	2.595201	-1.858236	28407.765492
HLA A*3101	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.217241	2.358631	-1.858610	16490.772388
HLA B*1801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.254086	2.394415	-1.859671	17950.874938
HLA B*4002	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.611423	2.750896	-1.860528	40871.774558
HLA B*5301	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.574278	2.713718	-1.860560	37521.322406
HLA B*1503	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.111918	2.251319	-1.860600	12939.523503
HLA A*0101	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-3.972937	2.111966	-1.860971	9395.866725
HLA A*2402	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.574809	2.713718	-1.861091	37567.225341
HLA A*6802	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.534979	1.673173	-1.861806	3427.510127
HLA B*3901	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.635767	1.772257	-1.863510	4322.818031
HLA A*6901	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.005757	1.140721	-1.865036	1013.344815
HLA A*3101	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.259713	2.394415	-1.865298	18184.972047
HLA B*7301	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.616200	2.750896	-1.865304	41323.775853
HLA A*0203	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.780317	1.914570	-1.865747	6029.991077
HLA A*6901	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.810590	0.943730	-1.866861	646.532305
HLA A*0211	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.298486	2.431446	-1.867040	19883.195779
HLA B*1517	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.299586	2.431446	-1.868140	19933.600395
HLA A*0211	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.478938	2.610483	-1.868455	30125.785838
HLA A*6901	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.007914	1.139224	-1.868690	1018.389885
HLA B*1503	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-3.058903	1.190075	-1.868827	1145.256066
HLA A*0301	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.263582	2.394415	-1.869167	18347.725736
HLA A*3001	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.194014	2.324609	-1.869405	15631.979927
HLA A*3201	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.584357	2.713718	-1.870639	38402.316884
HLA B*1801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-2.679470	0.807656	-1.871814	478.046531
HLA B*0803	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.266376	2.394415	-1.871961	18466.125265
HLA B*5801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.303542	2.431446	-1.872096	20116.030273
HLA B*4002	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.511295	2.639184	-1.872112	32456.037154
HLA A*3001	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.280651	2.407496	-1.873155	19083.202032
HLA B*1502	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.038525	2.164911	-1.873614	10927.607090
HLA A*3201	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.515153	2.641207	-1.873947	32745.629690
HLA B*5801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.300632	1.426359	-1.874273	1998.166689
HLA A*0203	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.647232	1.772257	-1.874976	4438.461336
HLA B*4601	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.233934	2.358631	-1.875303	17136.972049
HLA B*1503	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.170514	2.294422	-1.876092	14808.614911
HLA A*3001	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.210479	2.334336	-1.876143	16236.005120
HLA A*3002	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.210498	2.334336	-1.876162	16236.707815
HLA A*2402	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-3.589797	1.713482	-1.876315	3888.632761
HLA B*3501	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.843297	1.966426	-1.876871	6971.030205
HLA A*0250	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.463674	2.586427	-1.877247	29085.315581
HLA A*0219	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-2.533459	0.656026	-1.877433	341.553764
HLA B*1509	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.274251	2.396811	-1.877440	18804.043666
HLA B*3501	1:479-487	9	DAMTADWTR	1.140857	0.484835	-3.504064	1.625692	-1.878373	3192.009851
HLA A*6802	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-2.514710	0.635184	-1.879526	327.122326
HLA A*0211	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.475008	2.595201	-1.879806	29854.355224
HLA A*2403	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.835154	1.954913	-1.880241	6841.536519
HLA A*2402	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.277209	2.396811	-1.880398	18932.556111
HLA A*0203	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-2.783430	0.902116	-1.881314	607.337620
HLA A*3001	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.710725	1.828772	-1.881952	5137.181664
HLA A*0250	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.597066	2.713718	-1.883348	39542.651875
HLA A*0201	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.208069	2.324609	-1.883460	16146.136064
HLA B*0702	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.741545	1.858036	-1.883510	5514.999381
HLA A*2402	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.315170	2.431446	-1.883724	20661.882231
HLA A*0202	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.597641	2.713718	-1.883923	39595.097358
HLA B*7301	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.281142	2.396811	-1.884331	19104.790978
HLA A*0250	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.315962	2.431446	-1.884516	20699.585941
HLA A*0203	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-2.921636	1.036964	-1.884673	834.903514
HLA B*1501	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.292984	2.407496	-1.885487	19632.865662
HLA B*1801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-2.767350	0.881518	-1.885832	585.261974
HLA A*0206	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.481363	2.595201	-1.886162	30294.448653

HLA A*6802	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.181776	1.295300	-1.886476	1519.763351
HLA A*2602	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.439618	1.553110	-1.886508	2751.806229
HLA A*6802	1:51-59	9	EEIRARQPV	0.859860	0.021658	-2.768384	0.881518	-1.886866	586.656762
HLA B*0801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.138510	2.251319	-1.887191	13756.557095
HLA A*3001	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.184748	2.297367	-1.887381	15301.979643
HLA A*0201	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.301238	1.412655	-1.888583	2000.957580
HLA A*0202	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-2.179270	0.290570	-1.888700	151.101756
HLA A*0211	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.530108	2.641207	-1.888901	33892.828828
HLA B*3901	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.296708	2.407496	-1.889211	19801.934911
HLA A*8001	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.187323	2.297367	-1.889956	15392.978239
HLA A*2902	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.214614	2.324609	-1.890005	16391.332995
HLA A*3001	1:27-35	9	AQLIARRVR	1.168509	0.724756	-3.783366	1.893265	-1.890102	6072.482908
HLA B*4601	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.322153	2.431446	-1.890707	20996.772914
HLA A*0219	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.151183	2.260158	-1.891025	14163.900823
HLA B*4402	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.322987	2.431446	-1.891541	21037.136186
HLA A*3201	1:487-495	9	RVPYEVLER	0.866973	0.808043	-3.566777	1.675016	-1.891760	3687.879113
HLA B*3501	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-3.715250	1.822872	-1.892378	5190.988083
HLA B*1501	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.152757	2.260158	-1.892599	14215.332816
HLA A*0219	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.102782	1.210159	-1.892622	1267.014493
HLA A*2602	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-3.274327	1.381432	-1.892895	1880.731855
HLA B*4501	1:86-94	9	GVPVLGICY	1.484470	1.266426	-4.645778	2.750896	-1.894882	44236.184820
HLA B*2705	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.220056	2.324609	-1.895447	16597.996951
HLA A*0216	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.207630	1.311116	-1.896514	1612.982666
HLA A*2403	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.293733	2.396811	-1.896922	19666.776423
HLA B*4002	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.250944	2.352019	-1.898926	17821.504303
HLA A*2501	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.252504	2.352019	-1.900486	17885.637230
HLA A*0202	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.332164	2.431446	-1.900718	21486.402491
HLA A*6802	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.235210	2.334336	-1.900874	17187.387113
HLA A*0301	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-3.999030	2.097879	-1.901151	9977.695096
HLA A*3201	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.868314	1.966426	-1.901888	7384.384139
HLA A*0203	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.334017	2.431446	-1.902572	21578.311118
HLA B*3901	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.011548	2.108491	-1.903057	10269.476004
HLA B*5401	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-3.621980	1.718496	-1.903484	4187.744494
HLA B*3501	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.156573	2.251319	-1.905254	14340.774132
HLA A*1101	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-3.601563	1.695841	-1.905722	3995.426553
HLA A*0206	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.860678	1.954913	-1.905765	7255.685579
HLA A*2602	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.516281	2.610483	-1.905798	32830.772298
HLA B*1517	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.070802	2.164911	-1.905891	11770.700142
HLA B*5301	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.240614	2.334336	-1.906278	17402.581416
HLA B*0803	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.337990	2.431446	-1.906545	21776.617836
HLA B*1502	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.303366	2.396811	-1.906555	20107.870017
HLA A*0206	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.548333	2.641207	-1.907126	35345.389626
HLA A*0202	1:291-299	9	TFLEALSGV	0.900311	0.134202	-2.942862	1.034513	-1.908348	876.721257
HLA B*5401	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.549799	2.641207	-1.908592	35464.909183
HLA B*5401	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.548182	2.639184	-1.908999	35333.154007
HLA A*2603	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.267682	2.358631	-1.909051	18521.753113
HLA B*5701	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.189572	1.280105	-1.909467	1547.289429
HLA A*0202	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.207411	2.297367	-1.910044	16121.696913
HLA B*0801	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.503749	1.593295	-1.910455	3189.696721
HLA B*0803	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.235783	2.324609	-1.911174	17210.089667
HLA B*1503	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.146548	1.235042	-1.911505	1401.353779
HLA A*3201	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.206598	2.294422	-1.912176	16091.548197
HLA A*2603	1:394-402	9	EEIVARQPF	0.860370	0.918985	-3.692286	1.779355	-1.912931	4923.638574
HLA A*6802	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.226346	1.313175	-1.913170	1684.014000
HLA B*3901	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.248341	2.334336	-1.914005	17714.998929
HLA B*4002	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.627969	2.713718	-1.914251	42458.883286
HLA A*0219	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.324413	1.410054	-1.914359	2110.635321
HLA A*2301	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.322498	2.407496	-1.915001	21013.477316
HLA A*2603	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.554841	2.639184	-1.915657	35879.042692
HLA A*0212	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.240816	2.324609	-1.916207	17410.679859
HLA A*0206	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-2.828597	0.911989	-1.916607	673.901903
HLA A*2602	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.122331	2.204297	-1.918035	13253.518886
HLA A*2601	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.746832	1.828772	-1.918059	5582.539559
HLA A*0211	1:54-62	9	RARQPVALV	0.737262	0.289291	-2.944699	1.026553	-1.918146	880.438112
HLA A*0250	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-2.351736	0.433361	-1.918375	224.768687

HLA A*6901	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.179128	2.260158	-1.918969	15105.240757
HLA A*3002	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.316775	2.396811	-1.919963	20738.368160
HLA A*0101	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.352616	2.431446	-1.921170	22522.467752
HLA B*5401	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.515252	1.593295	-1.921958	3275.310448
HLA A*6802	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.247230	2.324609	-1.922621	17669.726364
HLA A*0212	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.354242	2.431446	-1.922796	22606.941859
HLA B*0802	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.354900	2.431446	-1.923454	22641.212102
HLA B*3801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.282634	2.358631	-1.924004	19170.534135
HLA B*4601	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.320877	2.396811	-1.924066	20935.183933
HLA B*1502	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.184531	2.260158	-1.924373	15294.365592
HLA A*2402	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.128722	2.204297	-1.924425	13449.985015
HLA A*2602	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.278984	1.353717	-1.925266	1901.006316
HLA A*0203	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.010054	2.084113	-1.925941	10234.202643
HLA B*4001	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.323165	2.396811	-1.926354	21045.787416
HLA A*3001	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.091548	2.164911	-1.926637	12346.624748
HLA A*0202	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.568191	2.641207	-1.926984	36999.054050
HLA B*4501	1:170-178	9	DRRLAGVQY	1.516148	1.197570	-4.641335	2.713718	-1.927617	43785.951104
HLA B*7301	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.083602	2.155890	-1.927713	12122.781862
HLA A*2501	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.322254	2.394415	-1.927839	21001.657861
HLA A*8001	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.359331	2.431446	-1.927885	22873.404061
HLA B*5701	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.875400	1.947300	-1.928100	7505.857717
HLA A*0250	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.567606	2.639184	-1.928422	36949.247569
HLA B*4403	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.523701	2.595201	-1.928499	33396.486015
HLA A*1101	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-3.432499	1.503120	-1.929379	2707.066408
HLA A*2501	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.288179	2.358631	-1.929548	19416.859948
HLA B*2705	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.324692	2.394415	-1.930277	21119.923682
HLA A*0202	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.832029	1.901679	-1.930350	6792.487290
HLA A*0211	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-2.937763	1.007289	-1.930474	866.489200
HLA A*0201	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.362002	2.431446	-1.930556	23014.532975
HLA A*0211	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-2.951973	1.020890	-1.931083	895.308771
HLA B*4601	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.251750	2.320077	-1.931673	17854.604444
HLA A*3001	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.790062	1.858036	-1.932027	6166.835067
HLA A*3201	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-3.309419	1.377330	-1.932088	2039.007337
HLA B*4801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.329081	2.396811	-1.932270	21334.436797
HLA B*5401	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.542905	2.610483	-1.932422	34906.432312
HLA A*2603	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.982997	2.050505	-1.932492	9616.063947
HLA B*4501	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.225885	1.293038	-1.932847	1682.229322
HLA A*2602	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-2.714055	0.781170	-1.932885	517.671898
HLA A*3001	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.917959	1.984120	-1.933839	8278.638120
HLA B*0802	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.330815	2.396811	-1.934004	21419.784760
HLA A*0216	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.365872	2.431446	-1.934426	23220.510753
HLA B*1801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-3.648205	1.713482	-1.934724	4448.413272
HLA A*0301	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.366180	2.431446	-1.934734	23236.972857
HLA A*2403	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-3.985399	2.050505	-1.934893	9669.377514
HLA A*0250	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.522926	1.587869	-1.935057	3333.695191
HLA B*4601	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.342711	2.407496	-1.935214	22014.587133
HLA A*2301	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.530547	2.595201	-1.935346	33927.133833
HLA B*1501	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.019490	2.084113	-1.935376	10458.985087
HLA A*3001	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.892011	1.954913	-1.937098	7798.501976
HLA A*0250	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.578479	2.641207	-1.937272	37886.022730
HLA A*2402	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.532833	2.595201	-1.937632	34106.191080
HLA A*0219	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.369088	2.431446	-1.937642	23393.123474
HLA A*3002	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.289866	2.352019	-1.937847	19492.427534
HLA A*0211	1:155-163	9	VASSAGAPV	0.740279	0.203451	-2.881714	0.943730	-1.937984	761.577035
HLA B*2705	1:112-120	9	TREYGRTEL	1.503201	0.420922	-3.862323	1.924123	-1.938200	7283.214389
HLA B*4403	1:35-43	9	REARVFSEV	0.807139	0.210046	-2.955756	1.017185	-1.938571	903.140899
HLA B*4403	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.346489	2.407496	-1.938992	22206.929657
HLA B*4002	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-2.832079	0.892605	-1.939473	679.326599
HLA A*3101	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.336313	2.396811	-1.939502	21692.664393
HLA A*3101	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-3.604298	1.663852	-1.940446	4020.665581
HLA B*5801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.337328	2.396811	-1.940517	21743.421002
HLA B*1503	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.013520	1.072837	-1.940683	1031.620463
HLA B*7301	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.348624	2.407496	-1.941128	22316.403167
HLA A*3002	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.247563	2.306412	-1.941152	17683.305538
HLA A*3002	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.238548	2.297367	-1.941182	17320.023499

HLA A*6901	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.221431	1.280105	-1.941326	1665.062635
HLA A*1101	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.336367	2.394415	-1.941952	21695.363724
HLA A*6901	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.373545	2.431446	-1.942099	23634.432908
HLA B*5701	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.373639	2.431446	-1.942193	23639.547848
HLA A*0201	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-2.751891	0.809432	-1.942458	564.794809
HLA B*5801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.350079	2.407496	-1.942582	22391.259851
HLA A*3001	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.090127	1.147258	-1.942869	1230.629315
HLA B*5401	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.538944	2.595201	-1.943743	34589.495789
HLA A*2602	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.583046	2.639184	-1.943863	38286.565911
HLA A*3101	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.278283	2.334336	-1.943947	18979.421344
HLA A*0216	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.298038	1.353717	-1.944321	1986.268170
HLA B*7301	1:53-61	9	IRARQPVAL	1.567292	0.450462	-3.963055	2.017754	-1.945301	9184.487217
HLA A*0202	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.280346	2.334336	-1.946010	19069.785809
HLA B*3901	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.847737	1.901679	-1.946058	7042.672467
HLA A*0250	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.542706	2.595201	-1.947504	34890.384608
HLA A*0202	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.094826	1.147258	-1.947568	1244.016745
HLA B*4501	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.588892	2.641207	-1.947685	38805.379322
HLA A*3101	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.380182	2.431446	-1.948737	23998.410694
HLA B*1509	1:112-120	9	TREYGRTEL	1.503201	0.420922	-3.872962	1.924123	-1.948839	7463.826958
HLA A*6802	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.343312	2.394415	-1.948897	22045.096953
HLA B*2705	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.307583	2.358631	-1.948953	20304.083685
HLA B*4002	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.590715	2.641207	-1.949508	38968.629604
HLA B*0702	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.308737	2.358631	-1.950106	20358.088213
HLA A*2301	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.347489	2.396811	-1.950678	22258.167049
HLA B*3901	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.077172	1.126421	-1.950751	1194.461610
HLA B*4801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.285261	2.334336	-1.950925	19286.833785
HLA A*0203	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.245428	2.294422	-1.951006	17596.559770
HLA A*0250	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.933804	1.982154	-1.951649	8586.255859
HLA A*2601	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.212429	2.260158	-1.952271	16309.072080
HLA B*4403	1:51-59	9	EEIRARQPV	0.859860	0.021658	-2.833808	0.881518	-1.952290	682.036851
HLA A*2601	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.286696	2.334336	-1.952361	19350.690780
HLA A*2902	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.383857	2.431446	-1.952411	24202.324292
HLA A*8001	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.065117	2.111966	-1.953151	11617.603293
HLA B*0801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.289735	1.336347	-1.953388	1948.654313
HLA A*0211	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.267683	1.313175	-1.954507	1852.177213
HLA A*2601	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.937037	1.982154	-1.954882	8650.410499
HLA A*0250	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-2.999620	1.044058	-1.955563	999.126309
HLA B*1501	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.250131	2.294422	-1.955709	17788.176826
HLA B*1503	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.940862	1.984120	-1.956741	8726.933743
HLA A*0202	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-3.590539	1.632644	-1.957895	3895.286161
HLA A*0301	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.365423	2.407496	-1.957927	23196.529651
HLA B*4402	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.113854	2.155890	-1.957965	12997.333401
HLA B*1517	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.252453	2.294422	-1.958030	17883.508652
HLA A*2603	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.114310	2.155890	-1.958421	13010.981504
HLA A*2402	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.071446	2.111966	-1.959480	11788.160902
HLA A*2301	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.391192	2.431446	-1.959746	24614.565164
HLA B*0801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.367514	2.407496	-1.960018	23308.485639
HLA A*2601	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.391540	2.431446	-1.960094	24634.281042
HLA A*0202	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.907663	1.947300	-1.960364	8084.691558
HLA A*6802	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.254931	2.294422	-1.960509	17985.869411
HLA A*6901	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.355400	2.394415	-1.960985	22667.316753
HLA B*5401	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.482613	1.521566	-1.961047	3038.179471
HLA A*0101	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.368931	2.407496	-1.961434	23384.645878
HLA A*3301	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.556953	2.595201	-1.961752	36053.965091
HLA B*4002	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.370169	2.407496	-1.962673	23451.410903
HLA A*2601	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.260316	2.297367	-1.962950	18210.272953
HLA A*3201	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.516822	1.553110	-1.963712	3287.168197
HLA A*8001	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.315790	2.352019	-1.963771	20691.412835
HLA A*1101	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.062133	2.097879	-1.964254	11538.057437
HLA B*1801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.316509	2.352019	-1.964490	20725.694307
HLA B*7301	1:331-339	9	EFLVQGTLY	1.312322	1.328885	-4.605851	2.641207	-1.964644	40350.648206
HLA A*2501	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.298991	2.334336	-1.964655	19906.335900
HLA B*3901	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-3.960306	1.995235	-1.965071	9126.536953
HLA B*4403	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.604800	2.639184	-1.965617	40253.189329
HLA A*0202	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.601916	1.635727	-1.966189	3998.670091

HLA A*2601	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.324852	2.358631	-1.966221	21127.694550
HLA A*0206	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-2.611011	0.644580	-1.966430	408.329613
HLA A*8001	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.363684	2.396811	-1.966873	23103.852199
HLA B*4402	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.361476	2.394415	-1.967061	22986.660507
HLA B*0801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.262636	1.295300	-1.967336	1830.778667
HLA A*2902	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.364199	2.396811	-1.967388	23131.241073
HLA B*0702	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.264759	2.297367	-1.967393	18397.522028
HLA B*3501	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.399399	2.431446	-1.967953	25084.122853
HLA B*4501	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.724047	1.756081	-1.967965	5297.201626
HLA B*4403	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.578676	2.610483	-1.968193	37903.243214
HLA A*3101	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.376228	2.407496	-1.968732	23780.900622
HLA A*3301	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.555534	2.586427	-1.969107	35936.348392
HLA B*4002	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.366017	2.396811	-1.969206	23228.300524
HLA A*0301	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.366097	2.396811	-1.969286	23232.573443
HLA B*0801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.053703	2.084113	-1.969590	11316.255498
HLA B*7301	1:112-120	9	TREYGRTEL	1.503201	0.420922	-3.893886	1.924123	-1.969763	7832.241599
HLA A*1101	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.304426	2.334336	-1.970090	20156.990303
HLA A*6802	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.328811	2.358631	-1.970180	21321.167977
HLA B*5401	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.556631	2.586427	-1.970204	36027.253421
HLA B*4801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.054450	2.084113	-1.970337	11335.740114
HLA B*4002	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.403743	2.431446	-1.972297	25336.295575
HLA B*1501	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.954475	1.982154	-1.972320	9004.810852
HLA A*3201	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.645696	1.673173	-1.972523	4422.785508
HLA A*6901	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.830760	1.858036	-1.972724	6772.673080
HLA B*3801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.380309	2.407496	-1.972813	24005.422470
HLA B*1509	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.023582	2.050505	-1.973077	10558.016750
HLA B*0702	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.224538	2.251319	-1.973220	16770.209880
HLA A*6801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-3.201873	1.228391	-1.973482	1591.744881
HLA A*0101	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.325790	2.352019	-1.973771	21173.348901
HLA B*0802	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.381397	2.407496	-1.973901	24065.626107
HLA A*2601	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.381470	2.407496	-1.973974	24069.662409
HLA B*1502	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.876213	1.901679	-1.974534	7519.920501
HLA A*6801	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.614614	2.639184	-1.975431	41173.150032
HLA A*3002	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.059882	2.084113	-1.975769	11478.414138
HLA A*0250	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.959916	1.984120	-1.975796	9118.344622
HLA A*6901	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.372648	2.396811	-1.975837	23585.640951
HLA B*5301	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.058608	2.082473	-1.976136	11444.806887
HLA A*2301	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.282601	2.306412	-1.976190	19169.082244
HLA B*4801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.384092	2.407496	-1.976596	24215.421023
HLA B*1501	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.301343	2.324609	-1.976734	20014.427070
HLA A*2902	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.384282	2.407496	-1.976786	24226.034571
HLA B*0802	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.328926	2.352019	-1.976907	21326.820639
HLA A*0219	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.085421	2.108491	-1.976929	12173.649455
HLA A*2603	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.924420	1.947300	-1.977120	8402.721754
HLA A*2601	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.371771	2.394415	-1.977356	23538.095740
HLA A*6901	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.272353	2.294422	-1.977931	18722.026996
HLA A*3001	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.298343	2.320077	-1.978266	19876.635343
HLA B*1801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.375991	2.396811	-1.979180	23767.910316
HLA A*0202	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.574884	2.595201	-1.979683	37573.729409
HLA B*0802	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.338369	2.358631	-1.979738	21795.593362
HLA A*0203	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.277153	2.297367	-1.979786	18930.098118
HLA A*3201	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.305196	2.324609	-1.980587	20192.789499
HLA B*5801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.092568	2.111966	-1.980602	12375.647345
HLA A*3002	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.185077	2.204297	-1.980780	15313.573514
HLA A*8001	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.389026	2.407496	-1.981529	24492.095425
HLA B*4001	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.375951	2.394415	-1.981536	23765.724526
HLA B*5801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.287975	2.306412	-1.981563	19407.723352
HLA B*1503	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.008140	1.026553	-1.981587	1018.918923
HLA A*3002	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.413306	2.431446	-1.981860	25900.343319
HLA B*5101	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-3.095395	1.113445	-1.981950	1245.646470
HLA A*6802	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.280019	2.297367	-1.982653	19055.451205
HLA A*0201	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.390217	2.407496	-1.982721	24559.364894
HLA A*2902	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.937883	1.954913	-1.982969	8667.274110
HLA A*2402	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.317355	2.334336	-1.983019	20766.098174
HLA A*6801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-3.360478	1.377330	-1.983147	2293.389377

HLA B*5701	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.281300	2.297367	-1.983933	19111.717005
HLA A*0203	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.380977	2.396811	-1.984166	24042.332953
HLA A*0206	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-3.807434	1.822872	-1.984562	6418.513004
HLA B*5701	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-3.997616	2.013049	-1.984567	9945.253061
HLA B*2705	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.279094	2.294422	-1.984671	19014.877837
HLA B*2705	1:31-39	9	ARRVREARV	0.936445	0.312607	-3.233751	1.249052	-1.984700	1712.975985
HLA B*0803	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.392332	2.407496	-1.984835	24679.233569
HLA B*4402	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-3.776402	1.791215	-1.985187	5975.887700
HLA A*6802	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.417161	2.431446	-1.985715	26131.300594
HLA A*6901	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.393598	2.407496	-1.986102	24751.301514
HLA B*1503	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.125501	1.138932	-1.986569	1335.060979
HLA B*0702	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.383662	2.396811	-1.986851	24191.459385
HLA A*3301	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.626284	2.639184	-1.987100	42294.508927
HLA B*5801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.238429	2.251319	-1.987110	17315.245489
HLA B*5701	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.395085	2.407496	-1.987589	24836.206646
HLA B*1509	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.346637	2.358631	-1.988006	22214.499579
HLA B*3901	1:423-431	9	LRHADSIVR	1.231621	0.752419	-3.972082	1.984040	-1.988042	9377.382593
HLA A*3001	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.177798	2.188431	-1.989367	15059.059291
HLA A*0211	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.955833	1.966426	-1.989406	9033.012207
HLA B*1502	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.341587	2.352019	-1.989569	21957.732560
HLA A*0301	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.323924	2.334336	-1.989588	21082.594852
HLA B*3901	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.314373	2.324609	-1.989765	20624.024047
HLA B*0801	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.485306	1.495512	-1.989794	3057.073882
HLA A*0211	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-2.803062	0.813260	-1.989802	635.422340
HLA B*1509	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.194235	2.204297	-1.989938	15639.931273
HLA B*4002	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.600545	2.610483	-1.990062	39860.741989
HLA A*6901	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-3.972763	1.982154	-1.990609	9392.106014
HLA A*3201	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.147414	2.156591	-1.990824	14041.525829
HLA A*0250	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.253985	1.263068	-1.990917	1794.671803
HLA A*0203	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.325418	2.334336	-1.991082	21155.258449
HLA B*4402	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.288564	2.297367	-1.991198	19434.094654
HLA A*1101	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.288672	2.297367	-1.991306	19438.931526
HLA A*6901	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.316105	2.324609	-1.991496	20706.417999
HLA B*0801	1:75-83	9	APKLDPALL	1.420023	0.333020	-3.744825	1.753043	-1.991782	5556.807461
HLA B*1501	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.042317	2.050505	-1.991812	11023.439935
HLA A*0301	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-3.712816	1.720897	-1.991919	5161.975815
HLA B*0803	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.344200	2.352019	-1.992181	22090.223937
HLA A*2403	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.243811	2.251319	-1.992493	17531.187043
HLA B*4001	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.958929	1.966426	-1.992503	9097.649864
HLA B*1509	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.854645	1.861603	-1.993042	7155.582233
HLA A*0201	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.158067	2.164911	-1.993156	14390.201266
HLA A*3002	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.006610	2.013049	-1.993561	10153.357243
HLA B*1801	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.780491	1.786784	-1.993707	6032.405558
HLA A*3001	1:115-123	9	YGRTELKVL	1.725445	0.240391	-3.959836	1.965836	-1.994000	9116.667582
HLA B*1509	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.388742	2.394415	-1.994327	24476.068229
HLA B*4001	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.352982	2.358631	-1.994352	22541.483448
HLA B*2705	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.078645	2.084113	-1.994532	11985.188728
HLA A*3201	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.301444	2.306412	-1.995032	20019.083472
HLA B*4402	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.353763	2.358631	-1.995132	22582.006208
HLA B*4501	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.426857	2.431446	-1.995412	26721.285693
HLA A*2902	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.200052	2.204297	-1.995756	15850.835729
HLA B*4402	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.424243	1.428368	-1.995875	2656.090200
HLA A*6801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-3.979943	1.984040	-1.995903	9548.672809
HLA A*2301	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.293425	2.297367	-1.996059	19652.843605
HLA A*2902	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.768447	1.772257	-1.996190	5867.418574
HLA A*3301	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.354883	2.358631	-1.996253	22640.354714
HLA A*2601	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.348610	2.352019	-1.996591	22315.678803
HLA A*1101	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.428918	2.431446	-1.997472	26848.365330
HLA A*0201	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.394773	2.396811	-1.997962	24818.343044
HLA A*3301	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.907847	1.909820	-1.998027	8088.103786
HLA A*0203	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.957106	1.958921	-1.998185	9059.537312
HLA B*0702	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.392907	2.394415	-1.998492	24711.965676
HLA B*1801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.430071	2.431446	-1.998626	26919.776251
HLA A*2602	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.357289	2.358631	-1.998658	22766.124129
HLA A*3002	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.049192	2.050505	-1.998687	11199.322042

HLA B*7301	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.638316	2.639184	-1.999132	43482.619535
HLA A*2601	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.396594	2.396811	-1.999783	24922.616458
HLA B*4801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.394526	2.394415	-2.000111	24804.249276
HLA A*0250	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.073375	1.072837	-2.000538	1184.064685
HLA A*3001	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.260739	2.260158	-2.000581	18228.014390
HLA A*3002	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.253282	2.251319	-2.001963	17917.693256
HLA B*7301	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-2.905876	0.903619	-2.002257	805.148417
HLA A*0216	1:1-9	9	VVQPADIDV	0.757996	0.154834	-2.915227	0.912830	-2.002397	822.672336
HLA B*4001	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.410101	2.407496	-2.002604	25709.925804
HLA A*0101	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.399718	2.396811	-2.002907	25102.585160
HLA A*6802	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.254339	2.251319	-2.003021	17961.366125
HLA A*8001	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.337636	2.334336	-2.003300	21758.835928
HLA B*7301	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.599622	2.595201	-2.004421	39776.084632
HLA A*0202	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.677668	1.673173	-2.004495	4760.665524
HLA A*0203	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.412711	2.407496	-2.005215	25864.917718
HLA A*2402	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.302868	2.297367	-2.005501	20084.821591
HLA B*5801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.210536	2.204297	-2.006239	16238.113296
HLA A*2902	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.090420	2.084113	-2.006307	12314.605281
HLA B*5101	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.438043	2.431446	-2.006597	27418.472004
HLA A*2602	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.865016	1.858036	-2.006980	7328.508634
HLA A*2402	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.287362	1.280105	-2.007257	1938.035925
HLA A*2403	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.313753	2.306412	-2.007341	20594.589619
HLA A*3201	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.240255	1.232655	-2.007600	1738.820089
HLA A*0201	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.267941	2.260158	-2.007782	18532.778463
HLA A*0211	1:384-392	9	RAVGRELGL	1.384772	0.599348	-3.992691	1.984120	-2.008571	9833.119517
HLA B*5301	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.328715	2.320077	-2.008637	21316.439350
HLA A*0211	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-2.616668	0.607629	-2.009040	413.683726
HLA B*0801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.368090	2.358631	-2.009459	23339.399721
HLA A*0101	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.260817	2.251319	-2.009498	18231.268861
HLA B*0802	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.316034	2.306412	-2.009623	20703.057689
HLA B*5801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.269794	2.260158	-2.009636	18612.052888
HLA B*3501	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-2.911924	0.902116	-2.009808	816.438578
HLA B*4403	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.441436	2.431446	-2.009990	27633.500610
HLA A*0206	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.358974	1.348830	-2.010144	2285.462639
HLA B*4801	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.368863	2.358631	-2.010232	23380.977424
HLA A*8001	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.330474	2.320077	-2.010397	21402.988942
HLA A*0219	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.094734	2.084113	-2.010621	12437.530262
HLA A*0216	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-2.916369	0.905240	-2.011128	824.838158
HLA B*4402	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.168348	2.156591	-2.011758	14734.934666
HLA A*3001	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.263218	2.251319	-2.011899	18332.347014
HLA A*3002	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.177013	2.164911	-2.012102	15031.873600
HLA B*5801	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.874080	1.861603	-2.012477	7483.071881
HLA B*3501	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.420283	2.407496	-2.012787	26319.854937
HLA A*0206	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.333186	2.320077	-2.013108	21537.026023
HLA A*0219	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.972349	1.958921	-2.013428	9383.167665
HLA A*8001	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.273998	2.260158	-2.013839	18793.060273
HLA A*6901	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.311387	2.297367	-2.014021	20482.700321
HLA B*5701	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.064788	2.050505	-2.014283	11608.807632
HLA B*7301	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.625062	2.610483	-2.014579	42175.695651
HLA B*1502	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.203017	2.188431	-2.014586	15959.424084
HLA A*0101	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.348995	2.334336	-2.014659	22335.486546
HLA A*0202	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.022161	1.007289	-2.014872	1052.352784
HLA A*3301	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.339990	2.324609	-2.015381	21877.104504
HLA A*2902	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.204300	2.188431	-2.015869	16006.634713
HLA A*0206	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-3.037358	1.020890	-2.016468	1089.827652
HLA B*0802	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.350884	2.334336	-2.016548	22432.847466
HLA B*1517	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.424120	2.407496	-2.016624	26553.403828
HLA A*0203	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.803920	1.787266	-2.016653	6366.776372
HLA A*0212	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.424186	2.407496	-2.016690	26557.426360
HLA B*4501	1:249-257	9	IGDRLTCVF	1.654851	0.984333	-4.656754	2.639184	-2.017571	45368.503887
HLA A*2403	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.376235	2.358631	-2.017605	23781.286581
HLA B*3801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.126100	2.108491	-2.017608	13369.026225
HLA B*5401	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.399968	1.381752	-2.018216	2511.701011
HLA A*3002	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.973303	1.954913	-2.018390	9403.799645
HLA A*3002	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.000586	1.982154	-2.018431	10013.492744

HLA B*7301	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.605047	2.586427	-2.018620	40276.061180
HLA B*4501	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.614114	2.595201	-2.018912	41125.733273
HLA A*3001	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.116871	2.097879	-2.018992	13087.931043
HLA A*0219	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.792854	1.772257	-2.020597	6206.596633
HLA A*6802	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.428422	2.407496	-2.020926	26817.735765
HLA B*5801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.345828	2.324609	-2.021219	22173.196798
HLA B*3501	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-3.116028	1.094025	-2.022003	1306.255040
HLA A*0212	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.356937	2.334336	-2.022601	22747.657291
HLA B*4402	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.329267	2.306412	-2.022855	21343.556684
HLA B*3801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.417629	2.394415	-2.023214	26159.447863
HLA A*2501	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.320663	2.297367	-2.023296	20924.880080
HLA A*0216	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.321044	2.297367	-2.023677	20943.226726
HLA B*0801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-2.554243	0.530534	-2.023709	358.296545
HLA A*2603	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.228138	2.204297	-2.023841	16909.778112
HLA A*0301	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.348765	2.324609	-2.024156	22323.648099
HLA B*0702	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.432158	2.407496	-2.024661	27049.409488
HLA B*4002	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.611393	2.586427	-2.024966	40868.900206
HLA A*0301	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-3.253445	1.228391	-2.025054	1792.440127
HLA B*3801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.331715	2.306412	-2.025303	21464.212298
HLA A*0301	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.322871	2.297367	-2.025505	21031.560305
HLA A*0211	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.453997	1.428368	-2.025629	2844.439478
HLA B*3901	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.420098	2.394415	-2.025683	26308.608728
HLA B*1517	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.182976	2.156591	-2.026386	15239.689134
HLA B*4002	1:107-115	9	VAHTGTREY	1.258906	1.336295	-4.622053	2.595201	-2.026851	41884.425638
HLA B*1801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.815033	1.787266	-2.027766	6531.796714
HLA A*0201	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.362413	2.334336	-2.028077	23036.331855
HLA B*0801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.353020	2.324609	-2.028411	22543.434683
HLA A*0212	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.387250	2.358631	-2.028619	24392.130349
HLA A*3001	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.233199	2.204297	-2.028902	17107.978648
HLA A*0219	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.326546	2.297367	-2.029179	21210.264687
HLA B*4402	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.349395	2.320077	-2.029318	22356.037521
HLA A*6802	1:288-296	9	AAETFLEAL	1.587358	0.379068	-3.996277	1.966426	-2.029850	9914.632748
HLA A*0219	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.438593	2.407496	-2.031097	27453.203412
HLA B*5701	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.291560	2.260158	-2.031402	19568.606807
HLA A*2902	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.338037	2.306412	-2.031626	21778.974145
HLA A*0211	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.291847	2.260158	-2.031688	19581.526477
HLA A*0201	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.115969	2.084113	-2.031856	13060.770430
HLA B*3501	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.429002	2.396811	-2.032191	26853.594720
HLA A*0212	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.429014	2.396811	-2.032203	26854.321104
HLA A*0250	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.116331	2.084113	-2.032217	13071.656191
HLA A*2501	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.292464	2.260158	-2.032306	19609.406919
HLA A*3101	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.338815	2.306412	-2.032403	21818.008111
HLA A*0201	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.391138	2.358631	-2.032507	24611.502627
HLA A*0202	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.338928	2.306412	-2.032516	21823.674431
HLA B*4601	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.329936	2.297367	-2.032570	21376.489954
HLA B*2705	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.329981	2.297367	-2.032614	21378.687312
HLA A*0219	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.430144	2.396811	-2.033333	26924.291252
HLA B*3801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.237635	2.204297	-2.033338	17283.612755
HLA A*2601	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.328724	2.294422	-2.034302	21316.900633
HLA B*5301	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.429042	2.394415	-2.034627	26856.064508
HLA A*3002	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.354723	2.320077	-2.034646	22632.027482
HLA B*1502	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.674341	1.639403	-2.034937	4724.336234
HLA B*4601	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.359984	2.324609	-2.035375	22907.830380
HLA B*0801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.662593	1.627062	-2.035531	4598.258412
HLA B*1503	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-3.708187	1.672339	-2.035849	5107.254267
HLA B*3501	1:285-293	9	TVDAAETFL	1.547755	0.411166	-3.995060	1.958921	-2.036138	9886.887642
HLA B*1517	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.865114	1.828772	-2.036342	7330.173973
HLA B*5301	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.296872	2.260158	-2.036714	19809.435171
HLA A*0216	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.247012	1.210159	-2.036852	1766.085675
HLA A*0216	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.444385	2.407496	-2.036888	27821.754141
HLA A*2501	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.468833	2.431446	-2.037387	29432.913182
HLA A*3001	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.447489	1.410054	-2.037435	2802.132222
HLA A*0216	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.371842	2.334336	-2.037506	23541.916205
HLA A*0211	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.334891	2.297367	-2.037525	21621.780737
HLA A*1101	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.445064	2.407496	-2.037567	27865.286306

HLA A*3101	1:212-220	9	ANALIEQVR	1.205252	0.651982	-3.894896	1.857234	-2.037662	7850.482577
HLA B*5101	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.432287	2.394415	-2.037872	27057.459072
HLA A*0212	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.335427	2.297367	-2.038060	21648.466679
HLA A*2603	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.445773	2.407496	-2.038277	27910.849445
HLA A*6901	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-3.993518	1.954913	-2.038605	9851.862379
HLA B*4001	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.364013	2.324609	-2.039404	23121.357327
HLA B*1503	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.388347	1.348830	-2.039518	2445.385809
HLA B*4001	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.359632	2.320077	-2.039554	22889.248597
HLA A*2602	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.447058	2.407496	-2.039562	27993.565819
HLA B*4403	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.796011	1.756081	-2.039930	6251.888578
HLA A*0219	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.374306	2.334336	-2.039970	23675.895766
HLA A*0201	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.334407	2.294422	-2.039985	21597.698042
HLA B*1503	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.268782	1.228069	-2.040713	1856.872549
HLA A*0212	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.023094	1.982154	-2.040939	10546.142950
HLA B*4501	1:371-379	9	LVEPLRLLF	1.507257	1.103226	-4.651499	2.610483	-2.041016	44822.766687
HLA A*6901	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.870725	1.828772	-2.041952	7425.485466
HLA A*0206	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.449772	2.407496	-2.042275	28169.029044
HLA A*0101	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.340067	2.297367	-2.042701	21881.010492
HLA B*5801	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.337706	2.294422	-2.043284	21762.367601
HLA B*1509	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.451391	2.407496	-2.043894	28274.222595
HLA A*0206	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.350504	2.306412	-2.044092	22413.195885
HLA A*2402	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.200846	2.156591	-2.044256	15879.846171
HLA A*3101	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.295613	2.251319	-2.044294	19752.076941
HLA A*0216	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.364415	2.320077	-2.044338	23142.756584
HLA A*6802	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.441185	2.396811	-2.044373	27617.509362
HLA B*4402	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.946209	1.901679	-2.044530	8835.051931
HLA A*2603	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.438967	2.394415	-2.044552	27476.828058
HLA A*0301	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.365021	2.320077	-2.044944	23175.080672
HLA A*0203	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.011858	1.966426	-2.045432	10276.812111
HLA A*3201	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.296771	2.251319	-2.045452	19804.827532
HLA A*3001	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.154514	2.108491	-2.046023	14272.973085
HLA A*2301	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.050409	2.004292	-2.046117	11230.750170
HLA A*3002	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.185122	1.138932	-2.046189	1531.516337
HLA B*4001	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.381484	2.334336	-2.047148	24070.443707
HLA A*0101	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.371800	2.324609	-2.047191	23539.623852
HLA B*4801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.367335	2.320077	-2.047258	23298.904289
HLA A*3201	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-3.949113	1.901679	-2.047434	8894.326545
HLA A*3101	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.307830	2.260158	-2.047672	20315.620460
HLA B*2705	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.354277	2.306412	-2.047865	22608.776450
HLA B*4001	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.835281	1.787266	-2.048014	6843.535456
HLA A*0206	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-3.995515	1.947300	-2.048216	9897.269561
HLA B*1517	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.384621	1.336347	-2.048274	2424.493948
HLA B*1801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.299753	2.251319	-2.048434	19941.258404
HLA B*5101	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.456529	2.407496	-2.049033	28610.733789
HLA A*1101	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.446036	2.396811	-2.049225	27927.765965
HLA B*5101	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.401380	2.352019	-2.049361	25198.781165
HLA B*0801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.034179	1.984120	-2.050058	10818.785842
HLA A*0301	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.357385	2.306412	-2.050974	22771.174339
HLA B*0702	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.101510	2.050505	-2.051005	12633.103819
HLA A*0216	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.410049	2.358631	-2.051419	25706.866053
HLA B*1517	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.376170	2.324609	-2.051561	23777.684539
HLA A*6901	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.160078	2.108491	-2.051587	14456.994884
HLA B*4501	1:284-292	9	VTVDAAETF	1.414591	1.171836	-4.638210	2.586427	-2.051783	43472.035197
HLA A*6801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.007643	1.954913	-2.052730	10177.554587
HLA A*0202	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-3.665432	1.612498	-2.052933	4628.407108
HLA A*2902	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.347400	2.294422	-2.052978	22253.591779
HLA B*4801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.359408	2.306412	-2.052997	22877.487931
HLA B*2705	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.373160	2.320077	-2.053083	23613.473223
HLA B*4402	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.405345	2.352019	-2.053327	25429.947623
HLA A*2402	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.360012	2.306412	-2.053600	22909.317574
HLA A*0219	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.378434	2.324609	-2.053826	23902.012240
HLA B*1501	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.347311	1.293038	-2.054273	2224.904030
HLA B*4001	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.360830	2.306412	-2.054418	22952.488229
HLA A*6802	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.314583	2.260158	-2.054424	20633.956496
HLA A*0216	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.349052	2.294422	-2.054630	22338.386714

HLA B*1517	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.342518	1.287816	-2.054702	2200.484598
HLA A*6901	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.211447	2.156591	-2.054857	16272.233494
HLA B*0802	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.352433	2.297367	-2.055066	22512.965921
HLA B*1801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.462687	2.407496	-2.055191	29019.304304
HLA A*0101	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.375521	2.320077	-2.055444	23742.207871
HLA A*0201	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.050855	1.995235	-2.055620	11242.299956
HLA B*1502	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.487223	2.431446	-2.055777	30705.959199
HLA A*0216	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.316018	2.260158	-2.055860	20702.273695
HLA A*0301	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.316020	2.260158	-2.055862	20702.385692
HLA B*4002	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-3.287907	1.231855	-2.056052	1940.469870
HLA A*0216	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.381167	2.324609	-2.056558	24052.870636
HLA A*0250	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.351157	2.294422	-2.056735	22446.929553
HLA A*6901	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.363316	2.306412	-2.056904	23084.237214
HLA A*0301	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.061207	2.004292	-2.056915	11513.490301
HLA B*1501	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.844674	1.787266	-2.057407	6993.164797
HLA A*0201	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.355008	2.297367	-2.057641	22646.847180
HLA B*3801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.309113	2.251319	-2.057794	20375.717442
HLA A*2501	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.364547	2.306412	-2.058135	23149.768832
HLA B*4001	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.246795	2.188431	-2.058364	17652.050827
HLA A*6802	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.328055	1.269596	-2.058459	2128.408102
HLA A*2403	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.916728	1.858036	-2.058692	8255.203218
HLA B*4001	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.356857	2.297367	-2.059490	22743.473558
HLA B*0801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.171896	2.111966	-2.059930	14855.796337
HLA A*2601	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.385528	2.324609	-2.060919	24295.596134
HLA B*1509	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.395475	2.334336	-2.061139	24858.520611
HLA B*5801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-3.775059	1.713482	-2.061577	5957.424156
HLA B*1502	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.469190	2.407496	-2.061694	29457.125913
HLA B*1503	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.170604	2.108491	-2.062112	14811.659517
HLA B*5101	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-2.810576	0.748391	-2.062185	646.511319
HLA A*3001	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.144717	2.082473	-2.062245	13954.590430
HLA B*4402	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.386895	2.324609	-2.062286	24372.212719
HLA A*0202	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.044441	1.982154	-2.062287	11077.482548
HLA A*0250	1:428-436	9	SIVREELTA	1.468906	-0.179470	-3.351912	1.289436	-2.062475	2248.596727
HLA A*0202	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.819699	1.756081	-2.063617	6602.352949
HLA A*6801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.398036	2.334336	-2.063700	25005.538858
HLA A*2301	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.836042	1.772257	-2.063785	6855.541352
HLA A*0101	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.370827	2.306412	-2.064415	23486.961291
HLA A*2601	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.384663	2.320077	-2.064586	24247.275624
HLA B*4001	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.221686	2.156591	-2.065096	16660.430646
HLA A*2501	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.221644	2.155890	-2.065754	16658.808366
HLA B*0801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.385960	2.320077	-2.065883	24319.792487
HLA B*3501	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.048097	1.982154	-2.065942	11171.124016
HLA B*4801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.317266	2.251319	-2.065947	20761.829606
HLA A*0203	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.424733	2.358631	-2.066103	26590.923213
HLA B*4001	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.981592	1.914570	-2.067022	9585.005153
HLA A*2403	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-3.780754	1.713482	-2.067272	6036.061746
HLA A*6901	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.449157	1.381752	-2.067405	2812.915968
HLA B*1502	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.319157	2.251319	-2.067838	20852.443726
HLA B*0702	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.362423	2.294422	-2.068000	23036.830356
HLA A*0202	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.475668	2.407496	-2.068171	29899.773696
HLA A*3002	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.392900	2.324609	-2.068291	24711.564612
HLA A*6901	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.388443	2.320077	-2.068366	24459.257577
HLA A*2402	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.081497	2.013049	-2.068449	12064.161766
HLA B*2705	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.052594	1.984120	-2.068473	11287.396666
HLA B*2705	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.272823	2.204297	-2.068526	18742.294777
HLA B*0803	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.375152	2.306412	-2.068741	23722.050926
HLA A*2902	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.320195	2.251319	-2.068877	20902.365147
HLA A*0211	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.234437	1.165167	-2.069271	1715.684091
HLA B*1509	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.142319	1.072837	-2.069481	1387.773902
HLA B*5701	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.273878	2.204297	-2.069581	18787.875901
HLA A*2501	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.466517	2.396811	-2.069706	29276.331574
HLA B*2705	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.404359	2.334336	-2.070023	25372.232474
HLA A*0201	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.390114	2.320077	-2.070037	24553.519598
HLA A*2501	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.478069	2.407496	-2.070573	30065.544599
HLA B*5401	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-3.165334	1.094025	-2.071309	1463.303028

HLA B*4801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.368914	2.297367	-2.071548	23383.760337
HLA A*0202	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.236777	1.165167	-2.071611	1724.953575
HLA B*5701	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.396584	2.324609	-2.071975	24922.077150
HLA B*4403	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.264299	1.191820	-2.072480	1837.804364
HLA A*1101	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.397153	2.324609	-2.072544	24954.726330
HLA B*1801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.397320	2.324609	-2.072711	24964.313335
HLA B*1509	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.379130	2.306412	-2.072718	23940.317844
HLA A*8001	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.379142	2.306412	-2.072730	23940.965425
HLA B*5101	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.431469	2.358631	-2.072839	27006.567499
HLA A*0211	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.027877	1.954913	-2.072964	10662.945887
HLA A*2403	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.367439	2.294422	-2.073017	23304.450906
HLA B*1501	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.039643	1.965836	-2.073808	10955.783113
HLA B*5301	1:75-83	9	APKLDPALL	1.420023	0.333020	-3.826865	1.753043	-2.073822	6712.196568
HLA A*0219	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.394185	2.320077	-2.074108	24784.799611
HLA A*2601	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.380608	2.306412	-2.074196	24021.921205
HLA A*2403	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.846530	1.772257	-2.074273	7023.116229
HLA A*0212	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-3.264981	1.190433	-2.074548	1840.689899
HLA B*3901	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.471521	2.396811	-2.074710	29615.635770
HLA B*4801	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.369138	2.294422	-2.074715	23395.781263
HLA A*3001	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-3.990253	1.914570	-2.075683	9778.056725
HLA A*0301	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.327030	2.251319	-2.075711	21233.915370
HLA A*0206	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-3.112851	1.036964	-2.075888	1296.735723
HLA A*0202	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.240799	2.164911	-2.075888	17410.020542
HLA A*3101	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.373578	2.297367	-2.076211	23636.223011
HLA A*0203	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.339614	1.263068	-2.076546	2185.819871
HLA B*4001	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.024142	1.947300	-2.076842	10571.619517
HLA B*4002	1:493-501	9	LERISTRIT	1.013477	-0.322582	-2.768027	0.690895	-2.077132	586.174551
HLA B*5701	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.371567	2.294422	-2.077145	23527.019899
HLA A*0216	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.474063	2.396811	-2.077252	29789.499254
HLA A*2402	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-3.700007	1.622722	-2.077285	5011.948193
HLA A*0250	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.401934	2.324609	-2.077325	25230.973848
HLA B*3501	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.402148	2.324609	-2.077539	25243.398113
HLA B*1502	1:394-402	9	EEIVARQPF	0.860370	0.918985	-3.857384	1.779355	-2.078029	7200.861810
HLA B*0802	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.398316	2.320077	-2.078239	25021.642027
HLA B*0803	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.412589	2.334336	-2.078253	25857.642572
HLA B*0802	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.402886	2.324609	-2.078277	25286.315646
HLA B*3501	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.600163	1.521566	-2.078597	3982.564870
HLA B*5301	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.940443	1.861603	-2.078840	8718.534097
HLA B*0801	1:301-309	9	APEGKRKII	1.207147	0.122555	-3.409037	1.329702	-2.079335	2564.702249
HLA B*0801	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.374010	2.294422	-2.079588	23659.762685
HLA A*2403	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.284476	2.204297	-2.080180	19252.015814
HLA B*3901	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-3.990375	1.909820	-2.080555	9780.807819
HLA A*2603	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.064877	1.984120	-2.080757	11611.194367
HLA B*2705	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.178662	2.097879	-2.080783	15089.069319
HLA B*3901	1:394-402	9	EEIVARQPF	0.860370	0.918985	-3.860152	1.779355	-2.080797	7246.898354
HLA A*3002	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.488320	2.407496	-2.080823	30783.633372
HLA B*0702	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.401107	2.320077	-2.081030	25182.972703
HLA A*3001	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-2.938247	0.857166	-2.081081	867.455386
HLA B*0801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.341841	2.260158	-2.081683	21970.565510
HLA B*3901	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.065859	1.984120	-2.081739	11637.480862
HLA B*3901	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.246720	2.164911	-2.081809	17648.995231
HLA A*2603	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.165985	2.084113	-2.081872	14654.959839
HLA B*0803	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.379306	2.297367	-2.081939	23950.033400
HLA B*4001	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.333449	2.251319	-2.082130	21550.079424
HLA A*0250	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.164655	2.082473	-2.082182	14610.155023
HLA A*6801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-3.610815	1.528166	-2.082649	4081.458862
HLA A*0201	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.378061	1.295300	-2.082762	2388.148575
HLA A*2603	1:109-117	9	HTGTREYGR	1.076414	0.591236	-3.751164	1.667650	-2.083514	5638.508762
HLA A*2501	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.378117	2.294422	-2.083695	23884.562136
HLA B*4601	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.288078	2.204297	-2.083781	19412.343622
HLA A*0212	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.404244	2.320077	-2.084166	25365.507578
HLA B*4403	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.240372	2.155890	-2.084482	17392.887075
HLA A*6802	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.031848	1.947300	-2.084548	10760.881152
HLA B*1501	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.112506	2.027725	-2.084781	12957.035689
HLA A*3101	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.672682	1.587869	-2.084813	4706.326605

HLA A*3101	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.404894	2.320077	-2.084817	25403.547282
HLA A*0101	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.379804	2.294422	-2.085382	23977.517367
HLA A*2902	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.242359	2.156591	-2.085769	17472.672694
HLA B*5101	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.420342	2.334336	-2.086006	26323.414865
HLA B*0802	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.243320	2.156591	-2.086730	17511.376313
HLA A*0201	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.393314	2.306412	-2.086902	24735.104698
HLA B*0702	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.105340	2.017754	-2.087586	12744.996653
HLA B*4402	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.348037	2.260158	-2.087879	22286.241251
HLA B*3901	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.244288	2.155890	-2.088399	17550.450500
HLA A*0219	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.447326	2.358631	-2.088695	28010.835542
HLA B*1501	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-2.991078	0.902116	-2.088962	979.665169
HLA A*0211	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.036354	1.947300	-2.089054	10873.119149
HLA A*3001	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.084387	1.995235	-2.089152	12144.706354
HLA B*0802	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.201316	2.111966	-2.089350	15897.037111
HLA B*4002	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.395854	2.306412	-2.089442	24880.181619
HLA A*2402	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.254584	2.164911	-2.089672	17971.474544
HLA A*0211	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.117501	2.027725	-2.089776	13106.920346
HLA B*5401	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.216276	1.126421	-2.089855	1645.416337
HLA A*1101	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.410012	2.320077	-2.089934	25704.641009
HLA A*0202	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.074374	1.984120	-2.090253	11867.890030
HLA A*0203	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.072799	1.982154	-2.090645	11824.951236
HLA B*0801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.388180	2.297367	-2.090813	24444.442017
HLA A*0212	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.351105	2.260158	-2.090947	22444.258133
HLA B*1509	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.388575	2.297367	-2.091208	24466.668725
HLA A*0203	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.119361	2.027725	-2.091636	13163.199160
HLA A*2402	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-3.817415	1.725080	-2.092335	6567.726176
HLA B*4403	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.489358	2.396811	-2.092547	30857.330379
HLA B*1503	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-3.330757	1.237896	-2.092861	2141.690998
HLA A*3101	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-3.596253	1.503120	-2.093133	3946.874484
HLA A*0206	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.075412	1.982154	-2.093258	11896.302140
HLA B*1503	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.048252	1.954913	-2.093339	11175.113408
HLA B*3501	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.388004	2.294422	-2.093582	24434.525899
HLA B*4403	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.250202	2.156591	-2.093611	17791.064023
HLA A*6801	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.445855	2.352019	-2.093837	27916.134757
HLA A*0202	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.723967	1.629570	-2.094397	5296.227369
HLA B*1509	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.419417	2.324609	-2.094808	26267.366358
HLA B*4001	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.389313	2.294422	-2.094890	24508.265702
HLA A*0101	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.355438	2.260158	-2.095280	22669.278881
HLA A*0203	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.401781	2.306412	-2.095370	25222.103118
HLA A*0250	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.406546	1.311116	-2.095430	2550.037097
HLA A*0250	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.050653	1.954913	-2.095740	11237.070688
HLA A*0250	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.305993	1.210159	-2.095834	2022.987687
HLA A*3101	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.178470	2.082473	-2.095997	15082.377128
HLA A*3101	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.284540	2.188431	-2.096108	19254.828103
HLA B*4801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.356295	2.260158	-2.096137	22714.086079
HLA B*5301	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.448167	2.352019	-2.096148	28065.137824
HLA B*4601	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.390755	2.294422	-2.096333	24589.809477
HLA B*1502	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.300932	2.204297	-2.096635	19995.487766
HLA B*4801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.525454	1.428368	-2.097086	3353.157357
HLA A*0101	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.002336	0.905240	-2.097096	1005.394256
HLA B*5101	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.494271	2.396811	-2.097460	31208.372679
HLA A*6801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.685510	1.587869	-2.097641	4847.415539
HLA B*4501	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.399193	1.301147	-2.098046	2507.220964
HLA A*1101	1:46-54	9	HTASIEEIR	1.076887	0.539178	-3.714634	1.616065	-2.098570	5183.635635
HLA A*6801	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.493355	2.394415	-2.098940	31142.596896
HLA A*3101	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.811525	0.712255	-2.099271	647.925876
HLA B*1503	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.197397	2.097879	-2.099518	15754.232378
HLA A*8001	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.424496	2.324609	-2.099887	26576.397933
HLA B*0803	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.458730	2.358631	-2.100100	28756.131695
HLA A*0203	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.084246	1.984120	-2.100126	12140.764903
HLA A*6802	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.230767	1.130410	-2.100357	1701.247220
HLA B*4601	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.360780	2.260158	-2.100622	22949.880798
HLA B*0702	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.425290	2.324609	-2.100681	26625.038464
HLA B*1503	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.813198	0.712255	-2.100944	650.426396
HLA B*3801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.421942	2.320077	-2.101865	26420.572728

HLA B*3801	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.436222	2.334336	-2.101886	27303.756211
HLA B*5101	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.427132	2.324609	-2.102523	26738.204472
HLA B*1501	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.439294	1.336347	-2.102946	2749.752594
HLA B*1517	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.017577	1.914570	-2.103007	10413.028642
HLA A*2603	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.427821	2.324609	-2.103212	26780.620742
HLA A*6801	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.965141	1.861603	-2.103538	9228.715475
HLA A*0203	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.363757	2.260158	-2.103599	23107.727192
HLA B*0802	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.398271	2.294422	-2.103849	25019.070237
HLA A*0219	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.398544	2.294422	-2.104121	25034.775811
HLA B*4001	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.364497	2.260158	-2.104339	23147.138990
HLA A*6901	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.188643	2.084113	-2.104530	15439.849616
HLA A*0212	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.064261	1.958921	-2.105340	11594.748423
HLA B*2705	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.356756	2.251319	-2.105437	22738.183467
HLA A*0211	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.465572	2.358631	-2.106942	29212.731311
HLA A*0216	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.402717	1.295300	-2.107417	2527.649419
HLA B*3801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.263697	2.155890	-2.107808	18352.590079
HLA B*0801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.296788	2.188431	-2.108356	19805.577540
HLA B*2705	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.368839	2.260158	-2.108681	23379.712574
HLA B*3501	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.217373	2.108491	-2.108881	16495.769087
HLA B*0803	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.369558	2.260158	-2.109400	23418.448012
HLA A*0216	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.392976	1.283502	-2.109474	2471.586834
HLA A*0201	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.218054	2.108491	-2.109563	16521.669080
HLA A*1101	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.747015	1.637421	-2.109594	5584.895728
HLA A*2402	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.429677	2.320077	-2.109599	26895.321021
HLA A*0206	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.506550	2.396811	-2.109738	32103.289277
HLA B*3901	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.404265	2.294422	-2.109842	25366.742629
HLA A*6901	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.275001	2.164911	-2.110089	18836.522849
HLA B*3801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.275304	2.164911	-2.110393	18849.672988
HLA B*3901	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.407932	2.297367	-2.110566	25581.867704
HLA B*3501	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.299480	2.188431	-2.111049	19928.748250
HLA A*2301	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.445799	2.334336	-2.111463	27912.510435
HLA A*1101	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.006567	1.893265	-2.113303	10152.368578
HLA A*0211	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.028347	1.914570	-2.113777	10674.489202
HLA A*3001	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.393892	1.280105	-2.113787	2476.807033
HLA A*0212	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-2.758883	0.644580	-2.114302	573.961502
HLA A*6901	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.080811	1.966426	-2.114385	12045.119204
HLA A*2501	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.318701	2.204297	-2.114405	20830.570181
HLA B*5301	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.545887	2.431446	-2.114441	35146.894642
HLA B*4002	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-3.901785	1.787266	-2.114519	7975.998142
HLA A*0203	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.434822	2.320077	-2.114745	27215.862649
HLA A*0211	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.522531	2.407496	-2.115034	33306.632806
HLA B*3501	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.271307	2.155890	-2.115418	18677.009784
HLA B*0801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.271310	2.155890	-2.115420	18677.110825
HLA A*0301	1:487-495	9	RVPYEVLER	0.866973	0.808043	-3.790777	1.675016	-2.115760	6176.985427
HLA B*1503	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.427405	1.311116	-2.116289	2675.501670
HLA A*2902	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-3.830027	1.713482	-2.116545	6761.251226
HLA B*5301	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.889370	1.772257	-2.117114	7751.225388
HLA B*1501	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.061003	0.943730	-2.117273	1150.808445
HLA B*1517	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.225850	2.108491	-2.117358	16820.910904
HLA A*3201	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.890047	1.772257	-2.117790	7763.311583
HLA A*2301	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.200367	2.082473	-2.117894	15862.330564
HLA B*1509	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.438158	2.320077	-2.118081	27425.741181
HLA B*5301	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.525580	2.407496	-2.118084	33541.336268
HLA B*1517	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.073114	1.954913	-2.118201	11833.526549
HLA A*3001	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.275370	2.156591	-2.118779	18852.528494
HLA B*3801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.307287	2.188431	-2.118856	20290.248203
HLA B*4002	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.033530	1.914570	-2.118960	10802.644048
HLA A*2602	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.425391	2.306412	-2.118980	26631.232841
HLA B*4402	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.413545	2.294422	-2.119123	25914.639298
HLA B*3501	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.074068	1.954913	-2.119155	11859.546448
HLA A*3002	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.145525	2.025736	-2.119789	13980.584129
HLA B*0702	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.379978	2.260158	-2.119820	23987.118251
HLA B*1801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.417241	2.297367	-2.119874	26136.107529
HLA B*0802	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.380312	2.260158	-2.120154	24005.552337
HLA A*0250	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.285223	2.164911	-2.120312	19285.164423

HLA B*1502	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.444972	2.324609	-2.120363	27859.407750
HLA B*5101	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.426834	2.306412	-2.120422	26719.840140
HLA B*5301	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.086943	1.966426	-2.120517	12216.400390
HLA A*3301	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.514944	2.394415	-2.120529	32729.867115
HLA A*0203	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.793779	1.673173	-2.120607	6219.840080
HLA A*2402	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.022831	1.901679	-2.121151	10539.754897
HLA B*4403	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.515661	2.394415	-2.121246	32783.916505
HLA A*0211	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.416426	2.294422	-2.122003	26087.090027
HLA A*0206	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.795203	1.673173	-2.122030	6240.264621
HLA A*2402	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.104221	1.982154	-2.122067	12712.219141
HLA A*2501	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.373416	2.251319	-2.122097	23627.401673
HLA A*2601	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.373970	2.251319	-2.122652	23657.586841
HLA A*0301	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.327211	2.204297	-2.122914	21242.762443
HLA B*4402	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.040579	1.917562	-2.123017	10979.397816
HLA A*3002	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.440732	1.317518	-2.123214	2758.871706
HLA B*1801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.443706	2.320077	-2.123628	27778.289984
HLA B*0702	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.105861	1.982154	-2.123707	12760.312530
HLA A*3001	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.174321	2.050505	-2.123816	14938.968290
HLA B*1801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.328508	2.204297	-2.124211	21306.293643
HLA B*4601	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.236378	2.111966	-2.124412	17233.661278
HLA B*0702	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.083513	1.958921	-2.124592	12120.289968
HLA A*0203	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-2.415242	0.290570	-2.124673	260.161117
HLA B*4601	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.376393	2.251319	-2.125074	23789.907970
HLA B*1501	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.109268	1.984120	-2.125148	12860.802374
HLA B*5401	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.484281	2.358631	-2.125650	30498.684919
HLA A*0212	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.432308	2.306412	-2.125896	27058.776505
HLA A*8001	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.377405	2.251319	-2.126087	23845.442719
HLA A*6802	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.432623	2.306412	-2.126211	27078.399204
HLA B*5401	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.557961	2.431446	-2.126515	36137.737837
HLA B*0803	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.377936	2.251319	-2.126618	23874.614820
HLA A*0201	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.679834	1.553110	-2.126724	4784.470652
HLA A*0202	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.604791	1.477798	-2.126994	4025.235961
HLA A*2301	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.177563	2.050505	-2.127058	15050.914710
HLA A*3001	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.111307	1.984040	-2.127267	12921.335936
HLA B*4601	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.178211	2.050505	-2.127706	15073.404459
HLA A*6802	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.448978	2.320077	-2.128901	28117.567840
HLA A*3101	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-3.524204	1.394918	-2.129286	3343.520639
HLA A*3301	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.481377	2.352019	-2.129358	30295.432007
HLA A*0211	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.111632	1.982154	-2.129477	12930.986151
HLA B*4801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.112308	1.982154	-2.130154	12951.148952
HLA A*1101	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.436671	2.306412	-2.130259	27331.983458
HLA A*0212	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.424832	2.294422	-2.130410	26596.965766
HLA A*0212	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.441779	1.311116	-2.130663	2765.536378
HLA A*0211	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.527993	2.396811	-2.131182	33728.209109
HLA A*6901	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-3.764641	1.632644	-2.131997	5816.221073
HLA A*2603	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.563459	2.431446	-2.132013	36598.118405
HLA A*3201	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.419840	1.287816	-2.132023	2629.298445
HLA A*6901	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.427692	1.295300	-2.132392	2677.268101
HLA A*0203	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.065425	0.932998	-2.132427	1162.585149
HLA A*3301	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-3.556754	1.424271	-2.132483	3603.742683
HLA B*5301	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.558892	1.426359	-2.132533	3621.527647
HLA A*0219	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.439725	2.306412	-2.133314	27524.882881
HLA A*3101	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.088334	1.954913	-2.133421	12255.588016
HLA A*0219	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.298613	2.164911	-2.133702	19889.005186
HLA B*1509	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.890118	1.756081	-2.134036	7764.571645
HLA A*0211	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.129563	1.995235	-2.134328	13476.059385
HLA B*0802	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.216936	2.082473	-2.134463	16479.178743
HLA A*3201	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-3.516559	1.381432	-2.135127	3285.177080
HLA B*4001	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.119568	1.984120	-2.135448	13169.467259
HLA A*0211	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-2.569021	0.433361	-2.135660	370.698544
HLA B*4801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-3.993781	1.858036	-2.135746	9857.833506
HLA B*4601	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.218359	2.082473	-2.135887	16533.292619
HLA B*1517	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.053994	1.917562	-2.136432	11323.849286
HLA A*0219	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-2.949854	0.813260	-2.136593	890.950557
HLA B*4002	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.531031	2.394415	-2.136616	33964.964567

HLA B*7301	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.121250	1.984040	-2.137210	13220.577859
HLA A*2501	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.457499	2.320077	-2.137422	28674.729766
HLA A*3001	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.293331	2.155890	-2.137442	19648.591277
HLA A*0250	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.472172	2.334336	-2.137836	29660.049234
HLA A*3101	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.302762	2.164911	-2.137851	20079.932636
HLA A*2902	1:275-283	9	FVAATGANL	1.478982	0.382621	-3.999759	1.861603	-2.138155	9994.442384
HLA A*2402	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.389484	2.251319	-2.138165	24517.946465
HLA B*5101	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.458683	2.320077	-2.138606	28753.020514
HLA B*0801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.105269	1.966426	-2.138843	12742.928350
HLA B*5701	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.390598	2.251319	-2.139279	24580.898206
HLA B*4402	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.328022	2.188431	-2.139590	21282.447207
HLA A*8001	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.434933	2.294422	-2.140510	27222.783565
HLA A*1101	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-3.865603	1.725080	-2.140522	7338.426944
HLA A*0201	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.095519	1.954913	-2.140606	12460.023988
HLA B*0803	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.435503	2.294422	-2.141081	27258.594253
HLA B*1801	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.435846	2.294422	-2.141424	27280.132790
HLA B*0802	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.345943	2.204297	-2.141647	22179.075350
HLA B*1503	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.054077	0.911989	-2.142087	1132.600525
HLA A*0212	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.250759	2.108491	-2.142267	17813.889353
HLA B*0802	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.193055	2.050505	-2.142550	15597.514528
HLA A*0216	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.137828	1.995235	-2.142593	13734.991796
HLA B*5101	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.393950	2.251319	-2.142632	24771.394935
HLA A*0250	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.109146	1.966426	-2.142720	12857.184956
HLA B*3901	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.464083	2.320077	-2.144005	29112.707081
HLA A*0202	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.540852	2.396811	-2.144041	34741.775789
HLA A*2602	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.575519	2.431446	-2.144073	37628.652333
HLA A*0202	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.077905	0.933159	-2.144746	1196.479427
HLA B*0801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.973581	1.828772	-2.144808	9409.804636
HLA A*0203	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.254123	2.108491	-2.145632	17952.428801
HLA A*0216	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.127942	1.982154	-2.145787	13425.849405
HLA B*4403	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.480635	2.334336	-2.146299	30243.685453
HLA B*1502	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.141667	1.995235	-2.146432	13856.944032
HLA A*6802	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-3.759693	1.612498	-2.147195	5750.331608
HLA A*0211	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.245082	2.097879	-2.147203	17582.571603
HLA A*6901	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.464997	1.317518	-2.147479	2917.406769
HLA A*2601	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.303765	2.155890	-2.147876	20126.371352
HLA B*5301	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.445308	2.297367	-2.147941	27880.968521
HLA B*0802	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.399540	2.251319	-2.148221	25092.266314
HLA A*3201	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.468380	2.320077	-2.148303	29402.198062
HLA B*0803	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.468547	2.320077	-2.148469	29413.493678
HLA B*5801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.232691	2.084113	-2.148578	17087.999034
HLA A*0250	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.118561	0.969193	-2.149367	1313.895193
HLA B*1502	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.305720	2.155890	-2.149831	20217.164887
HLA B*0803	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.777098	1.627062	-2.150036	5985.464717
HLA B*5401	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-2.170064	0.019419	-2.150645	147.932716
HLA B*0702	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-3.264327	1.113445	-2.150883	1837.923676
HLA A*0202	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.739027	1.587869	-2.151158	5483.108251
HLA B*5801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.069068	1.917562	-2.151507	11723.799331
HLA B*4402	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.147043	1.995235	-2.151808	14029.528787
HLA B*1501	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.053867	1.901679	-2.152188	11320.541687
HLA B*3801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.449847	2.297367	-2.152480	28173.905988
HLA A*3101	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.148096	1.995235	-2.152860	14063.572417
HLA B*1502	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.780824	1.627062	-2.153762	6037.041458
HLA A*0101	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.358163	2.204297	-2.153867	22811.986603
HLA B*0702	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.119784	1.965836	-2.153949	13176.023463
HLA B*0702	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.097834	0.943730	-2.154104	1252.661031
HLA B*3801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.479216	2.324609	-2.154607	30145.023282
HLA B*5101	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.452805	2.297367	-2.155438	28366.454869
HLA B*5801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.013315	1.856944	-2.156371	10311.339761
HLA A*2603	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.313391	2.156591	-2.156801	20577.438940
HLA B*5801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.313579	2.156591	-2.156989	20586.346600
HLA B*4001	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.266021	2.108491	-2.157530	18451.046572
HLA A*3201	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-3.770919	1.612498	-2.158421	5900.906449
HLA B*1501	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.346857	2.188431	-2.158426	22225.799182
HLA B*4001	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.240952	2.082473	-2.158479	17416.143727

HLA B*4001	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.363015	2.204297	-2.158718	23068.257702
HLA B*4601	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.315337	2.156591	-2.158746	20669.820028
HLA B*0702	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.323842	2.164911	-2.158931	21078.603322
HLA A*6901	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.654629	1.495512	-2.159117	4514.697120
HLA A*3001	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.871743	0.712255	-2.159488	744.290756
HLA B*5401	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.567131	2.407496	-2.159635	36908.891575
HLA B*1501	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.257842	2.097879	-2.159963	18106.830985
HLA A*2402	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.348612	2.188431	-2.160181	22315.799529
HLA A*0216	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.089944	0.929716	-2.160228	1230.110134
HLA B*4002	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.411607	2.251319	-2.160288	25799.235877
HLA B*4402	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.916634	1.756081	-2.160553	8253.417022
HLA B*3901	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.467200	2.306412	-2.160789	29322.456949
HLA B*1501	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.243341	2.082473	-2.160869	17512.228945
HLA A*3001	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-3.839773	1.678625	-2.161148	6914.690357
HLA B*1502	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.019443	1.858036	-2.161407	10457.853510
HLA A*3001	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.165707	2.004292	-2.161416	14645.607583
HLA B*1801	1:479-487	9	DAMTADWTR	1.140857	0.484835	-3.787440	1.625692	-2.161749	6129.715360
HLA A*0211	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.481906	2.320077	-2.161829	30332.330818
HLA A*6802	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.394696	1.232655	-2.162041	2481.393819
HLA B*5801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.351044	2.188431	-2.162613	22441.101411
HLA B*5401	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.559465	2.396811	-2.162654	36263.075432
HLA A*2403	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.245533	2.082473	-2.163061	17600.844086
HLA B*5401	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.063165	0.899837	-2.163327	1156.550409
HLA A*2601	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.319939	2.156591	-2.163349	20890.043117
HLA A*2501	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.487991	2.324609	-2.163382	30760.327153
HLA B*7301	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.516105	2.352019	-2.164086	32817.454187
HLA A*2301	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.352567	2.188431	-2.164135	22519.909173
HLA B*1501	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.475546	1.311116	-2.164430	2989.139434
HLA B*4402	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.416036	2.251319	-2.164717	26063.673251
HLA B*1501	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-2.943049	0.778023	-2.165027	877.100776
HLA A*6802	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.937840	1.772257	-2.165584	8666.430149
HLA A*0211	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.472040	2.306412	-2.165629	29651.064970
HLA A*6802	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.292117	1.126421	-2.165696	1959.373278
HLA B*5401	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.560390	2.394415	-2.165975	36340.452479
HLA A*0216	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.472933	2.306412	-2.166521	29712.083078
HLA A*6901	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.477670	1.311116	-2.166554	3003.793744
HLA A*0250	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.464762	2.297367	-2.167395	29158.259175
HLA A*6801	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.464802	2.297367	-2.167435	29160.940929
HLA A*0250	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.521173	1.353717	-2.167456	3320.268252
HLA A*0201	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.152325	1.984120	-2.168204	14201.189636
HLA B*4402	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.333122	2.164911	-2.168211	21533.880404
HLA B*0801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.266319	2.097879	-2.168440	18463.727828
HLA A*0201	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.357797	2.188431	-2.169365	22792.742715
HLA B*3501	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.153678	1.984120	-2.169558	14245.510927
HLA A*0250	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.577107	2.407496	-2.169610	37766.515451
HLA B*4801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.326210	2.156591	-2.169620	21193.862471
HLA B*2705	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.195612	2.025736	-2.169875	15689.591580
HLA A*1101	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.430093	2.260158	-2.169934	26921.086980
HLA B*1501	1:382-390	9	EVRAVGREL	1.480172	0.348600	-3.999063	1.828772	-2.170291	9978.450819
HLA A*0201	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.137528	1.966426	-2.171101	13725.484076
HLA B*1517	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.255258	2.084113	-2.171145	17999.399414
HLA A*2301	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.529986	2.358631	-2.171355	33883.295633
HLA B*3501	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.336515	2.164911	-2.171604	21702.759263
HLA B*1517	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.584717	1.412655	-2.172063	3843.415561
HLA B*0702	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.284187	2.111966	-2.172222	19239.209469
HLA B*5101	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.765628	1.593295	-2.172333	5829.451445
HLA B*4001	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.032858	1.859882	-2.172976	10785.942815
HLA A*6801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-3.885216	1.711364	-2.173853	7677.440792
HLA B*1502	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.258392	2.084113	-2.174279	18129.767191
HLA A*6901	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.487463	1.313175	-2.174287	3072.293924
HLA B*4002	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.339447	2.164911	-2.174536	21849.782103
HLA A*0219	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.225135	2.050505	-2.174630	16793.269864
HLA B*4801	1:431-439	9	REELTAAGL	1.365493	0.421291	-3.961467	1.786784	-2.174683	9150.960109
HLA A*3001	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.286751	2.111966	-2.174785	19353.098687
HLA A*0206	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.257427	2.082473	-2.174954	18089.501080

HLA A*0206	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.804803	1.629570	-2.175233	6379.740329
HLA A*0202	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.557012	1.381752	-2.175260	3605.887865
HLA A*0216	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.160069	1.984120	-2.175948	14456.682044
HLA B*4801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.284490	2.108491	-2.175999	19252.640732
HLA B*1503	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.472736	1.295300	-2.177437	2969.861456
HLA B*1517	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.136574	1.958921	-2.177653	13695.370301
HLA B*1502	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.159951	1.982154	-2.177797	14452.772121
HLA A*0203	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-3.552572	1.374504	-2.178068	3569.206624
HLA B*5101	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.438612	2.260158	-2.178454	27454.391588
HLA B*4403	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.475839	2.297367	-2.178473	29911.584104
HLA A*0301	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.366978	2.188431	-2.178547	23279.753401
HLA A*0211	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.094281	0.915104	-2.179177	1242.456366
HLA B*4001	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.080919	1.901679	-2.179240	12048.117064
HLA B*1503	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-3.464419	1.284024	-2.180395	2913.526771
HLA A*0250	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.539097	2.358631	-2.180466	34601.661075
HLA A*6802	1:421-429	9	DTLRHADSI	0.987060	0.113427	-3.281446	1.100487	-2.180959	1911.814803
HLA A*0301	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.345936	2.164911	-2.181025	22178.715394
HLA B*5801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.337441	2.155890	-2.181551	21749.067951
HLA A*2601	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.386037	2.204297	-2.181741	24324.134598
HLA B*5801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.346726	2.164911	-2.181815	22219.066812
HLA B*4501	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.091882	1.909820	-2.182062	12356.113121
HLA A*2603	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.578977	2.396811	-2.182166	37929.499003
HLA A*2402	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.541562	2.358631	-2.182931	34798.582826
HLA A*3301	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.443231	2.260158	-2.183073	27747.950516
HLA B*0702	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.564869	1.381752	-2.183117	3671.714417
HLA B*1509	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.477634	2.294422	-2.183212	30035.469168
HLA B*4002	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.093183	1.909820	-2.183363	12393.200913
HLA B*4801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.372326	2.188431	-2.183895	23568.166816
HLA A*0203	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.497129	1.313175	-2.183953	3141.438365
HLA A*3301	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.388396	2.204297	-2.184100	24456.611283
HLA B*3501	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.268761	2.084113	-2.184647	18567.802352
HLA B*4501	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.519018	2.334336	-2.184682	33038.342345
HLA A*0206	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-3.913189	1.728396	-2.184794	8188.218899
HLA A*0211	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-3.903340	1.718496	-2.184844	8004.614167
HLA A*3301	1:260-268	9	HGLLRAGER	1.105522	0.436138	-3.726626	1.541660	-2.184966	5328.760952
HLA A*6802	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-2.966380	0.781170	-2.185210	925.507370
HLA A*2902	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.211245	2.025736	-2.185509	16264.664591
HLA B*5401	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.537567	2.352019	-2.185549	34480.013972
HLA A*8001	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.342288	2.156591	-2.185697	21993.160201
HLA B*2705	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.374191	2.188431	-2.185760	23669.620483
HLA A*0202	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.539499	1.353717	-2.185782	3463.372114
HLA B*5701	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.044216	1.858036	-2.186180	11071.730958
HLA B*0803	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.298164	2.111966	-2.186199	19868.464713
HLA A*6802	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.268812	2.082473	-2.186340	18570.012378
HLA A*6802	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.270711	2.084113	-2.186597	18651.363109
HLA B*1501	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-2.959665	0.772641	-2.187024	911.307728
HLA B*5101	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.481969	2.294422	-2.187547	30336.761695
HLA B*1509	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.448064	2.260158	-2.187906	28058.458131
HLA B*1502	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.017690	1.828772	-2.188917	10415.732993
HLA A*2602	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.586324	2.396811	-2.189513	38576.599825
HLA A*2402	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.345415	2.155890	-2.189525	22152.094848
HLA A*2602	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.298728	2.108491	-2.190237	19894.278153
HLA B*1501	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.346503	2.155890	-2.190613	22207.650491
HLA B*5301	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.587510	2.396811	-2.190699	38682.134960
HLA B*4501	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.598330	2.407496	-2.190833	39657.909217
HLA B*4601	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.203962	2.013049	-2.190913	15994.170016
HLA B*1517	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.484117	1.293038	-2.191079	3048.716880
HLA B*4002	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.826916	1.635727	-2.191190	6712.995484
HLA B*5401	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.526149	2.334336	-2.191813	33585.277114
HLA A*2603	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.356746	2.164911	-2.191835	22737.691428
HLA A*3301	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-3.864522	1.672339	-2.192183	7320.187613
HLA A*3002	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.486739	2.294422	-2.192316	30671.758398
HLA A*6801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.151263	1.958921	-2.192342	14166.506317
HLA A*1101	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.444081	2.251319	-2.192763	27802.344789
HLA A*0211	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-2.483678	0.290570	-2.193108	304.563733

HLA A*2403	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.140671	1.947300	-2.193371	13825.195497
HLA A*0250	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.820596	1.627062	-2.193534	6616.011332
HLA A*3101	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.350323	2.156591	-2.193732	22403.861356
HLA A*6901	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.382405	2.188431	-2.193974	24121.543496
HLA A*6802	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.256964	1.062990	-2.193974	1807.025105
HLA A*2602	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.160576	1.966426	-2.194150	14473.585072
HLA B*0803	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.398499	2.204297	-2.194203	25032.202671
HLA A*2601	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.382870	2.188431	-2.194439	24147.395325
HLA B*3901	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.279277	2.084113	-2.195164	19022.903264
HLA B*1503	1:10-18	9	PETPARPVL	1.635476	0.153516	-3.984304	1.788992	-2.195311	9645.031634
HLA A*0301	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.307377	2.111966	-2.195411	20294.419815
HLA A*3201	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.213270	2.017754	-2.195517	16340.689124
HLA A*0203	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-2.727964	0.532233	-2.195730	534.519485
HLA A*2301	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.490486	2.294422	-2.196064	30937.563180
HLA B*1501	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-2.908545	0.712255	-2.196290	810.111801
HLA A*0101	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.385048	2.188431	-2.196617	24268.797882
HLA A*0250	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.593626	2.396811	-2.196815	39230.707941
HLA B*1801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.089465	0.892605	-2.196859	1228.753312
HLA A*0203	1:291-299	9	TFLEALSGV	0.900311	0.134202	-3.231406	1.034513	-2.196893	1703.752431
HLA B*1503	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.870481	1.673173	-2.197308	7421.308852
HLA B*4402	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.057485	1.859882	-2.197603	11415.249685
HLA A*6901	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.353523	2.155890	-2.197633	22569.548698
HLA A*0203	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-2.496784	0.299099	-2.197685	313.894434
HLA A*3101	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.309651	2.111966	-2.197685	20400.975840
HLA A*6801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-3.739398	1.541660	-2.197738	5487.797010
HLA A*3301	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.629197	2.431446	-2.197752	42579.185372
HLA B*1801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-3.916873	1.718496	-2.198377	8257.972586
HLA B*0803	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.355090	2.156591	-2.198499	22651.135679
HLA A*2402	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.493294	2.294422	-2.198872	31138.216776
HLA A*3001	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.226630	2.027725	-2.198904	16851.149807
HLA B*0801	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.060728	1.861603	-2.199124	11500.790822
HLA B*1509	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.364051	2.164911	-2.199140	23123.358757
HLA A*0203	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.387762	2.188431	-2.199331	24420.914320
HLA B*5301	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.505835	2.306412	-2.199424	32050.535397
HLA A*2301	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.450907	2.251319	-2.199588	28242.730301
HLA B*4501	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.551742	2.352019	-2.199723	35623.933889
HLA A*8001	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.404037	2.204297	-2.199740	25353.434688
HLA B*4501	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-2.950206	0.750232	-2.199974	891.673842
HLA B*0702	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.388570	2.188431	-2.200139	24466.404002
HLA A*1101	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.404951	2.204297	-2.200654	25406.845825
HLA A*2501	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.357587	2.156591	-2.200997	22781.771104
HLA A*1101	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.440299	1.239243	-2.201056	2756.126837
HLA A*3001	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.219125	2.017754	-2.201372	16562.476856
HLA A*6802	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.358459	2.156591	-2.201869	22827.541604
HLA B*4403	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.522070	2.320077	-2.201993	33271.335226
HLA B*5301	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.406290	2.204297	-2.201993	25485.312229
HLA B*1501	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-3.123683	0.921448	-2.202235	1329.482427
HLA A*3101	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.149703	1.947300	-2.202403	14115.709159
HLA A*2402	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.220262	2.017754	-2.202509	16605.900644
HLA B*3801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.463021	2.260158	-2.202862	29041.605622
HLA A*0101	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.359566	2.156591	-2.202975	22885.781667
HLA B*5801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.161901	1.958921	-2.202980	14517.813990
HLA A*3101	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.253545	2.050505	-2.203040	17928.553012
HLA A*2501	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.060314	1.856944	-2.203370	11489.845665
HLA A*6802	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.369029	2.164911	-2.204118	23389.959832
HLA B*2705	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.360947	2.156591	-2.204357	22958.697590
HLA B*4601	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.393093	2.188431	-2.204662	24722.529364
HLA B*0702	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.171482	1.966426	-2.205056	14841.658264
HLA B*5301	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.529779	2.324609	-2.205170	33867.168644
HLA B*0801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.218496	2.013049	-2.205447	16538.481143
HLA A*0216	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.028338	1.822872	-2.205465	10674.258213
HLA A*0301	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.362378	2.156591	-2.205788	23034.462571
HLA B*5701	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.394221	2.188431	-2.205789	24786.810938
HLA B*1517	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.701346	1.495512	-2.205834	5027.427074
HLA A*6801	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.466310	2.260158	-2.206152	29262.397301

HLA B*3801	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.500807	2.294422	-2.206385	31681.620745
HLA B*0802	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.224863	2.017754	-2.207109	16782.734601
HLA B*5801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.233859	2.025736	-2.208123	17134.005614
HLA B*0801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.109860	1.901679	-2.208181	12878.347360
HLA A*2602	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-3.841088	1.632644	-2.208444	6935.670438
HLA B*3901	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.468845	2.260158	-2.208687	29433.709337
HLA B*1503	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-3.964798	1.756081	-2.208717	9221.429109
HLA A*0206	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.563022	1.353717	-2.209305	3656.134800
HLA A*3201	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.119249	1.909820	-2.209429	13159.781454
HLA B*1801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.365578	2.155890	-2.209689	23204.813513
HLA A*0212	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.505084	1.295300	-2.209784	3199.513150
HLA B*4403	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.569004	2.358631	-2.210373	37068.374538
HLA A*2403	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.072165	1.861603	-2.210562	11807.691492
HLA B*0802	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.399070	2.188431	-2.210639	25065.131721
HLA B*4601	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.366797	2.155890	-2.210908	23270.057973
HLA B*3501	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.637562	1.426359	-2.211203	4340.721883
HLA B*0702	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.295352	2.084113	-2.211239	19740.219425
HLA B*0803	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.399808	2.188431	-2.211376	25107.746175
HLA B*4402	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.415686	2.204297	-2.211389	26042.672480
HLA A*0206	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.400026	2.188431	-2.211595	25120.381554
HLA A*0211	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-2.989800	0.778023	-2.211777	976.786273
HLA A*0301	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.367676	2.155890	-2.211787	23317.187910
HLA B*3501	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.848550	1.635727	-2.212824	7055.867439
HLA A*8001	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.377784	2.164911	-2.212872	23866.220960
HLA B*5401	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.538416	2.324609	-2.213807	34547.418202
HLA B*1509	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.296301	2.082473	-2.213829	19783.410736
HLA A*2601	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.379196	2.164911	-2.214284	23943.944523
HLA B*1509	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.169617	1.954913	-2.214704	14778.043359
HLA B*3901	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.403250	2.188431	-2.214818	25307.527944
HLA A*0101	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.379800	2.164911	-2.214888	23977.257937
HLA B*5101	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.297612	2.082473	-2.215140	19843.221507
HLA B*5801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.323854	2.108491	-2.215362	21079.173495
HLA A*3001	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.117472	1.901679	-2.215793	13106.069490
HLA A*0203	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.569596	1.353717	-2.215879	3711.898214
HLA B*0702	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.371948	2.155890	-2.216058	23547.648065
HLA A*0203	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.843142	1.627062	-2.216080	6968.541624
HLA A*3101	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.200381	1.984040	-2.216341	15862.845453
HLA B*4403	1:464-472	9	RTYGHPIVL	1.770618	0.581401	-4.568839	2.352019	-2.216820	37054.339690
HLA B*4601	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.182689	1.965836	-2.216854	15229.634159
HLA B*2705	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.230048	2.013049	-2.216999	16984.315168
HLA A*0202	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-3.966194	1.749103	-2.217091	9251.109596
HLA B*7301	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.245050	2.027725	-2.217324	17581.239977
HLA B*5401	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.512362	2.294422	-2.217940	32535.850065
HLA B*4001	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.373996	2.155890	-2.218107	23658.994717
HLA A*2402	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.222438	2.004292	-2.218146	16689.297572
HLA A*0211	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.406967	2.188431	-2.218535	25525.050520
HLA A*6801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.554912	1.336347	-2.218564	3588.490306
HLA A*0212	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.375603	2.156591	-2.219013	23746.703791
HLA A*8001	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.407446	2.188431	-2.219015	25553.235959
HLA B*4601	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.327975	2.108491	-2.219483	21280.144618
HLA A*3001	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.186181	1.966426	-2.219755	15352.560083
HLA B*0802	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.375951	2.155890	-2.220062	23765.724526
HLA A*8001	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.376087	2.155890	-2.220198	23773.182752
HLA A*0203	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.078466	1.858036	-2.220431	11980.262012
HLA B*3501	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.238466	2.017754	-2.220713	17316.744330
HLA B*4403	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.138308	1.917562	-2.220746	13750.158339
HLA A*0202	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.579816	2.358631	-2.221185	38002.824183
HLA B*3801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.304040	2.082473	-2.221568	20139.114513
HLA B*5101	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.425911	2.204297	-2.221614	26663.091798
HLA B*0702	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.743543	1.521566	-2.221976	5540.417983
HLA A*3001	1:487-495	9	RVPYEVLER	0.866973	0.808043	-3.897124	1.675016	-2.222107	7890.847785
HLA A*6802	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.249896	2.027725	-2.222171	17778.556222
HLA B*5801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.305170	2.082473	-2.222698	20191.587887
HLA A*2602	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.306839	2.084113	-2.222725	20269.293344
HLA A*6901	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.334701	2.111966	-2.222735	21612.308126

HLA B*1503	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.370040	1.147258	-2.222782	2344.445819
HLA A*2403	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.438664	1.215498	-2.223166	2745.768753
HLA B*7301	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.427738	2.204297	-2.223442	26775.550415
HLA B*5301	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.474843	2.251319	-2.223524	29843.051751
HLA A*0250	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.484053	2.260158	-2.223895	30482.684651
HLA B*1503	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.412389	2.188431	-2.223958	25845.754912
HLA B*5701	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.380697	2.156591	-2.224106	24026.860038
HLA A*3101	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-3.601591	1.377330	-2.224261	3995.685940
HLA A*0202	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.084302	1.859882	-2.224420	12142.341330
HLA A*2902	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.380493	2.155890	-2.224603	24015.554208
HLA B*5801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.207444	1.982154	-2.225289	16122.917992
HLA A*0219	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.413752	2.188431	-2.225321	25926.979424
HLA A*0216	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.413782	2.188431	-2.225351	25928.802895
HLA B*4501	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.619992	2.394415	-2.225577	41686.176786
HLA B*2705	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.253383	2.027725	-2.225658	17921.861848
HLA B*1503	1:480-488	9	AMTADWTRV	0.947260	0.174566	-3.347546	1.121826	-2.225720	2226.108004
HLA B*7301	1:191-199	9	VLSRFLHDF	1.282229	1.112186	-4.620145	2.394415	-2.225730	41700.838008
HLA A*0101	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.381696	2.155890	-2.225806	24082.166219
HLA B*1503	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.654647	1.428368	-2.226280	4514.892516
HLA A*0250	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.414741	2.188431	-2.226310	25986.097058
HLA B*4403	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.221644	1.995235	-2.226409	16658.808366
HLA B*1517	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.170245	0.943730	-2.226515	1479.941998
HLA A*2301	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-3.951646	1.725080	-2.226565	8946.348561
HLA A*3301	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.634087	2.407496	-2.226590	43061.249401
HLA A*0216	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.324944	2.097879	-2.227065	21132.152661
HLA A*0202	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.547221	2.320077	-2.227144	35255.060721
HLA B*0801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-3.999524	1.772257	-2.227267	9989.036964
HLA B*0702	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.175035	1.947300	-2.227735	14963.557225
HLA A*0212	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.416515	2.188431	-2.228084	26092.453452
HLA A*2403	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.384160	2.155890	-2.228271	24219.220401
HLA A*0202	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-3.855777	1.627062	-2.228716	7174.265238
HLA B*1503	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-3.344492	1.115576	-2.228916	2210.507031
HLA B*0801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.394190	2.164911	-2.229279	24785.067778
HLA B*1517	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.417831	2.188431	-2.229399	26171.621390
HLA A*0202	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.247159	2.017754	-2.229406	17666.858858
HLA B*5401	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.536275	2.306412	-2.229864	34377.573272
HLA B*4501	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.626831	2.396811	-2.230020	42347.854947
HLA A*8001	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.281051	2.050505	-2.230546	19100.760566
HLA A*0203	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.140732	1.909820	-2.230912	13827.140246
HLA A*6801	1:55-63	9	ARQPVALVL	1.819352	0.612094	-4.662508	2.431446	-2.231063	45973.582398
HLA B*4501	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.589785	2.358631	-2.231154	38885.235841
HLA A*2603	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.343862	2.111966	-2.231896	22073.021822
HLA A*0203	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.314583	2.082473	-2.232110	20633.956496
HLA A*3002	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.420629	2.188431	-2.232198	26340.794224
HLA B*1509	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.420770	2.188431	-2.232339	26349.345659
HLA A*0201	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.389517	2.156591	-2.232926	24519.803487
HLA B*0803	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.389118	2.155890	-2.233228	24497.263452
HLA A*3101	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.389122	2.155890	-2.233233	24497.528508
HLA B*1503	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.258980	2.025736	-2.233243	18154.303787
HLA A*3101	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.342269	2.108491	-2.233777	21992.208378
HLA A*0202	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.012308	0.778023	-2.234285	1028.744708
HLA B*3501	1:75-83	9	APKLDPALL	1.420023	0.333020	-3.987419	1.753043	-2.234376	9714.469151
HLA B*5701	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.316951	2.082473	-2.234478	20746.784288
HLA A*0219	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.391716	2.156591	-2.235126	24644.278225
HLA A*3001	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.248388	2.013049	-2.235340	17716.915756
HLA A*2603	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-3.847860	1.612498	-2.235361	7044.653949
HLA A*2501	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.344264	2.108491	-2.235772	22093.450825
HLA B*4002	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.570199	2.334336	-2.235863	37170.587923
HLA A*2602	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.248921	2.013049	-2.235873	17738.686288
HLA A*6901	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.374814	1.138932	-2.235882	2370.360241
HLA B*4801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.391772	2.155890	-2.235883	24647.478180
HLA B*5701	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.400947	2.164911	-2.236036	25173.710285
HLA B*3501	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.065084	1.828772	-2.236311	11616.723427
HLA A*0101	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.286840	2.050505	-2.236335	19357.077625
HLA B*1509	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.094415	1.858036	-2.236379	12428.382778

HLA A*3001	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.098122	1.861603	-2.236519	12534.935622
HLA A*3201	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.425001	2.188431	-2.236570	26607.327621
HLA A*0206	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.023408	1.786784	-2.236625	10553.790886
HLA A*0206	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-3.136812	0.900138	-2.236674	1370.286955
HLA A*3301	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.633518	2.396811	-2.236707	43004.910795
HLA B*4601	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.401894	2.164911	-2.236983	25228.653510
HLA A*2602	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.488419	2.251319	-2.237100	30790.628680
HLA A*2403	1:114-122	9	EYGRTELKV	1.003669	0.148169	-3.389142	1.151838	-2.237303	2449.861392
HLA A*1101	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-3.916140	1.678625	-2.237516	8244.045831
HLA B*0702	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.161803	1.924123	-2.237680	14514.515695
HLA B*1501	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.192604	1.954913	-2.237691	15581.321821
HLA A*2601	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.877200	1.639403	-2.237797	7537.026341
HLA A*2601	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.875673	1.637421	-2.238252	7510.569475
HLA B*7301	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.597223	2.358631	-2.238593	39556.987205
HLA A*3001	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-3.057770	0.819048	-2.238722	1142.273624
HLA A*0201	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.394705	2.155890	-2.238815	24814.449679
HLA A*6901	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.876570	1.637421	-2.239149	7526.106699
HLA B*4403	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.546547	2.306412	-2.240135	35200.364840
HLA A*2602	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.565122	2.324609	-2.240513	36738.565371
HLA A*2403	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.338942	2.097879	-2.241063	21824.382824
HLA A*2402	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.013395	1.772257	-2.241138	10313.236564
HLA A*6901	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.146562	0.905240	-2.241322	1401.399267
HLA A*0202	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.332843	1.091476	-2.241367	2152.004395
HLA B*1509	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.325580	2.084113	-2.241467	21163.156808
HLA B*4801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.324479	2.082473	-2.242006	21109.528904
HLA A*2603	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.099034	1.856944	-2.242090	12561.274549
HLA B*3801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.354150	2.111966	-2.242184	22602.172622
HLA A*0301	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.326645	2.084113	-2.242532	21215.084532
HLA B*1503	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.102751	1.859882	-2.242868	12669.240875
HLA B*1502	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.152968	1.909820	-2.243148	14222.255805
HLA B*0801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.101383	1.858036	-2.243347	12629.413799
HLA A*3201	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.352120	2.108491	-2.243629	22496.773325
HLA A*6901	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.326149	2.082473	-2.243676	21190.881613
HLA B*5701	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.161417	1.917562	-2.243855	14501.643811
HLA B*4001	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.483624	1.239243	-2.244381	3045.255270
HLA A*6802	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.432957	2.188431	-2.244525	27099.208938
HLA B*4001	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.880320	1.635727	-2.244593	7591.369823
HLA A*0212	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.146409	1.901679	-2.244730	14009.051234
HLA B*1503	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.073711	1.828772	-2.244939	11849.798315
HLA B*1503	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.534537	1.289353	-2.245184	3424.025918
HLA B*2705	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.159791	1.914570	-2.245221	14447.456322
HLA A*3301	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.579607	2.334336	-2.245271	37984.530983
HLA B*5801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.343592	2.097879	-2.245712	22059.293644
HLA B*0803	1:75-83	9	APKLDPALL	1.420023	0.333020	-3.998795	1.753043	-2.245752	9972.298733
HLA B*1509	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.839181	1.593295	-2.245886	6905.270037
HLA A*0216	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.273636	2.027725	-2.245911	18777.409864
HLA B*0801	1:31-39	9	ARRVREARV	0.936445	0.312607	-3.495005	1.249052	-2.245953	3126.112542
HLA A*0101	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.205094	1.958921	-2.246173	16035.930302
HLA B*3801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.264407	2.017754	-2.246653	18382.598801
HLA A*0202	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.212866	1.965836	-2.247031	16325.491170
HLA A*0250	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.567204	2.320077	-2.247127	36915.081957
HLA B*3501	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.583557	1.336347	-2.247209	3833.157802
HLA A*0101	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.330277	2.082473	-2.247805	21393.264977
HLA B*1501	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.214506	1.966426	-2.248080	16387.254439
HLA B*5701	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.404300	2.155890	-2.248410	25368.801181
HLA A*0203	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.405221	2.156591	-2.248630	25422.657289
HLA A*2601	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.360757	2.111966	-2.248791	22948.639269
HLA B*5401	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.568942	2.320077	-2.248865	37063.160974
HLA B*5701	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.361892	2.111966	-2.249926	23008.681934
HLA B*3801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.406985	2.156591	-2.250395	25526.155245
HLA A*0211	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.108629	1.858036	-2.250593	12841.891750
HLA B*4001	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.362667	2.111966	-2.250701	23049.795180
HLA A*8001	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.359364	2.108491	-2.250872	22875.136523
HLA A*0212	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.333858	2.082473	-2.251385	21570.374511
HLA B*0702	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.360073	2.108491	-2.251582	22912.540159

HLA A*0203	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.217598	1.965836	-2.251762	16504.338379
HLA A*0206	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.773536	1.521566	-2.251970	5936.576325
HLA A*2501	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.416893	2.164911	-2.251982	26115.189674
HLA B*1502	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.546655	2.294422	-2.252233	35209.125713
HLA A*0216	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.391787	1.139224	-2.252563	2464.830354
HLA A*0202	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.185568	0.932998	-2.252570	1533.091360
HLA B*4801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.200719	1.947300	-2.253420	15875.207806
HLA A*3301	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.559998	2.306412	-2.253586	36307.635470
HLA A*3001	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.212580	1.958921	-2.253658	16314.719795
HLA A*2301	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.033220	1.779355	-2.253865	10794.932576
HLA B*0802	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.419064	2.164911	-2.254153	26246.059473
HLA B*0702	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.155882	1.901679	-2.254203	14317.983154
HLA A*0301	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.362716	2.108491	-2.254225	23052.413962
HLA B*5401	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.505723	2.251319	-2.254404	32042.213765
HLA B*1517	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.352414	2.097879	-2.254535	22511.991601
HLA B*1503	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-3.976268	1.721649	-2.254619	9468.221683
HLA B*2705	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.367025	2.111966	-2.255060	23282.272355
HLA A*8001	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.339306	2.084113	-2.255193	21842.690960
HLA A*3001	1:241-249	9	AAALVQRAI	1.328858	0.344315	-3.929377	1.673173	-2.256205	8499.187220
HLA A*0250	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-2.923107	0.666703	-2.256404	837.735783
HLA A*2403	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.240905	1.984120	-2.256785	17414.259441
HLA A*0216	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.172049	0.915104	-2.256945	1486.103645
HLA B*4601	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.223542	1.966426	-2.257116	16731.786574
HLA B*1503	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.044319	1.786784	-2.257535	11074.366733
HLA A*3002	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.606596	1.348830	-2.257766	4041.994781
HLA B*1509	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.172681	1.914570	-2.258111	14882.663586
HLA B*0801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.045733	1.787266	-2.258467	11110.492006
HLA A*6802	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.414619	2.155890	-2.258729	25978.787827
HLA A*0206	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.116796	1.858036	-2.258760	13085.665503
HLA A*6801	1:14-22	9	ARPVLVVDF	1.224972	1.182524	-4.666359	2.407496	-2.258863	46383.033922
HLA A*3001	1:31-39	9	ARRVREARV	0.936445	0.312607	-3.508030	1.249052	-2.258978	3221.292442
HLA A*2601	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.213900	1.954913	-2.258987	16364.397860
HLA A*0201	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-2.903818	0.644580	-2.259237	801.341795
HLA B*1503	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.895249	1.635727	-2.259522	7856.855699
HLA B*1501	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.368442	2.108491	-2.259951	23358.346943
HLA B*4002	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.580568	2.320077	-2.260490	38068.670303
HLA B*5301	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.720245	1.459325	-2.260920	5251.036499
HLA A*2403	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.256238	1.995235	-2.261002	18040.050523
HLA B*3501	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.118102	1.856944	-2.261158	13125.085110
HLA B*5401	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.558558	2.297367	-2.261191	36187.429264
HLA B*3901	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.176139	1.914570	-2.261569	15001.652694
HLA B*1502	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.370317	2.108491	-2.261826	23459.405046
HLA A*0101	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.034103	1.772257	-2.261847	10816.913094
HLA A*0212	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.360433	2.097879	-2.262554	22931.513019
HLA A*1101	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.451139	2.188431	-2.262708	28257.860567
HLA B*0802	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.346944	2.084113	-2.262831	22230.248475
HLA B*4402	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.051828	1.788992	-2.262836	11267.507487
HLA B*5701	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.245158	1.982154	-2.263003	17585.615699
HLA B*1509	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.419666	2.156591	-2.263075	26282.433653
HLA A*0206	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.289333	2.025736	-2.263596	19468.504651
HLA A*1101	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.428631	2.164911	-2.263720	26830.651081
HLA A*0219	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.420535	2.155890	-2.264645	26335.094810
HLA A*6802	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.373411	2.108491	-2.264920	23627.146031
HLA B*4002	1:482-490	9	TADWTRVPY	1.136050	1.222581	-4.623711	2.358631	-2.265081	42044.704136
HLA B*0803	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.260516	1.995235	-2.265281	18218.648701
HLA A*0202	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-2.938383	0.673013	-2.265370	867.727613
HLA A*0211	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.122378	1.856944	-2.265434	13254.952965
HLA B*0803	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.430560	2.164911	-2.265649	26950.084965
HLA B*3501	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.316422	2.050505	-2.265917	20721.546145
HLA B*2705	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.374555	2.108491	-2.266064	23689.476561
HLA A*2601	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.374659	2.108491	-2.266167	23695.116159
HLA B*3801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.249530	1.982154	-2.267376	17763.558469
HLA B*1801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.376019	2.108491	-2.267528	23769.453347
HLA A*2902	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.433130	2.164911	-2.268219	27110.059785
HLA A*2902	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.170012	1.901679	-2.268332	14791.480657

HLA B*5401	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.528517	2.260158	-2.268359	33768.923553
HLA A*0216	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.224383	1.954913	-2.269470	16764.223100
HLA A*0301	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-3.626111	1.356576	-2.269534	4227.762389
HLA A*2601	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.320360	2.050505	-2.269855	20910.282209
HLA B*1801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.127077	1.856944	-2.270133	13399.147286
HLA A*0250	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.576599	2.306412	-2.270188	37722.409690
HLA A*6802	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.382424	2.111966	-2.270458	24122.587478
HLA A*3301	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-3.774123	1.503120	-2.271003	5944.610812
HLA A*0250	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.430591	1.159455	-2.271136	2695.200807
HLA A*2403	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.299085	2.027725	-2.271360	19910.644009
HLA B*4403	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.060460	1.788992	-2.271468	11493.700157
HLA B*1801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.460018	2.188431	-2.271587	28841.509170
HLA A*0201	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.049758	0.778023	-2.271736	1121.394457
HLA B*0801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.254591	1.982154	-2.272436	17971.766217
HLA A*1101	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.429202	2.156591	-2.272612	26865.945932
HLA B*4801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.384745	2.111966	-2.272779	24251.867186
HLA A*6801	1:305-313	9	KRKIIGRQF	1.175348	1.221463	-4.669728	2.396811	-2.272917	46744.262698
HLA B*1503	1:31-39	9	ARRVREARV	0.936445	0.312607	-3.522057	1.249052	-2.273005	3327.028944
HLA A*0101	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.370916	2.097879	-2.273037	23491.790138
HLA B*3801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.197275	1.924123	-2.273152	15749.801111
HLA A*2601	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.286212	2.013049	-2.273164	19329.137664
HLA B*4002	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.597801	2.324609	-2.273192	39609.665983
HLA A*2403	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-2.719872	0.446544	-2.273328	524.652703
HLA A*0211	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.655456	1.381752	-2.273704	4523.302563
HLA A*0202	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.178994	0.905240	-2.273754	1510.059907
HLA B*4801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.324751	2.050505	-2.274246	21122.780286
HLA A*2603	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.569025	2.294422	-2.274602	37070.179404
HLA A*0206	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.588030	1.313175	-2.274855	3872.845019
HLA A*1101	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.234028	1.958921	-2.275107	17140.680815
HLA A*6901	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.259306	1.984120	-2.275186	18167.960497
HLA A*6901	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.701614	1.426359	-2.275255	5030.528582
HLA B*1517	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.588533	1.313175	-2.275357	3877.331271
HLA A*3201	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.431378	2.155890	-2.275488	27000.870101
HLA A*0203	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.431415	2.155890	-2.275526	27003.207350
HLA A*0206	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.059622	0.783681	-2.275941	1147.153523
HLA A*2301	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.230971	1.954913	-2.276058	17020.463704
HLA A*2602	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.596549	2.320077	-2.276472	39495.617171
HLA A*2602	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.048914	1.772257	-2.276658	11192.175046
HLA B*1517	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.063547	1.786784	-2.276764	11575.695298
HLA A*3101	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.081596	1.804702	-2.276894	12066.903240
HLA B*1503	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.689753	1.412655	-2.277099	4895.008166
HLA B*0702	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-3.371492	1.094025	-2.277467	2352.297149
HLA B*3501	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.068697	1.791215	-2.277482	11713.782549
HLA B*1501	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.170942	1.893265	-2.277677	14823.202651
HLA B*4403	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.538239	2.260158	-2.278081	34533.403718
HLA A*0250	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.614476	1.336347	-2.278129	4116.005261
HLA A*2601	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.135230	1.856944	-2.278286	13653.056075
HLA A*0203	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.283964	1.005151	-2.278814	1922.934397
HLA A*0301	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.361300	2.082473	-2.278827	22977.335752
HLA B*1509	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.292605	2.013049	-2.279557	19615.773035
HLA A*0211	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.297321	2.017754	-2.279567	19829.914617
HLA B*3901	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.330080	2.050505	-2.279575	21383.545429
HLA B*3901	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.391676	2.111966	-2.279710	24642.011841
HLA A*3002	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.307569	2.027725	-2.279844	20303.424639
HLA B*5101	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.388389	2.108491	-2.279898	24456.214364
HLA A*6801	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.604758	2.324609	-2.280149	40249.269745
HLA A*2603	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.600228	2.320077	-2.280151	39831.640920
HLA A*0202	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.362926	2.082473	-2.280453	23063.515914
HLA A*0206	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.246304	1.965836	-2.280468	17632.103518
HLA B*0801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.389111	2.108491	-2.280619	24496.865873
HLA B*0803	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.363222	2.082473	-2.280749	23079.242428
HLA A*0211	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.190678	1.909820	-2.280858	15512.354464
HLA A*1101	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.393159	2.111966	-2.281193	24726.274539
HLA A*0250	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.183070	1.901679	-2.281391	15242.987292
HLA A*0201	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.264285	1.982154	-2.282130	18377.428241

HLA B*1501	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.038412	1.756081	-2.282331	10924.769836
HLA A*6802	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.300401	2.017754	-2.282647	19971.055523
HLA A*3101	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-3.958666	1.675762	-2.282904	9092.139198
HLA A*0301	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.238182	1.954913	-2.283269	17305.412558
HLA A*0212	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.439319	2.155890	-2.283430	27499.134096
HLA A*0212	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.267708	1.984120	-2.283588	18522.855353
HLA A*2501	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.296715	2.013049	-2.283666	19802.256293
HLA B*1509	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.396876	2.111966	-2.284910	24938.801142
HLA A*0206	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.667010	1.381752	-2.285259	4645.264053
HLA A*2402	1:25-33	9	QYAQLIARR	0.855428	0.838712	-3.979854	1.694140	-2.285714	9546.710034
HLA A*3002	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.368487	2.082473	-2.286014	23360.748021
HLA B*4001	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.196279	1.909820	-2.286459	15713.715730
HLA B*3801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.370705	2.084113	-2.286592	23480.355004
HLA A*6802	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.219636	0.932998	-2.286638	1658.194875
HLA B*5401	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.490994	2.204297	-2.286697	30973.735968
HLA A*3002	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.442683	2.155890	-2.286794	27712.996143
HLA A*0202	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.115908	1.828772	-2.287135	13058.933469
HLA B*1503	1:77-85	9	KLDPALLDL	1.284905	0.332102	-3.904308	1.617007	-2.287302	8022.475344
HLA B*7301	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.611997	2.324609	-2.287388	40925.761454
HLA B*3801	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.074933	1.786784	-2.288149	11883.180416
HLA B*0801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.212551	1.924123	-2.288428	16313.660699
HLA B*0803	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.397059	2.108491	-2.288567	24949.326822
HLA B*0801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.316963	2.027725	-2.289237	20747.345484
HLA B*4002	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.478168	2.188431	-2.289737	30072.376728
HLA A*2501	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.401723	2.111966	-2.289757	25218.692129
HLA B*3901	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.244784	1.954913	-2.289871	17570.495542
HLA B*7301	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.610218	2.320077	-2.290141	40758.501475
HLA A*3002	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.204737	1.914570	-2.290167	16022.749326
HLA A*2301	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.843574	1.553110	-2.290465	6975.481700
HLA A*0211	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.438175	1.147258	-2.290917	2742.680795
HLA A*0301	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.341705	2.050505	-2.291200	21963.672808
HLA B*4001	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.389155	2.097879	-2.291276	24499.383983
HLA A*0201	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.389381	2.097879	-2.291502	24512.111027
HLA B*4801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.389430	2.097879	-2.291551	24514.895949
HLA B*7301	1:158-166	9	SAGAPVAAF	1.236468	1.097868	-4.625976	2.334336	-2.291640	42264.545619
HLA A*0203	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.120499	1.828772	-2.291726	13197.710663
HLA A*6802	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.276568	1.984120	-2.292447	18904.615262
HLA A*0206	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-2.965647	0.673013	-2.292634	923.946537
HLA A*0201	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.375385	2.082473	-2.292912	23734.759362
HLA A*0212	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.259395	1.966426	-2.292969	18171.695773
HLA B*0803	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.390953	2.097879	-2.293073	24600.986380
HLA B*4402	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.377290	2.084113	-2.293177	23839.122497
HLA A*0219	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.375676	2.082473	-2.293204	23750.686603
HLA A*3101	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.275407	1.982154	-2.293253	18854.160406
HLA B*5301	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.588081	2.294422	-2.293659	38733.020053
HLA A*2902	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.392311	2.097879	-2.294431	24678.031991
HLA B*1501	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.312221	2.017754	-2.294468	20522.075363
HLA B*4801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.196580	1.901679	-2.294900	15724.600709
HLA A*2301	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.450836	2.155890	-2.294947	28238.146972
HLA A*2603	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.546308	2.251319	-2.294989	35180.946331
HLA A*0219	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.392907	2.097879	-2.295028	24711.965676
HLA A*8001	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.392950	2.097879	-2.295070	24714.372195
HLA B*3801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.345732	2.050505	-2.295227	22168.279208
HLA B*3501	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.323043	2.027725	-2.295318	21039.867769
HLA B*1801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.308530	2.013049	-2.295482	20348.398640
HLA B*5101	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.346005	2.050505	-2.295499	22182.195214
HLA B*1801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.378084	2.082473	-2.295612	23882.753225
HLA A*0211	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.197477	1.901679	-2.295798	15757.130418
HLA B*4402	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.407951	2.111966	-2.295985	25582.974889
HLA B*4402	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.404977	2.108491	-2.296485	25408.357801
HLA B*1502	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.566330	1.269596	-2.296735	3684.090367
HLA A*0203	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.314547	2.017754	-2.296794	20632.282153
HLA B*5701	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.394726	2.097879	-2.296847	24815.657899
HLA B*4601	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.381002	2.084113	-2.296889	24043.763725
HLA B*3501	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.198736	1.901679	-2.297057	15802.887688

HLA B*1517	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.154171	1.856944	-2.297227	14261.704117
HLA B*7301	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.462154	2.164911	-2.297242	28983.689170
HLA A*2602	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.462384	2.164911	-2.297473	28999.059501
HLA A*0202	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.323229	2.025736	-2.297492	21048.861736
HLA B*7301	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.604408	2.306412	-2.297996	40216.838948
HLA B*4001	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.348514	2.050505	-2.298009	22310.729613
HLA A*3001	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.247810	1.949733	-2.298077	17693.353187
HLA B*5101	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.486621	2.188431	-2.298190	30663.462980
HLA A*2402	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.324107	2.025736	-2.298371	21091.492980
HLA A*6901	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.531027	1.232655	-2.298372	3396.463195
HLA A*3201	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.928893	1.629570	-2.299324	8489.720686
HLA A*3101	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-3.908467	1.608922	-2.299545	8099.663555
HLA A*0101	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.408285	2.108491	-2.299793	25602.635389
HLA A*0212	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.254722	1.954913	-2.299809	17977.211657
HLA A*0301	1:491-499	9	EVLERISTR	1.036599	0.600822	-3.937337	1.637421	-2.299917	8656.402687
HLA B*4002	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.597315	2.297367	-2.299948	39565.334043
HLA A*3002	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.456604	2.156591	-2.300014	28615.687207
HLA A*2601	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.398043	2.097879	-2.300164	25005.944693
HLA A*0101	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.384900	2.084113	-2.300787	24260.527926
HLA B*5801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.255796	1.954913	-2.300883	18021.712052
HLA A*2601	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.385069	2.084113	-2.300956	24269.979534
HLA B*5701	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.409459	2.108491	-2.300968	25671.982847
HLA A*0201	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.326720	2.025736	-2.300984	21218.757530
HLA B*5101	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.466244	2.164911	-2.301333	29257.965060
HLA A*0203	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.650296	1.348830	-2.301466	4469.883144
HLA A*6901	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.329210	2.027725	-2.301485	21340.785673
HLA A*0211	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.931107	1.629570	-2.301537	8533.095712
HLA B*4801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.268298	1.966426	-2.301871	18548.024292
HLA A*3101	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.329678	2.027725	-2.301953	21363.772850
HLA A*3001	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.023996	1.721649	-2.302347	10568.074252
HLA B*1501	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.328127	2.025736	-2.302391	21287.628944
HLA B*4801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.058792	1.756081	-2.302710	11449.637287
HLA B*4601	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.400701	2.097879	-2.302821	25159.414712
HLA A*0219	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.298423	1.995235	-2.303187	19880.291713
HLA A*0202	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.566584	1.263068	-2.303516	3686.243492
HLA A*6901	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.402244	2.097879	-2.304365	25248.997857
HLA A*0216	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.461322	2.156591	-2.304731	28928.235601
HLA B*1509	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.300284	1.995235	-2.305048	19965.654194
HLA B*4501	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.544410	1.239243	-2.305167	3502.753530
HLA B*1502	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.594994	1.289353	-2.305641	3935.446307
HLA B*1509	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.271740	1.965836	-2.305904	18695.610502
HLA A*0202	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-2.605123	0.299099	-2.306024	402.831170
HLA A*2301	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-3.928748	1.622722	-2.306026	8486.873600
HLA B*0802	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.414851	2.108491	-2.306360	25992.705247
HLA A*2501	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.168259	1.861603	-2.306656	14731.905831
HLA B*0801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.332678	2.025736	-2.306942	21511.873930
HLA A*2501	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.495563	2.188431	-2.307132	31301.369574
HLA A*2902	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.320247	2.013049	-2.307199	20904.853043
HLA B*0801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.936990	1.629570	-2.307420	8649.474595
HLA A*0101	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.273998	1.966426	-2.307571	18793.060273
HLA B*0802	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.335578	2.027725	-2.307852	21655.963388
HLA A*0216	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.390525	2.082473	-2.308052	24576.776174
HLA A*2301	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.169805	1.861603	-2.308202	14784.440549
HLA B*5301	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-3.400179	1.091915	-2.308265	2512.924231
HLA B*1801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.473295	2.164911	-2.308384	29736.847210
HLA A*0203	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.937977	1.629570	-2.308407	8669.149872
HLA B*0803	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.392595	2.084113	-2.308482	24694.191435
HLA A*2601	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.255810	1.947300	-2.308510	18022.297034
HLA B*0702	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.336928	2.027725	-2.309203	21723.433180
HLA B*1503	1:207-215	9	TPANIANAL	1.335334	0.257961	-3.902513	1.593295	-2.309219	7989.385637
HLA A*3301	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.264224	1.954913	-2.309311	18374.843507
HLA B*4501	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.604119	2.294422	-2.309697	40190.086907
HLA B*4601	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.327603	2.017754	-2.309850	21261.962921
HLA B*1801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.422001	2.111966	-2.310035	26424.146279
HLA A*0301	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.257467	1.947300	-2.310167	18091.164814

HLA B*1509	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.269745	1.958921	-2.310824	18609.938536
HLA B*0702	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.408785	2.097879	-2.310906	25632.154474
HLA A*0206	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.026827	0.715584	-2.311244	1063.720261
HLA A*3001	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.606568	1.295300	-2.311268	4041.732389
HLA B*7301	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.571952	2.260158	-2.311794	37320.903254
HLA B*4403	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.636413	2.324609	-2.311804	43292.495120
HLA B*7301	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.606527	2.294422	-2.312105	40413.565457
HLA B*5101	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.468213	2.155890	-2.312323	29390.906784
HLA A*0203	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.410742	2.097879	-2.312863	25747.924840
HLA B*4002	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.214708	1.901679	-2.313029	16394.880390
HLA B*5701	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.397155	2.084113	-2.313042	24954.861333
HLA A*2603	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.866463	1.553110	-2.313353	7352.971567
HLA B*3501	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.026858	1.713482	-2.313376	10637.939810
HLA A*3101	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.297652	1.984120	-2.313532	19845.046535
HLA A*6801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.364244	2.050505	-2.313739	23133.618807
HLA B*0801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.309019	1.995235	-2.313784	20371.308704
HLA A*2403	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.318243	2.004292	-2.313951	20808.607008
HLA A*3101	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.327432	2.013049	-2.314383	21253.567764
HLA A*2601	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.396899	2.082473	-2.314427	24940.150340
HLA A*0201	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.261780	1.947300	-2.314480	18271.751690
HLA A*0211	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.397059	2.082473	-2.314586	24949.326822
HLA B*5801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.342328	2.027725	-2.314603	21995.182964
HLA A*3201	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-3.654549	1.339557	-2.314992	4513.866780
HLA B*5701	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.340901	2.025736	-2.315165	21923.073584
HLA A*0216	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.471307	2.155890	-2.315418	29601.059584
HLA B*4403	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.503890	2.188431	-2.315459	31907.289672
HLA B*4501	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.612901	2.297367	-2.315535	41011.090761
HLA B*1503	1:263-271	9	LRAGERAQV	0.865849	0.254971	-3.436394	1.120820	-2.315574	2731.456924
HLA B*1503	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-3.688715	1.372792	-2.315923	4883.317347
HLA A*0201	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.225817	1.909820	-2.315997	16819.636963
HLA A*0206	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.603847	1.287816	-2.316030	4016.491489
HLA B*1517	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.471930	2.155890	-2.316040	29643.526707
HLA B*0802	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.413989	2.097879	-2.316110	25941.149765
HLA B*5801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.775773	1.459325	-2.316447	5967.229835
HLA B*4501	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.623159	2.306412	-2.316747	41991.285660
HLA B*5801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.174931	1.858036	-2.316896	14959.995797
HLA B*4601	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.344741	2.027725	-2.317015	22117.727346
HLA A*0201	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.344905	2.027725	-2.317180	22126.104744
HLA A*3301	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.637463	2.320077	-2.317386	43397.312602
HLA A*3301	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.122350	1.804702	-2.317648	13254.092499
HLA A*6801	1:309-317	9	IGRQFIRAF	1.287673	1.018739	-4.624278	2.306412	-2.317866	42099.557069
HLA B*4501	1:443-451	9	IWQCPVVLL	1.826862	0.497747	-4.642627	2.324609	-2.318018	43916.427548
HLA B*4501	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.506752	2.188431	-2.318320	32118.228822
HLA B*0702	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.233267	1.914570	-2.318697	17110.662875
HLA A*0203	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.220413	1.901679	-2.318734	16611.651149
HLA A*3201	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.401450	2.082473	-2.318977	25202.871176
HLA B*2705	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-3.282108	0.962750	-2.319358	1914.733672
HLA A*2501	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.148185	1.828772	-2.319413	14066.463844
HLA A*1101	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.402047	2.082473	-2.319574	25237.526544
HLA B*4801	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.181181	1.861603	-2.319578	15176.831122
HLA A*2403	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.286140	1.966426	-2.319713	19325.896312
HLA B*2705	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.370298	2.050505	-2.319793	23458.389766
HLA B*4002	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.476509	2.156591	-2.319918	29957.737906
HLA B*1501	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.589745	1.269596	-2.320150	3888.169973
HLA B*4501	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.476854	2.156591	-2.320264	29981.571384
HLA A*3301	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.016134	1.695841	-2.320293	10378.497360
HLA A*8001	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.304712	1.984120	-2.320592	20170.298439
HLA A*8001	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.275555	1.954913	-2.320642	18860.587433
HLA A*2301	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.485609	2.164911	-2.320697	30592.049430
HLA B*5101	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.816612	1.495512	-2.321100	6555.585921
HLA A*8001	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.403590	2.082473	-2.321118	25327.387816
HLA A*8001	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.280520	1.958921	-2.321599	19077.421579
HLA A*2402	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.178822	1.856944	-2.321878	15094.621194
HLA A*6802	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-3.351009	1.028966	-2.322043	2243.930347
HLA A*2603	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.035790	1.713482	-2.322309	10859.010941

HLA B*1502	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.277334	1.954913	-2.322421	18937.985310
HLA A*0219	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.304628	1.982154	-2.322473	20166.370535
HLA A*0203	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.348495	2.025736	-2.322759	22309.764045
HLA A*2402	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.277787	1.954913	-2.322874	18957.768949
HLA B*0801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.277884	1.954913	-2.322970	18961.974352
HLA A*0301	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.048604	1.725080	-2.323524	11184.185507
HLA A*3301	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.621186	2.297367	-2.323819	41800.897291
HLA A*0206	1:428-436	9	SIVREELTA	1.468906	-0.179470	-3.613301	1.289436	-2.323865	4104.886739
HLA B*3901	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.337065	2.013049	-2.324016	21730.250489
HLA B*0803	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.374610	2.050505	-2.324104	23692.424365
HLA B*2705	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.271437	1.947300	-2.324137	18682.567842
HLA A*0211	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.107950	0.783681	-2.324270	1282.184285
HLA A*0202	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.481091	2.156591	-2.324500	30275.443423
HLA B*0802	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.308627	1.984120	-2.324506	20352.912526
HLA A*0250	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.422419	2.097879	-2.324540	26449.603937
HLA B*4001	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.342382	2.017754	-2.324628	21997.919939
HLA A*6801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-3.681262	1.356576	-2.324686	4800.233703
HLA A*6901	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.272062	1.947300	-2.324762	18709.471980
HLA A*3002	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.422675	2.097879	-2.324796	26465.205284
HLA B*5801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.343180	2.017754	-2.325427	22038.419319
HLA B*4501	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.645841	2.320077	-2.325764	44242.646739
HLA A*0212	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.273067	1.947300	-2.325767	18752.842692
HLA A*3301	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-3.720818	1.394918	-2.325900	5257.972512
HLA A*0250	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-3.457051	1.131046	-2.326005	2864.514520
HLA A*0202	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.339151	2.013049	-2.326102	21834.893361
HLA A*0211	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.149035	1.822872	-2.326163	14094.038315
HLA A*2603	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-3.107424	0.781170	-2.326255	1280.631455
HLA A*6901	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.339774	2.013049	-2.326725	21866.218764
HLA A*6802	1:46-54	9	HTASIEEIR	1.076887	0.539178	-3.942863	1.616065	-2.326799	8767.250993
HLA A*0250	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.185401	1.858036	-2.327365	15325.010356
HLA A*0212	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.355153	2.027725	-2.327428	22654.444504
HLA A*2402	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.410054	2.082473	-2.327581	25707.144198
HLA A*0202	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.237430	1.909820	-2.327610	17275.479958
HLA B*3501	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.293550	1.965836	-2.327714	19658.479358
HLA A*3301	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.579449	2.251319	-2.328131	37970.765507
HLA A*1101	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.484030	2.155890	-2.328140	30481.035616
HLA B*7301	1:144-152	9	AVTAAPDGF	1.150799	1.146568	-4.625680	2.297367	-2.328313	42235.745976
HLA A*0202	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.151239	1.822872	-2.328367	14165.739945
HLA B*0803	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.243320	1.914570	-2.328750	17511.376313
HLA B*4402	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.411355	2.082473	-2.328883	25784.306101
HLA B*3901	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.294800	1.965836	-2.328964	19715.139157
HLA B*3801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.313558	1.984120	-2.329438	20585.344296
HLA A*8001	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.347760	2.017754	-2.330006	22272.018992
HLA A*0301	1:109-117	9	HTGTREYGR	1.076414	0.591236	-3.997752	1.667650	-2.330102	9948.374108
HLA B*0802	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.355952	2.025736	-2.330216	22696.152582
HLA B*5701	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.102478	1.772257	-2.330221	12661.292823
HLA A*3101	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.297001	1.966426	-2.330575	19815.330224
HLA B*1509	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.314763	1.984040	-2.330723	20642.553598
HLA B*3501	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.232647	0.901531	-2.331116	1708.626023
HLA A*8001	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.359016	2.027725	-2.331291	22856.828564
HLA A*0101	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.344414	2.013049	-2.331365	22101.101629
HLA A*0206	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-3.291868	0.960386	-2.331482	1958.250001
HLA B*1509	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.188770	1.857234	-2.331536	15444.360780
HLA A*3301	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.415838	2.084113	-2.331725	26051.831809
HLA A*6802	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.429637	2.097879	-2.331758	26892.847622
HLA A*0211	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.488529	2.156591	-2.331938	30798.458649
HLA B*4001	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.256106	1.924123	-2.331983	18034.586049
HLA A*0219	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.316159	1.984120	-2.332039	20708.994606
HLA A*0212	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.119479	1.787266	-2.332213	13166.760214
HLA B*5801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-3.672231	1.339557	-2.332674	4701.440687
HLA A*3001	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.105307	1.772257	-2.333050	12744.031403
HLA B*0801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.282996	1.949733	-2.333263	19186.512202
HLA B*3901	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.280691	1.947300	-2.333391	19084.957159
HLA A*6901	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.351371	2.017754	-2.333617	22457.982895
HLA B*7301	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.108949	1.775111	-2.333837	12851.343584

HLA A*0301	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.227132	1.893265	-2.333868	16870.669955
HLA A*0301	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.361727	2.027725	-2.334002	22999.970374
HLA B*4801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.062584	1.728396	-2.334188	11550.048229
HLA A*2301	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.352242	2.017754	-2.334489	22503.102878
HLA A*2403	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.157381	1.822872	-2.334508	14367.487189
HLA B*2705	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.417135	2.082473	-2.334663	26129.745598
HLA B*7301	1:263-271	9	LRAGERAQV	0.865849	0.254971	-3.455618	1.120820	-2.334798	2855.077110
HLA A*0301	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.319246	1.984040	-2.335206	20856.730925
HLA B*3801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.330512	1.995235	-2.335277	21404.841627
HLA A*2902	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.386404	2.050505	-2.335899	24344.671439
HLA A*6802	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.889187	1.553110	-2.336077	7747.955283
HLA B*4801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.889309	1.553110	-2.336200	7750.135200
HLA A*0301	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.320592	1.984120	-2.336472	20921.484317
HLA A*3101	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.194521	1.858036	-2.336486	15650.257136
HLA B*4002	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.630952	2.294422	-2.336530	42751.603984
HLA B*5701	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.291720	1.954913	-2.336807	19575.806882
HLA B*0702	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.125917	1.788992	-2.336924	13363.386069
HLA B*0802	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.284455	1.947300	-2.337155	19251.078475
HLA A*0206	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.493289	2.155890	-2.337400	31137.879869
HLA A*1101	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.421583	2.084113	-2.337470	26398.713123
HLA B*1801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.765853	1.428368	-2.337486	5832.479753
HLA B*4402	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.350563	2.013049	-2.337514	22416.227413
HLA A*0219	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.292737	1.954913	-2.337824	19621.716608
HLA A*6801	1:361-369	9	GGLPDDLKF	1.386058	0.934019	-4.657929	2.320077	-2.337852	45491.389300
HLA A*2603	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.350910	2.013049	-2.337862	22434.182457
HLA B*3501	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.255561	1.917562	-2.337999	18011.965142
HLA B*4001	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.296933	1.958921	-2.338012	19812.221705
HLA B*1517	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.764373	1.426359	-2.338014	5812.635156
HLA A*3101	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.240066	1.901679	-2.338387	17380.659209
HLA B*0702	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.633817	1.295300	-2.338517	4303.451192
HLA B*1801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.422680	2.084113	-2.338567	26465.491633
HLA A*0201	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.816785	1.477798	-2.338988	6558.210855
HLA B*3901	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.092812	1.753043	-2.339769	12382.612196
HLA B*1517	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.367538	2.027725	-2.339813	23309.746637
HLA B*4801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.365634	2.025736	-2.339898	23207.826560
HLA A*3001	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-3.944583	1.604651	-2.339933	8802.038482
HLA B*1517	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-3.979421	1.639403	-2.340018	9537.211780
HLA A*0202	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.653402	1.313175	-2.340227	4501.965771
HLA A*0212	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.818026	1.477798	-2.340228	6576.970650
HLA A*1101	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-3.764895	1.424271	-2.340624	5819.620298
HLA B*0802	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.307682	1.966426	-2.341256	20308.697608
HLA B*7301	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.592614	2.251319	-2.341295	39139.341740
HLA A*0203	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.800926	1.459325	-2.341601	6323.046155
HLA B*0702	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.354970	2.013049	-2.341922	22644.886994
HLA B*5801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.346270	2.004292	-2.341978	22195.759723
HLA B*4002	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.533973	1.191820	-2.342154	3419.583139
HLA B*4403	1:239-247	9	AVAAALVQR	1.496975	0.797447	-4.636648	2.294422	-2.342225	43315.922216
HLA A*3301	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-3.964981	1.622722	-2.342260	9225.321109
HLA B*4501	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-2.975914	0.633434	-2.342480	946.050003
HLA A*2603	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.114959	1.772257	-2.342702	13030.423094
HLA A*8001	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.115010	1.772257	-2.342754	13031.974035
HLA A*2501	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.368562	2.025736	-2.342826	23364.792501
HLA B*1503	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.347231	2.004292	-2.342939	22244.925426
HLA B*3501	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.441041	2.097879	-2.343162	27608.396998
HLA A*0216	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.484136	1.140721	-2.343414	3048.848828
HLA B*7301	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.654882	1.311116	-2.343766	4517.335684
HLA A*2602	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.298911	1.954913	-2.343998	19902.674740
HLA B*4801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-3.979882	1.635727	-2.344155	9547.329814
HLA A*2501	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.428481	2.084113	-2.344368	26821.363035
HLA B*0803	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.202604	1.858036	-2.344568	15944.235702
HLA B*4002	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.548925	2.204297	-2.344628	35393.608576
HLA A*0301	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-3.139556	0.794851	-2.344705	1378.972870
HLA A*1101	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.453200	2.108491	-2.344708	28392.247763
HLA A*2602	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.202087	1.856944	-2.345143	15925.270550
HLA A*2601	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.372934	2.027725	-2.345209	23601.212765

HLA A*6802	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-3.535876	1.190433	-2.345443	3434.600667
HLA A*0202	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.443649	2.097879	-2.345770	27774.683559
HLA B*1517	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.372060	2.025736	-2.346324	23553.763587
HLA A*2601	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.372103	2.025736	-2.346366	23556.057317
HLA A*0301	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.359418	2.013049	-2.346369	22877.982995
HLA A*0219	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.659779	1.313175	-2.346603	4568.553246
HLA B*5801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.342069	1.995235	-2.346834	21982.097793
HLA A*0301	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.364638	2.017754	-2.346885	23154.653617
HLA B*4601	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.329203	1.982154	-2.347049	21340.439322
HLA B*0802	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.360886	2.013049	-2.347838	22955.468512
HLA A*3201	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.696821	1.348830	-2.347991	4975.316023
HLA B*4001	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.330785	1.982154	-2.348630	21418.278390
HLA B*5701	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.205973	1.856944	-2.349029	16068.408622
HLA A*0206	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.250897	1.901679	-2.349218	17819.576160
HLA A*2902	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.431937	2.082473	-2.349464	27035.657560
HLA A*3001	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.475513	1.125828	-2.349685	2988.913050
HLA A*0301	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.071437	1.721649	-2.349787	11787.905814
HLA A*0301	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.308749	1.958921	-2.349828	20358.638896
HLA A*0206	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.249681	0.899837	-2.349844	1776.972811
HLA B*4002	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.610145	2.260158	-2.349987	40751.666580
HLA B*2705	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.903101	1.553110	-2.349991	8000.198370
HLA A*3001	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.267894	1.917562	-2.350332	18530.773365
HLA A*1101	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.400884	2.050505	-2.350379	25170.033505
HLA B*4402	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.401513	2.050505	-2.351008	25206.552753
HLA A*6802	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-3.980620	1.629570	-2.351050	9563.561696
HLA A*0212	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.261465	1.909820	-2.351645	18258.510838
HLA A*2301	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.449948	2.097879	-2.352069	28180.460712
HLA A*0101	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.377979	2.025736	-2.352242	23876.939795
HLA A*3201	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-2.756707	0.404390	-2.352318	571.093399
HLA A*1101	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-3.957012	1.604651	-2.352361	9057.577080
HLA B*3501	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.296243	0.943730	-2.352513	1978.075558
HLA B*4402	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.450423	2.097879	-2.352544	28211.273085
HLA A*0101	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.370331	2.017754	-2.352577	23460.166535
HLA B*4601	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.357012	2.004292	-2.352720	22751.595626
HLA B*1502	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.318598	1.965836	-2.352762	20825.612364
HLA A*2602	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.465189	2.111966	-2.353224	29186.982530
HLA B*1509	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.142368	1.788992	-2.353375	13879.301479
HLA B*5101	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.371219	2.017754	-2.353466	23508.190209
HLA A*0212	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.371374	2.017754	-2.353621	23516.585370
HLA A*0101	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.357985	2.004292	-2.353693	22802.609347
HLA B*5701	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.381590	2.027725	-2.353865	24076.304250
HLA B*1502	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-3.431423	1.077535	-2.353887	2700.367334
HLA A*3001	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.278053	1.924123	-2.353930	18969.361708
HLA B*1503	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.256428	1.901679	-2.354749	18047.957424
HLA A*3101	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.372518	2.017754	-2.354765	23578.624231
HLA A*8001	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.368355	2.013049	-2.355307	23353.671866
HLA A*3301	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-3.943192	1.587869	-2.355323	8773.893688
HLA A*0219	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.373470	2.017754	-2.355716	23630.341753
HLA A*2402	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.351115	1.995235	-2.355879	22444.743822
HLA B*4001	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.368938	2.013049	-2.355889	23385.025407
HLA B*1509	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.184738	1.828772	-2.355966	15301.648518
HLA B*1509	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.257951	1.901679	-2.356271	18111.337519
HLA B*1517	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.179339	1.822872	-2.356467	15112.597139
HLA A*0216	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.143923	1.787266	-2.356657	13929.097183
HLA B*5301	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.546007	2.188431	-2.357576	35156.593161
HLA A*2603	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.313147	1.954913	-2.358234	20565.864743
HLA A*0201	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.145511	1.787266	-2.358245	13980.130335
HLA A*6901	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.384468	2.025736	-2.358732	24236.390536
HLA A*0201	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.642411	1.283502	-2.358909	4389.462042
HLA A*6801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.234024	0.874608	-2.359416	1714.051296
HLA B*5801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.325874	1.966426	-2.359448	21177.472940
HLA A*8001	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.354712	1.995235	-2.359476	22631.415307
HLA B*1509	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.306921	1.947300	-2.359621	20273.131620
HLA B*1801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-3.912804	1.553110	-2.359694	8180.957355
HLA B*1501	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.318835	1.958921	-2.359914	20836.994563

HLA A*0301	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.355177	1.995235	-2.359942	22655.670118
HLA A*0219	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.326478	1.966426	-2.360052	21206.937337
HLA A*3301	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.253376	1.893265	-2.360111	17921.570985
HLA B*0803	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.319674	1.958921	-2.360753	20877.276571
HLA A*6801	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.565150	2.204297	-2.360854	36740.950468
HLA B*0801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.308234	1.947300	-2.360934	20334.532961
HLA A*0211	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.576607	1.215498	-2.361109	3772.306065
HLA B*5301	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.473600	2.111966	-2.361635	29757.768062
HLA A*2601	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.366013	2.004292	-2.361721	23228.049200
HLA A*0101	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.389477	2.027725	-2.361752	24517.548550
HLA A*0101	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.344174	1.982154	-2.362020	22088.909413
HLA A*0206	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.379879	2.017754	-2.362126	23981.668629
HLA A*0201	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.380023	2.017754	-2.362269	23989.583963
HLA A*2501	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.460406	2.097879	-2.362527	28867.265509
HLA B*5701	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.380363	2.017754	-2.362610	24008.409589
HLA B*5301	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.471150	2.108491	-2.362658	29590.332252
HLA B*5301	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.775552	1.412655	-2.362897	5964.196093
HLA B*4801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.376433	2.013049	-2.363384	23792.095984
HLA B*7301	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.471963	2.108491	-2.363471	29645.771947
HLA B*4001	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.389254	2.025736	-2.363517	24504.951252
HLA A*3201	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.220855	1.856944	-2.363911	16628.554775
HLA B*4001	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.318922	1.954913	-2.364009	20841.165836
HLA A*0211	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.276225	0.911989	-2.364236	1888.970886
HLA A*6801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.718027	1.353717	-2.364310	5224.288154
HLA A*2601	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.348467	1.984120	-2.364346	22308.315772
HLA B*3901	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.462245	2.097879	-2.364366	28989.804958
HLA B*1517	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.359855	1.995235	-2.364619	22901.015309
HLA A*0216	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.382795	2.017754	-2.365041	24143.215375
HLA B*0702	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.390790	2.025736	-2.365054	24591.804980
HLA A*0206	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-3.687197	1.322138	-2.365060	4866.280973
HLA A*0250	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.390889	2.025736	-2.365153	24597.393250
HLA B*1503	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.040513	1.675016	-2.365497	10977.734817
HLA A*2402	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.283085	1.917562	-2.365523	19190.456890
HLA B*1501	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.188822	1.822872	-2.365949	15446.199039
HLA B*4501	1:88-96	9	PVLGICYGF	1.280744	0.979414	-4.626117	2.260158	-2.365959	42278.266636
HLA A*0202	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.224139	1.858036	-2.366103	16754.793724
HLA A*2601	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.224308	1.858036	-2.366272	16761.321188
HLA B*0702	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-3.275130	0.908582	-2.366549	1884.214772
HLA A*2501	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.720278	1.353717	-2.366561	5251.434219
HLA B*0803	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.380103	2.013049	-2.367054	23993.996922
HLA A*3101	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.326001	1.958921	-2.367080	21183.660504
HLA A*0216	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.392872	2.025736	-2.367136	24709.960422
HLA B*5301	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.351314	1.984120	-2.367194	22455.067200
HLA B*3901	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.225361	1.858036	-2.367325	16801.993703
HLA A*0250	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.749144	1.381752	-2.367392	5612.336504
HLA A*0206	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.465807	2.097879	-2.367928	29228.539350
HLA A*0201	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.282829	1.914570	-2.368259	19179.144037
HLA B*5801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.041434	1.673173	-2.368261	11001.039744
HLA A*0250	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.386214	2.017754	-2.368460	24334.005916
HLA B*4402	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.386282	2.017754	-2.368528	24337.823900
HLA A*0212	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.283182	1.914570	-2.368612	19194.713910
HLA A*2601	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.363957	1.995235	-2.368722	23118.355506
HLA A*0250	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.225882	1.856944	-2.368938	16822.184942
HLA A*0203	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.382241	2.013049	-2.369192	24112.410584
HLA A*2602	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.557641	2.188431	-2.369210	36111.159459
HLA B*4402	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.279307	1.909820	-2.369487	19024.241165
HLA B*5801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.353558	1.984040	-2.369518	22571.380253
HLA B*1801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.467562	2.097879	-2.369683	29346.896339
HLA A*6901	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.373994	2.004292	-2.369702	23658.866725
HLA B*3501	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.157014	1.787266	-2.369748	14355.366968
HLA A*3002	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.365174	1.995235	-2.369939	23183.231455
HLA A*2902	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.398142	2.027725	-2.370417	25011.627073
HLA A*0211	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.529913	1.159455	-2.370458	3387.764845
HLA A*2603	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.329525	1.958921	-2.370604	21356.261754
HLA B*1801	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.421134	2.050505	-2.370629	26371.449716

HLA B*0801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.329584	1.958921	-2.370663	21359.150325
HLA A*0301	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.352891	1.982154	-2.370736	22536.728019
HLA B*5101	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.482853	2.111966	-2.370887	30398.533061
HLA A*2601	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.329946	1.958921	-2.371025	21376.952537
HLA B*4801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.326062	1.954913	-2.371149	21186.640346
HLA B*5101	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.455528	2.084113	-2.371415	28544.873048
HLA B*1502	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.399166	2.027725	-2.371441	25070.691920
HLA B*4501	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.659483	1.287816	-2.371666	4565.440171
HLA B*0803	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.399629	2.027725	-2.371904	25097.425207
HLA B*1509	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.356206	1.984120	-2.372086	22709.417093
HLA A*2403	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.047773	1.675016	-2.372756	11162.787162
HLA B*3501	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.046307	1.673173	-2.373134	11125.167684
HLA A*6901	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.368538	1.995235	-2.373303	23363.528526
HLA A*0101	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.328275	1.954913	-2.373362	21294.885494
HLA A*2301	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.086854	1.713482	-2.373372	12213.889252
HLA B*2705	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.377899	2.004292	-2.373607	23872.548365
HLA B*4801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.332880	1.958921	-2.373959	21521.884668
HLA B*0802	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.369427	1.995235	-2.374191	23411.354379
HLA A*3002	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-3.281324	0.906788	-2.374536	1911.277058
HLA B*3901	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.400325	2.025736	-2.374588	25137.646592
HLA A*3101	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.289185	1.914570	-2.374615	19461.870467
HLA A*2603	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.563085	2.188431	-2.374654	36566.651250
HLA B*2705	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.614034	1.239243	-2.374791	4111.821168
HLA A*8001	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.379172	2.004292	-2.374881	23942.649218
HLA B*4601	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.400762	2.025736	-2.375025	25162.953812
HLA B*0801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.290012	1.914570	-2.375442	19498.966646
HLA B*4001	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.379750	2.004292	-2.375459	23974.534091
HLA B*4601	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.233521	1.858036	-2.375485	17120.663009
HLA A*2501	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.403285	2.027725	-2.375560	25309.581691
HLA B*1503	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.334527	1.958921	-2.375606	21603.657763
HLA B*3801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.334753	1.958921	-2.375832	21614.880523
HLA A*0203	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.380138	2.004292	-2.375846	23995.944074
HLA A*6801	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.627492	2.251319	-2.376173	42412.280217
HLA A*2403	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.342720	1.965836	-2.376884	22015.063524
HLA B*5301	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.532805	2.155890	-2.376916	34103.977023
HLA B*1503	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.694485	1.317518	-2.376967	4948.633416
HLA A*3001	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.873070	1.495512	-2.377558	7465.684599
HLA B*5401	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.566191	2.188431	-2.377760	36829.108724
HLA A*0201	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.390891	2.013049	-2.377843	24597.526320
HLA A*0216	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.234857	1.856944	-2.377914	17173.445491
HLA A*0206	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.134112	1.756081	-2.378030	13617.943221
HLA B*4801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.343869	1.965836	-2.378033	22073.380063
HLA B*1503	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.017544	1.639403	-2.378141	10412.240006
HLA A*3301	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.099076	1.720897	-2.378179	12562.497801
HLA B*1801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.236610	1.858036	-2.378574	17242.893738
HLA A*0216	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.325879	1.947300	-2.378579	21177.702076
HLA A*0206	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.097112	1.718496	-2.378616	12505.810089
HLA B*5701	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.344506	1.965836	-2.378670	22105.765137
HLA A*8001	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.404448	2.025736	-2.378712	25377.448926
HLA A*0212	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.404721	2.025736	-2.378984	25393.379470
HLA B*1501	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.383312	2.004292	-2.379020	24171.967148
HLA A*3201	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.648750	1.269596	-2.379155	4453.999956
HLA B*0803	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.240820	1.861603	-2.379217	17410.868240
HLA A*0216	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.293822	1.914570	-2.379253	19670.819852
HLA B*5801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-3.996657	1.617007	-2.379651	9923.325761
HLA B*3901	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.169048	1.788992	-2.380056	14758.708704
HLA B*1517	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.053285	1.673173	-2.380112	11305.363638
HLA B*4601	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.364281	1.984120	-2.380161	23135.621298
HLA B*0803	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.406215	2.025736	-2.380478	25480.900684
HLA A*0206	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.293423	0.912830	-2.380594	1965.275747
HLA A*6901	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.609265	1.228069	-2.381196	4066.911889
HLA A*0101	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.376487	1.995235	-2.381251	23795.056558
HLA A*3201	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.840811	1.459325	-2.381486	6931.244348
HLA B*5101	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.336543	1.954913	-2.381630	21704.168223
HLA A*0212	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.521277	1.139224	-2.382052	3321.058686

HLA B*4801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.366170	1.984040	-2.382130	23236.470024
HLA B*0803	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.348161	1.965836	-2.382326	22292.632171
HLA B*1503	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.332067	1.949733	-2.382334	21481.637218
HLA B*5301	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.509130	1.126421	-2.382709	3229.458534
HLA B*5701	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.341879	1.958921	-2.382958	21972.467325
HLA A*6802	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.408924	2.025736	-2.383187	25640.337140
HLA A*2601	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.401199	2.017754	-2.383445	25188.286510
HLA A*6801	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.539501	2.155890	-2.383612	34633.872937
HLA A*2403	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.342584	1.958921	-2.383663	22008.156862
HLA A*2501	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.342696	1.958921	-2.383775	22013.872566
HLA A*2902	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.342964	1.958921	-2.384043	22027.453310
HLA B*4002	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.468763	2.084113	-2.384650	29428.136706
HLA A*2902	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.367176	1.982154	-2.385021	23290.334840
HLA A*2403	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.402984	2.017754	-2.385231	25292.061737
HLA B*1517	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.057791	1.672339	-2.385452	11423.280689
HLA A*0206	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.577316	1.191820	-2.385497	3778.474245
HLA B*4001	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.243757	1.858036	-2.385721	17529.005818
HLA B*4801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.309891	1.924123	-2.385768	20412.236383
HLA B*0702	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.381010	1.995235	-2.385774	24044.153951
HLA A*2902	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.369946	1.984120	-2.385825	23439.361394
HLA B*4501	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.637176	2.251319	-2.385857	43368.679545
HLA B*4002	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.134962	1.749103	-2.385859	13644.638458
HLA B*2705	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.368101	1.982154	-2.385947	23340.031048
HLA A*3002	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.345006	1.958921	-2.386085	22131.252433
HLA B*4801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.390546	2.004292	-2.386254	24577.972822
HLA B*3501	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.412161	2.025736	-2.386425	25832.195671
HLA B*0801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.209563	1.822872	-2.386691	16201.785586
HLA B*5801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.352726	1.965836	-2.386891	22528.195151
HLA A*0211	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.542936	2.155890	-2.387046	34908.887317
HLA B*4601	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.335021	1.947300	-2.387721	21628.215123
HLA A*6901	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.000308	1.612498	-2.387810	10007.102501
HLA A*3201	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.305375	1.917562	-2.387813	20201.093503
HLA A*6802	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.400874	2.013049	-2.387826	25169.488842
HLA B*1501	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.372265	1.984040	-2.388225	23564.852019
HLA B*0801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.372363	1.984040	-2.388323	23570.206923
HLA A*0101	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.372483	1.984040	-2.388443	23576.710943
HLA B*4402	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.355158	1.966426	-2.388732	22654.689621
HLA A*6901	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.172608	0.783681	-2.388928	1488.018315
HLA A*2602	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.415044	2.025736	-2.389308	26004.238453
HLA A*2301	1:488-496	9	VPYEVLERI	1.256779	0.264787	-3.911333	1.521566	-2.389767	8153.298662
HLA B*4601	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.385107	1.995235	-2.389872	24272.080391
HLA A*0201	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.394275	2.004292	-2.389983	24789.895289
HLA B*2705	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.345041	1.954913	-2.390128	22133.048420
HLA B*3801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.403212	2.013049	-2.390164	25305.337464
HLA A*3101	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.251797	1.861603	-2.390194	17856.536377
HLA A*6802	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.250185	1.859882	-2.390303	17790.390302
HLA B*1503	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.213299	1.822872	-2.390426	16341.749975
HLA B*3901	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.340225	1.949733	-2.390492	21888.942977
HLA B*0802	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.314869	1.924123	-2.390746	20647.579536
HLA A*0216	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.293226	1.901679	-2.391547	19643.808508
HLA A*1101	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.404744	2.013049	-2.391695	25394.753261
HLA B*1509	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.489734	2.097879	-2.391855	30884.051500
HLA B*1801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.396152	2.004292	-2.391860	24897.281569
HLA B*5401	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.556814	2.164911	-2.391903	36042.459098
HLA B*4402	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.417716	2.025736	-2.391979	26164.684616
HLA B*3501	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.680609	1.287816	-2.392793	4793.019821
HLA A*0101	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.377095	1.984120	-2.392975	23828.420638
HLA A*3001	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.250573	1.857234	-2.393339	17806.277658
HLA A*3201	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.348481	1.954913	-2.393568	22309.039897
HLA B*0801	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.173672	1.779355	-2.394317	14916.679122
HLA A*8001	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.341667	1.947300	-2.394368	21961.771754
HLA A*2602	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.804441	1.410054	-2.394387	6374.427434
HLA A*2602	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.353387	1.958921	-2.394465	22562.468081
HLA A*2902	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.412359	2.017754	-2.394605	25843.937281
HLA A*2601	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.378893	1.984040	-2.394853	23927.240456

HLA B*3501	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.776623	1.381752	-2.394872	5978.927388
HLA A*0202	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.002900	0.607629	-2.395272	1006.700481
HLA A*2402	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.493263	2.097879	-2.395384	31136.026947
HLA A*3301	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.583944	2.188431	-2.395513	38365.769885
HLA A*6901	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.379583	1.984040	-2.395543	23965.327190
HLA B*1801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.361434	1.965836	-2.395598	22984.422221
HLA B*3801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.343058	1.947300	-2.395758	22032.220469
HLA B*3501	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.400153	2.004292	-2.395861	25127.721144
HLA A*6901	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.018601	1.622722	-2.395880	10437.618964
HLA A*2601	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.175373	1.779355	-2.396018	14975.218738
HLA A*2402	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.380382	1.984120	-2.396262	24009.448674
HLA B*0802	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.362174	1.965836	-2.396338	23023.623713
HLA A*3001	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.064078	1.667650	-2.396428	11589.856803
HLA B*1517	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-3.736405	1.339557	-2.396848	5450.104065
HLA A*2402	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.254887	1.858036	-2.396851	17984.020777
HLA B*3501	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.029574	1.632644	-2.396929	10704.676158
HLA A*0301	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.363508	1.966426	-2.397082	23094.479905
HLA A*0211	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.733557	1.336347	-2.397210	5414.485799
HLA A*0206	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.118957	1.721649	-2.397308	13150.956487
HLA A*3001	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.746273	1.348830	-2.397443	5575.356366
HLA B*4001	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.347203	1.949733	-2.397470	22243.481361
HLA B*5301	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.448188	2.050505	-2.397683	28066.504321
HLA A*0219	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.410756	2.013049	-2.397708	25748.760614
HLA B*1503	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.255213	1.857234	-2.397979	17997.549389
HLA A*2403	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.424160	2.025736	-2.398424	26555.846007
HLA A*3001	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.258444	1.859882	-2.398562	18131.925080
HLA B*4403	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.602996	2.204297	-2.398699	40086.292536
HLA A*2501	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.481264	2.082473	-2.398792	30287.566072
HLA A*0216	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.365338	1.966426	-2.398912	23192.012427
HLA A*0202	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.524749	1.125828	-2.398921	3347.719707
HLA A*2301	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.313690	1.914570	-2.399120	20591.581649
HLA A*3001	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.662227	1.263068	-2.399159	4594.379382
HLA B*5101	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.427113	2.027725	-2.399388	26737.047292
HLA A*0301	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.365754	1.965836	-2.399919	23214.230583
HLA A*3201	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.628056	1.228069	-2.399987	4246.742656
HLA A*6901	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.366161	1.965836	-2.400325	23235.967203
HLA B*1517	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.418113	2.017754	-2.400359	26188.617174
HLA B*1509	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.426404	2.025736	-2.400667	26693.400329
HLA B*0801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.405172	2.004292	-2.400880	25419.769244
HLA A*2602	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.310859	1.909820	-2.401039	20457.783433
HLA B*3501	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.350840	1.949733	-2.401107	22430.541759
HLA B*0802	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.383427	1.982154	-2.401273	24178.375613
HLA B*5801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.351359	1.949733	-2.401626	22457.375427
HLA B*3501	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.349160	1.947300	-2.401860	22343.946423
HLA B*5701	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.397197	1.995235	-2.401962	24957.291506
HLA B*4601	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.386005	1.984040	-2.401965	24322.292396
HLA A*0219	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.427762	2.025736	-2.402026	26776.998982
HLA A*0216	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.215453	0.813260	-2.402193	1642.303753
HLA B*4402	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.406647	2.004292	-2.402355	25506.277500
HLA A*2601	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.368832	1.966426	-2.402406	23379.333132
HLA A*0201	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.368447	1.965836	-2.402611	23358.599676
HLA A*0211	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.075830	1.673173	-2.402658	11907.763324
HLA B*0803	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.407505	2.004292	-2.403213	25556.692198
HLA B*3801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.431072	2.027725	-2.403347	26981.887455
HLA A*6802	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.327568	1.924123	-2.403445	21260.237618
HLA B*0702	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.359054	1.954913	-2.404140	22858.807097
HLA A*0219	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.431956	2.027725	-2.404231	27036.827665
HLA A*0101	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.370091	1.965836	-2.404256	23447.224582
HLA A*8001	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.386836	1.982154	-2.404682	24368.916667
HLA B*4403	1:82-90	9	LLDLGVPVL	1.833552	0.417767	-4.656024	2.251319	-2.404705	45292.236667
HLA B*2705	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.371219	1.966426	-2.404793	23508.190209
HLA A*2602	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.388981	1.984120	-2.404861	24489.578064
HLA A*2501	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.389061	1.984120	-2.404941	24494.082999
HLA B*5101	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.387273	1.982154	-2.405119	24393.449972
HLA A*0216	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.410178	2.004292	-2.405887	25714.516113

HLA B*4403	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.571097	2.164911	-2.406186	37247.483257
HLA A*0250	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.229078	1.822872	-2.406205	16946.409742
HLA B*4001	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.372237	1.965836	-2.406401	23563.322269
HLA A*3301	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.390609	1.984040	-2.406570	24581.563115
HLA B*1801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.042327	1.635727	-2.406600	11023.678480
HLA A*0206	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-2.840048	0.433361	-2.406687	691.907555
HLA A*2402	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.434446	2.027725	-2.406721	27192.315274
HLA B*1503	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.155872	1.749103	-2.406769	14317.673323
HLA A*0212	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.420060	2.013049	-2.407012	26306.331600
HLA B*2705	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.268695	1.861603	-2.407091	18564.989972
HLA A*6901	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.080416	1.673173	-2.407244	12034.176834
HLA A*3101	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.373228	1.965836	-2.407392	23617.178156
HLA A*0211	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-2.939953	0.532233	-2.407719	870.869085
HLA A*2501	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.355045	1.947300	-2.407746	22648.807536
HLA B*5401	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.563868	2.155890	-2.407978	36632.585191
HLA A*0206	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.421193	2.013049	-2.408144	26375.016623
HLA A*0201	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.392461	1.984040	-2.408421	24686.577817
HLA A*0250	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.374264	1.965836	-2.408428	23673.590367
HLA B*5101	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.270097	1.861603	-2.408494	18625.046321
HLA B*1502	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.459478	2.050505	-2.408973	28805.644733
HLA B*1509	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.196288	1.787266	-2.409022	15714.055771
HLA A*3001	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.232205	1.822872	-2.409332	17068.873800
HLA A*3001	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.642045	1.232655	-2.409390	4385.759151
HLA A*3001	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.105316	1.695841	-2.409475	12744.307181
HLA B*0803	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.393809	1.984040	-2.409770	24763.355610
HLA B*4403	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.201208	1.791215	-2.409993	15893.081548
HLA B*1502	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.507926	2.097879	-2.410047	32205.224457
HLA B*4601	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.272278	1.861603	-2.410674	18718.786185
HLA A*6901	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.697192	1.286148	-2.411044	4979.570554
HLA B*4501	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.567126	2.155890	-2.411237	36908.492231
HLA B*0803	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.366360	1.954913	-2.411447	23246.654501
HLA B*4402	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.395651	1.984040	-2.411612	24868.608795
HLA B*3501	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.406936	1.995235	-2.411701	25523.255443
HLA B*5401	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.494297	2.082473	-2.411824	31210.229907
HLA A*0301	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.090655	1.678625	-2.412031	12321.269148
HLA B*1509	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-3.455364	1.043287	-2.412077	2853.409467
HLA B*3501	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.270201	1.858036	-2.412165	18629.480264
HLA B*3801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.362054	1.949733	-2.412321	23017.272272
HLA A*0203	1:428-436	9	SIVREELTA	1.468906	-0.179470	-3.702065	1.289436	-2.412628	5035.756501
HLA A*0211	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.241793	1.828772	-2.413021	17449.906960
HLA B*4601	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.185316	1.772257	-2.413060	15322.026009
HLA B*5301	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.497227	2.084113	-2.413114	31421.490023
HLA B*0803	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.314801	1.901679	-2.413122	20644.340458
HLA A*3201	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.408466	1.995235	-2.413230	25613.302682
HLA B*4402	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.395682	1.982154	-2.413528	24870.357830
HLA A*0101	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.361044	1.947300	-2.413744	22963.790519
HLA A*2902	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.408987	1.995235	-2.413752	25644.082620
HLA A*3002	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.683391	1.269596	-2.413795	4823.819127
HLA A*0212	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.315950	0.902116	-2.413834	2069.904729
HLA A*0206	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.842320	1.428368	-2.413952	6955.359445
HLA A*0211	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.440792	2.025736	-2.415056	27592.569550
HLA B*3801	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.512947	2.097879	-2.415068	32579.707418
HLA A*0250	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.133722	1.718496	-2.415225	13605.719231
HLA B*5101	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.513159	2.097879	-2.415279	32595.574014
HLA B*5701	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.381959	1.966426	-2.415532	24096.762208
HLA B*5301	1:301-309	9	APEGKRKII	1.207147	0.122555	-3.745746	1.329702	-2.416045	5568.604156
HLA B*1801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.382743	1.966426	-2.416317	24140.342080
HLA A*0219	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.699988	1.283502	-2.416486	5011.731285
HLA B*5701	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.420944	2.004292	-2.416652	26359.896251
HLA B*4001	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.400740	1.984040	-2.416701	25161.728683
HLA B*5101	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.188972	1.772257	-2.416715	15451.547948
HLA A*8001	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.033746	1.617007	-2.416740	10808.021968
HLA A*8001	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.382645	1.965836	-2.416809	24134.857647
HLA A*2601	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.382736	1.965836	-2.416901	24139.950293
HLA A*0216	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.201565	1.784483	-2.417082	15906.155854

HLA A*0301	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.367143	1.949733	-2.417410	23288.570933
HLA A*3001	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.089828	1.672339	-2.417490	12297.828316
HLA A*6901	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.895376	1.477798	-2.417578	7859.151289
HLA A*3001	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.129112	1.711364	-2.417748	13462.069087
HLA A*0301	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.103216	1.685162	-2.418054	12682.818905
HLA A*6801	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.500554	2.082473	-2.418081	31663.115593
HLA B*5701	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.367942	1.949733	-2.418208	23331.446472
HLA B*0802	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.377429	1.958921	-2.418508	23846.732765
HLA B*3801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.444471	2.025736	-2.418735	27827.323665
HLA B*0802	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.278821	1.859882	-2.418939	19002.948849
HLA B*4402	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.312407	1.893265	-2.419142	20530.847987
HLA B*5701	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.403238	1.984040	-2.419198	25306.843398
HLA A*0202	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.575415	2.155890	-2.419526	37619.696458
HLA B*2705	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.321403	1.901679	-2.419724	20960.568884
HLA A*3301	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.528362	2.108491	-2.419871	33756.868420
HLA A*2501	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.199310	1.779355	-2.419955	15823.761478
HLA B*4402	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.404211	1.984120	-2.420090	25363.586506
HLA B*4601	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.375091	1.954913	-2.420178	23718.714486
HLA A*0211	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.386263	1.965836	-2.420427	24336.770603
HLA A*6802	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.511958	1.091476	-2.420482	3250.562289
HLA B*1503	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.211983	1.791215	-2.420768	16292.316941
HLA B*1501	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.212265	1.791215	-2.421050	16302.897130
HLA B*4501	1:442-450	9	QIWQCPVVL	1.590475	0.613822	-4.625466	2.204297	-2.421170	42214.958439
HLA B*5701	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.336214	1.914570	-2.421644	21687.736047
HLA A*2602	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.387783	1.965836	-2.421947	24422.103379
HLA B*5301	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.439967	2.017754	-2.422214	27540.224531
HLA A*3201	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.245418	1.822872	-2.422546	17596.178992
HLA B*0702	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.406696	1.984040	-2.422656	25509.175374
HLA B*1509	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.176045	1.753043	-2.423002	14998.406754
HLA B*5301	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.378348	1.954913	-2.423434	23897.228351
HLA B*1509	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.373303	1.949733	-2.423570	23621.267032
HLA A*0201	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.325254	1.901679	-2.423575	21147.248634
HLA A*0219	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.338214	1.914570	-2.423644	21787.812576
HLA A*0212	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.389714	1.965836	-2.423879	24530.948570
HLA B*0803	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.441650	2.017754	-2.423896	27647.107929
HLA B*4601	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.373898	1.949733	-2.424164	23653.619641
HLA A*2301	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.406396	1.982154	-2.424241	25491.517257
HLA A*0212	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.429510	1.005151	-2.424360	2688.502006
HLA A*0216	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.334356	1.909820	-2.424536	21595.127690
HLA B*3501	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.408644	1.984040	-2.424604	25623.835797
HLA B*1501	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.374628	1.949733	-2.424895	23693.449775
HLA A*0202	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.394287	0.969193	-2.425093	2479.059131
HLA B*2705	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.390988	1.965836	-2.425152	24602.982790
HLA A*0216	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.391133	1.965836	-2.425298	24611.236338
HLA A*1101	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.409807	1.984120	-2.425687	25692.545700
HLA A*0219	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.372988	1.947300	-2.425689	23604.149586
HLA A*2603	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.779476	1.353717	-2.425758	6018.323853
HLA B*5101	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.566720	1.140721	-2.425999	3687.400320
HLA B*1801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.335864	1.909820	-2.426044	21670.261182
HLA A*0206	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.359265	0.933159	-2.426106	2286.996302
HLA B*1501	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.591479	1.165167	-2.426312	3903.724515
HLA B*0802	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.410601	1.984040	-2.426561	25739.568591
HLA A*2403	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.341176	1.914570	-2.426606	21936.954340
HLA A*1101	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.454419	2.027725	-2.426694	28472.077617
HLA A*0212	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.249570	1.822872	-2.426698	17765.192225
HLA B*5801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.341613	1.914570	-2.427043	21959.039277
HLA A*6901	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.376975	1.949733	-2.427242	23821.847180
HLA A*0216	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.034910	0.607629	-2.427281	1083.701463
HLA A*0216	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.713554	1.286148	-2.427405	5170.751942
HLA B*0803	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.394021	1.966426	-2.427595	24775.415577
HLA B*4403	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.141118	1.713482	-2.427636	13839.413430
HLA B*0803	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.256571	1.828772	-2.427799	18053.914291
HLA B*3801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.345708	1.917562	-2.428147	22167.079961
HLA A*8001	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.342732	1.914570	-2.428162	22015.659027
HLA A*0250	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.584858	2.156591	-2.428267	38446.593624

HLA A*1101	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.423615	1.995235	-2.428380	26522.536824
HLA A*0219	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.394340	1.965836	-2.428505	24793.650670
HLA A*6801	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.585098	2.156591	-2.428507	38467.814643
HLA B*2705	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.215404	1.786784	-2.428620	16421.154989
HLA A*6802	1:481-489	9	MTADWTRVP	0.898983	0.129318	-3.456934	1.028301	-2.428632	2863.739790
HLA A*0201	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-3.328830	0.900138	-2.428693	2132.211265
HLA B*1503	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.661635	1.232655	-2.428980	4588.120169
HLA B*4601	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.343676	1.914570	-2.429106	22063.590243
HLA A*0219	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.331332	1.901679	-2.429653	21445.293242
HLA A*2501	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.447678	2.017754	-2.429925	28033.575095
HLA A*3101	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.380032	1.949733	-2.430299	23990.103092
HLA B*1801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.385229	1.954913	-2.430316	24278.909434
HLA A*0212	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.434836	2.004292	-2.430545	27216.746072
HLA A*3201	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.444201	2.013049	-2.431153	27810.016635
HLA B*1502	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.449297	2.017754	-2.431544	28138.262810
HLA B*1502	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.514035	2.082473	-2.431562	32661.414661
HLA A*8001	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.398029	1.966426	-2.431603	25005.133030
HLA B*5301	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.596584	2.164911	-2.431673	39498.822305
HLA B*1801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.449516	2.017754	-2.431762	28152.423286
HLA A*6801	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.540370	2.108491	-2.431879	34703.267569
HLA A*6901	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.341797	1.909820	-2.431977	21968.307317
HLA A*2301	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.458197	2.025736	-2.432461	28720.839551
HLA A*0101	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.382264	1.949733	-2.432531	24113.715074
HLA A*0201	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-3.088595	0.656026	-2.432569	1226.296227
HLA A*3101	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.671930	1.239243	-2.432687	4698.186227
HLA B*5801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.356988	1.924123	-2.432865	22750.364823
HLA B*4402	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.380255	1.947300	-2.432955	24002.435722
HLA A*6901	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.357345	1.924123	-2.433222	22769.080213
HLA B*0803	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.415545	1.982154	-2.433390	26034.220574
HLA B*5101	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.399552	1.965836	-2.433716	25092.945056
HLA A*0216	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.377559	0.943730	-2.433829	2385.385377
HLA A*0202	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.027309	1.593295	-2.434014	10648.995165
HLA B*0803	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.418171	1.984120	-2.434051	26192.159352
HLA B*5801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.336437	1.901679	-2.434758	21698.885095
HLA A*1101	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.401234	1.966426	-2.434808	25190.330581
HLA A*2301	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.430053	1.995235	-2.434817	26918.611212
HLA B*3501	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.207430	1.772257	-2.435173	16122.394661
HLA A*2902	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.402164	1.966426	-2.435738	25244.354079
HLA B*1801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.417915	1.982154	-2.435761	26176.718967
HLA A*6802	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.440153	2.004292	-2.435861	27551.997222
HLA B*5101	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.448938	2.013049	-2.435889	28114.982039
HLA A*0212	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.646067	1.210159	-2.435908	4426.567555
HLA B*1517	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.440353	2.004292	-2.436061	27564.669662
HLA B*4001	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.264905	1.828772	-2.436133	18403.693834
HLA A*2603	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.544700	2.108491	-2.436209	35051.004582
HLA B*4601	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.395142	1.958921	-2.436220	24839.431522
HLA B*1503	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.651720	1.215498	-2.436222	4484.561224
HLA B*5101	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.848926	1.412655	-2.436271	7061.977517
HLA A*2602	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.753800	1.317518	-2.436282	5672.838003
HLA A*3002	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.402972	1.966426	-2.436546	25291.377610
HLA A*6901	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.223904	1.787266	-2.436638	16745.732017
HLA B*1501	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.583966	1.147258	-2.436707	3836.767732
HLA B*1509	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.346669	1.909820	-2.436849	22216.182135
HLA A*0219	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.441229	2.004292	-2.436938	27620.348253
HLA A*3002	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.298662	1.861603	-2.437059	19891.264858
HLA B*4402	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.150835	1.713482	-2.437354	14152.564842
HLA B*1503	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-3.546548	1.109115	-2.437433	3520.040099
HLA A*0212	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.295589	1.858036	-2.437553	19751.008404
HLA B*4001	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.166215	1.728396	-2.437819	14662.731507
HLA B*0801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.194211	1.756081	-2.438130	15639.085193
HLA A*3301	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.550144	2.111966	-2.438179	35493.124001
HLA A*6802	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.433415	1.995235	-2.438179	27127.811747
HLA A*1101	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.456132	2.017754	-2.438378	28584.587772
HLA A*2403	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.422457	1.984040	-2.438417	26451.893467
HLA B*1509	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.298658	1.859882	-2.438775	19891.049640

HLA B*4001	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.300612	1.861603	-2.439009	19980.781598
HLA B*4601	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.356746	1.917562	-2.439185	22737.691428
HLA B*5401	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.301049	1.861603	-2.439446	20000.897166
HLA A*8001	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.301320	1.861603	-2.439716	20013.344341
HLA B*0702	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.444140	2.004292	-2.439849	27806.105233
HLA A*3001	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.296830	1.856944	-2.439886	19807.506261
HLA A*0212	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.424280	1.984040	-2.440240	26563.173891
HLA B*1503	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.193464	1.753043	-2.440421	15612.203704
HLA A*0250	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.596326	2.155890	-2.440436	39475.324030
HLA B*4801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.334006	1.893265	-2.440741	21577.727444
HLA A*1101	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.396375	1.954913	-2.441462	24910.080553
HLA B*5301	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.359056	1.917562	-2.441494	22858.930760
HLA A*0203	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.374767	0.933159	-2.441608	2370.103788
HLA A*0101	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.303232	1.861603	-2.441629	20101.670436
HLA B*1801	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.467372	2.025736	-2.441635	29334.039316
HLA B*3901	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.081337	1.639403	-2.441934	12059.724510
HLA B*0802	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.446264	2.004292	-2.441972	27942.425164
HLA A*3001	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.228871	1.786784	-2.442087	16938.343981
HLA B*4402	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.356857	1.914570	-2.442287	22743.473558
HLA A*2301	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.470255	2.027725	-2.442530	29529.404426
HLA A*2603	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.360299	1.917562	-2.442737	22924.442863
HLA A*0301	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.357501	1.914570	-2.442931	22777.211426
HLA B*4002	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.598856	2.155890	-2.442967	39705.996403
HLA B*5801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.352792	1.909820	-2.442972	22531.607911
HLA A*0301	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.367225	1.924123	-2.443102	23292.980951
HLA B*5401	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.551667	2.108491	-2.443175	35617.767334
HLA B*1801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.438633	1.995235	-2.443398	27455.728347
HLA B*4501	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.608388	2.164911	-2.443477	40587.094209
HLA A*0203	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.427529	1.984040	-2.443489	26762.661623
HLA A*1101	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.427696	1.984040	-2.443656	26772.943193
HLA A*0219	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.427748	1.984040	-2.443708	26776.129833
HLA A*0301	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.305429	1.861603	-2.443826	20203.607230
HLA A*2902	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.168973	1.725080	-2.443893	14756.153950
HLA B*7301	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.632355	2.188431	-2.443924	42889.902213
HLA A*6802	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-3.766300	1.322138	-2.444162	5838.477918
HLA A*6802	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.428267	1.984040	-2.444227	26808.162130
HLA B*2705	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.403339	1.958921	-2.444418	25312.731093
HLA A*0216	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-3.465434	1.020890	-2.444544	2920.343857
HLA A*3101	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-3.766802	1.322138	-2.444665	5845.241133
HLA A*3301	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.495345	2.050505	-2.444840	31285.625199
HLA B*5101	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.394958	1.949733	-2.445225	24828.952205
HLA B*4601	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.347012	1.901679	-2.445333	22233.736380
HLA A*0206	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-3.559197	1.113845	-2.445352	3624.075511
HLA B*4002	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.393095	1.947300	-2.445795	24722.663110
HLA A*0101	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.360470	1.914570	-2.445900	22933.498016
HLA B*5101	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.412638	1.966426	-2.446212	25860.580365
HLA A*2601	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.396847	1.949733	-2.447114	24937.182201
HLA B*4501	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.413757	1.966426	-2.447330	25927.259949
HLA B*3801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.165914	1.718496	-2.447418	14652.581581
HLA A*6901	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.362148	1.914570	-2.447578	23022.253646
HLA B*0802	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.402756	1.954913	-2.447843	25278.792976
HLA A*3001	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.235562	1.787266	-2.448296	17201.340052
HLA A*0211	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-3.492467	1.044058	-2.448410	3107.900920
HLA A*0212	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.036434	1.587869	-2.448565	10875.119294
HLA B*1501	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.366511	1.917562	-2.448949	23254.704651
HLA B*4801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.398715	1.949733	-2.448982	25044.664545
HLA A*6901	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.366610	1.917562	-2.449048	23259.989077
HLA A*2402	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.310769	1.861603	-2.449166	20453.578240
HLA A*8001	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.399131	1.949733	-2.449398	25068.657558
HLA A*0301	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.367098	1.917562	-2.449536	23286.177273
HLA A*2402	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.396941	1.947300	-2.449642	24942.579080
HLA B*5301	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.462755	2.013049	-2.449707	29023.857406
HLA A*6901	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.719460	1.269596	-2.449865	5241.556952
HLA A*0201	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.399688	1.949733	-2.449955	25100.819794
HLA A*0201	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.272842	1.822872	-2.449969	18743.105944

HLA A*0203	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.374560	1.924123	-2.450437	23689.732877
HLA B*4601	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.237797	1.787266	-2.450530	17290.065627
HLA B*1801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.279338	1.828772	-2.450565	19025.579159
HLA B*3501	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.365209	1.914570	-2.450639	23185.112812
HLA B*3801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.417502	1.966426	-2.451075	26151.806914
HLA B*1517	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.164730	1.713482	-2.451248	14612.684501
HLA B*3501	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.361396	1.909820	-2.451576	22982.432816
HLA B*1801	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.410721	1.958921	-2.451800	25746.671230
HLA A*2902	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.436002	1.984040	-2.451962	27289.874973
HLA A*3101	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.376473	1.924123	-2.452350	23794.284198
HLA A*2602	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.470151	2.017754	-2.452398	29522.376227
HLA A*2301	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.310602	1.858036	-2.452567	20445.723486
HLA A*0216	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.465746	2.013049	-2.452697	29224.428437
HLA A*0201	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.310741	1.858036	-2.452705	20452.250464
HLA A*0216	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.168638	0.715584	-2.453054	1474.475794
HLA A*6801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.346392	1.893265	-2.453128	22202.004585
HLA A*2403	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.181726	1.728396	-2.453331	15195.891435
HLA A*3201	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.412551	1.958921	-2.453630	25855.404477
HLA B*4403	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.537748	2.084113	-2.453635	34494.380009
HLA A*0212	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.366469	0.912830	-2.453639	2325.246414
HLA B*4601	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.276772	1.822872	-2.453900	18913.515009
HLA B*1801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.646030	1.191820	-2.454210	4426.184416
HLA A*2301	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.403995	1.949733	-2.454261	25350.965942
HLA B*0802	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.316009	1.861603	-2.454405	20701.825712
HLA A*2501	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.449734	1.995235	-2.454499	28166.590888
HLA A*6802	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.420408	1.965836	-2.454572	26327.402557
HLA A*0250	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.482366	2.027725	-2.454641	30364.510407
HLA B*4801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.372267	1.917562	-2.454705	23564.979502
HLA B*0802	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.369488	1.914570	-2.454918	23414.647585
HLA A*2402	1:114-122	9	EYGRTELKV	1.003669	0.148169	-3.606901	1.151838	-2.455063	4044.838458
HLA B*3901	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.183460	1.728396	-2.455065	15256.682277
HLA B*1517	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.594454	1.139224	-2.455229	3930.552577
HLA B*1509	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.421792	1.966426	-2.455366	26411.426640
HLA B*1517	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-3.628117	1.172675	-2.455442	4247.340033
HLA B*4501	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.450728	1.995235	-2.455493	28231.120645
HLA B*5401	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.568141	2.111966	-2.456176	36994.850913
HLA A*6901	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.915699	1.459325	-2.456373	8235.665411
HLA B*2705	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-3.646481	1.190075	-2.456405	4430.784276
HLA B*5801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.805240	1.348830	-2.456410	6386.163105
HLA A*0211	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.469498	2.013049	-2.456450	29478.009444
HLA B*0803	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.403807	1.947300	-2.456507	25339.996642
HLA A*2301	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.422490	1.965836	-2.456654	26453.896968
HLA B*1501	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.241375	1.784483	-2.456891	17433.111480
HLA B*3801	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.318506	1.861603	-2.456903	20821.218922
HLA A*3002	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.474970	2.017754	-2.457216	29851.771195
HLA B*2705	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.407051	1.949733	-2.457318	25530.022161
HLA A*3301	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.539882	2.082473	-2.457409	34664.239439
HLA A*6901	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.359519	1.901679	-2.457840	22883.305610
HLA B*1501	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.230156	1.772257	-2.457899	16988.542324
HLA A*0211	1:428-436	9	SIVREELTA	1.468906	-0.179470	-3.747410	1.289436	-2.457974	5589.973931
HLA A*0203	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.747400	1.289353	-2.458047	5589.852968
HLA A*8001	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.442120	1.984040	-2.458080	27677.037675
HLA B*4501	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.247242	1.788992	-2.458249	17670.204326
HLA B*4402	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.315393	1.856944	-2.458449	20672.503917
HLA A*2402	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.373134	1.914570	-2.458564	23612.068056
HLA A*0101	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.368555	1.909820	-2.458735	23364.413301
HLA A*2902	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.075901	1.617007	-2.458894	11909.696071
HLA A*6901	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.807857	1.348830	-2.459028	6424.766268
HLA A*0216	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.317216	1.858036	-2.459180	20759.471037
HLA B*5101	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.454607	1.995235	-2.459372	28484.402747
HLA B*4402	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.244136	1.784483	-2.459652	17544.280095
HLA A*3301	1:267-275	9	ERAQVQRDF	1.061262	1.094628	-4.615599	2.155890	-2.459709	41266.584861
HLA A*2601	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.369687	1.909820	-2.459867	23425.417066
HLA A*0203	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.283076	1.822872	-2.460204	19190.041621
HLA A*0250	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.809088	1.348830	-2.460259	6443.004918

HLA A*0301	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.361997	1.901679	-2.460318	23014.283964
HLA B*7301	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.617013	2.156591	-2.460422	41401.199030
HLA B*4001	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.244953	1.784483	-2.460470	17577.340794
HLA B*1501	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.317571	1.856944	-2.460627	20776.436237
HLA A*2501	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.427433	1.966426	-2.461007	26756.726177
HLA B*3501	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.385210	1.924123	-2.461087	24277.858687
HLA A*0101	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.385349	1.924123	-2.461226	24285.609014
HLA B*5801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.354660	1.893265	-2.461395	22628.721931
HLA B*5401	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.756770	1.295300	-2.461470	5711.762369
HLA A*3301	1:161-169	9	APVAAFEAF	1.105718	1.050873	-4.618272	2.156591	-2.461682	41521.424335
HLA B*5401	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.545859	2.084113	-2.461746	35144.613027
HLA B*0802	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.320170	1.858036	-2.462134	20901.121309
HLA B*4601	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.372020	1.909820	-2.462200	23551.597491
HLA A*2601	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.386627	1.924123	-2.462504	24357.186342
HLA A*0206	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.412518	1.949733	-2.462785	25853.446303
HLA B*0802	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.380432	1.917562	-2.462870	24012.176487
HLA B*1801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-3.738735	1.275786	-2.462949	5479.431272
HLA B*0803	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.413296	1.949733	-2.463563	25899.782853
HLA A*0250	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.378317	1.914570	-2.463747	23895.547753
HLA A*1101	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-3.589773	1.126026	-2.463748	3888.422396
HLA A*2403	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.320731	1.856944	-2.463787	20928.163175
HLA A*6901	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-3.654257	1.190433	-2.463824	4510.839775
HLA A*2501	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.381489	1.917562	-2.463927	24070.704145
HLA A*2403	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.374064	1.909820	-2.464244	23662.706792
HLA A*1101	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.411586	1.947300	-2.464286	25797.979769
HLA A*0301	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.052396	1.587869	-2.464528	11282.268492
HLA A*0203	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.414311	1.949733	-2.464578	25960.383300
HLA B*4601	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.388751	1.924123	-2.464628	24476.597886
HLA A*6801	1:165-173	9	AFEAFDRRL	1.631914	0.556517	-4.653099	2.188431	-2.464667	44988.204348
HLA B*4402	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.419694	1.954913	-2.464781	26284.139929
HLA A*2902	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.412185	1.947300	-2.464885	25833.593202
HLA A*2601	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.382537	1.917562	-2.464975	24128.852316
HLA B*5101	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.469294	2.004292	-2.465002	29464.138578
HLA A*0219	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.414769	1.949733	-2.465036	25987.784095
HLA A*3301	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.293905	1.828772	-2.465132	19674.544798
HLA B*5301	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.960832	1.495512	-2.465321	9137.603332
HLA A*0219	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.776562	1.311116	-2.465446	5978.086468
HLA B*1801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.367230	1.901679	-2.465551	23293.232977
HLA A*2403	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.415617	1.949733	-2.465884	26038.587050
HLA B*0801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.185044	1.718496	-2.466548	15312.413732
HLA B*5101	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.944494	1.477798	-2.466696	8800.229182
HLA A*0216	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.020091	1.553110	-2.466981	10473.480101
HLA A*0206	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.075086	0.607629	-2.467457	1188.737199
HLA B*1801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.382219	1.914570	-2.467650	24111.236603
HLA B*4001	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.361006	1.893265	-2.467741	22961.802900
HLA A*2602	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.565625	2.097879	-2.467746	36781.122836
HLA A*2601	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.369436	1.901679	-2.467757	23411.860996
HLA A*0301	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.272491	1.804702	-2.467789	18728.003711
HLA B*5701	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.329471	1.861603	-2.467868	21353.604614
HLA B*0801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.327979	1.859882	-2.468097	21280.374866
HLA B*0802	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.377986	1.909820	-2.468166	23877.327313
HLA A*3001	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.193798	1.725080	-2.468717	15624.201673
HLA B*5101	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.452927	1.984120	-2.468807	28374.435879
HLA A*2403	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.328804	1.859882	-2.468922	21320.821944
HLA A*2403	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.362547	1.893265	-2.469283	23043.436519
HLA A*0201	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.393518	1.924123	-2.469395	24746.749272
HLA A*2501	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.473753	2.004292	-2.469461	29768.234007
HLA B*4402	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.428636	1.958921	-2.469715	26830.941385
HLA B*3901	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.329692	1.859882	-2.469810	21364.466315
HLA B*0702	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.256809	1.786784	-2.470025	18063.781624
HLA A*0203	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.487294	1.017185	-2.470109	3071.097461
HLA B*5101	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.429157	1.958921	-2.470236	26863.184580
HLA A*0212	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.420413	1.949733	-2.470680	26327.687415
HLA B*5401	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.568611	2.097879	-2.470732	37034.900183
HLA B*5401	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.521403	2.050505	-2.470898	33220.256112

HLA B*4402	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.106853	1.635727	-2.471126	12789.477261
HLA B*0802	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.224322	1.753043	-2.471279	16761.865259
HLA B*4402	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.437266	1.965836	-2.471430	27369.418410
HLA B*0801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.381425	1.909820	-2.471605	24067.188466
HLA B*1502	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.185617	1.713482	-2.472135	15332.639663
HLA A*0216	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.060178	1.587869	-2.472309	11486.241021
HLA A*3301	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.637265	2.164911	-2.472354	43377.596012
HLA B*3801	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.261381	1.788992	-2.472388	18254.955229
HLA A*3101	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.247899	1.775111	-2.472788	17696.990886
HLA B*1509	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.259687	1.786784	-2.472903	18183.889914
HLA A*2301	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.390732	1.917562	-2.473170	24588.479231
HLA A*0216	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.423030	1.949733	-2.473297	26486.833364
HLA A*3001	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.226390	1.753043	-2.473347	16841.853761
HLA B*4402	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.423333	1.949733	-2.473600	26505.324333
HLA A*6901	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.026961	1.553110	-2.473851	10640.472315
HLA B*5401	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.491651	2.017754	-2.473898	31020.689575
HLA B*3901	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.391469	1.917562	-2.473908	24630.283305
HLA B*3501	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.027041	1.553110	-2.473931	10642.429663
HLA B*3901	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.478290	2.004292	-2.473998	30080.837706
HLA B*0801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.367592	1.893265	-2.474327	23312.647190
HLA A*0202	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.258054	0.783681	-2.474374	1811.566777
HLA B*5101	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.500533	2.025736	-2.474796	31661.573985
HLA B*1503	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.811288	1.336347	-2.474940	6475.712821
HLA B*3801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.389540	1.914570	-2.474971	24521.130017
HLA A*0216	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.193629	1.718496	-2.475133	15618.117044
HLA A*3002	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.203703	1.728396	-2.475308	15984.654912
HLA B*1501	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.399545	1.924123	-2.475422	25092.537809
HLA A*0202	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.425159	1.949733	-2.475425	26616.973530
HLA A*0206	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.502030	1.026553	-2.475477	3177.090376
HLA B*5101	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.333550	1.858036	-2.475514	21555.093100
HLA A*3001	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.264670	1.788992	-2.475678	18393.740332
HLA A*6801	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.587879	2.111966	-2.475914	38715.003689
HLA A*6801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-3.402989	0.926967	-2.476023	2529.236136
HLA A*6802	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.426059	1.949733	-2.476325	26672.180742
HLA A*6802	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.390913	1.914570	-2.476343	24598.723978
HLA A*0206	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.112294	1.635727	-2.476567	12950.728573
HLA B*1501	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-3.772225	1.295300	-2.476925	5918.682496
HLA B*1501	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.263777	1.786784	-2.476994	18355.966096
HLA A*2402	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.442855	1.965836	-2.477019	27723.942774
HLA B*4402	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.401159	1.924123	-2.477036	25185.970098
HLA B*3801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.461108	1.984040	-2.477068	28913.997738
HLA B*1801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.401215	1.924123	-2.477092	25189.240389
HLA A*0101	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.378869	1.901679	-2.477190	23925.946054
HLA B*3901	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.300103	1.822872	-2.477230	19957.339003
HLA A*2402	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.436366	1.958921	-2.477445	27312.768026
HLA A*6901	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.104738	1.627062	-2.477676	12727.357921
HLA B*1801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.395269	1.917562	-2.477707	24846.689025
HLA B*1801	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.462074	1.984040	-2.478034	28978.358510
HLA B*1503	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.888210	1.410054	-2.478156	7730.538008
HLA B*3801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.380079	1.901679	-2.478400	23992.698909
HLA A*2403	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.402620	1.924123	-2.478497	25270.862403
HLA A*0301	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.336007	1.857234	-2.478773	21677.413618
HLA A*0201	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.396356	1.917562	-2.478794	24909.002490
HLA B*1502	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.483431	2.004292	-2.479139	30439.015356
HLA A*3002	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.772220	1.293038	-2.479182	5918.618458
HLA A*2601	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.393847	1.914570	-2.479277	24765.499175
HLA A*2601	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.106505	1.627062	-2.479443	12779.241290
HLA B*4403	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.389303	1.909820	-2.479483	24507.735360
HLA A*2402	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.207946	1.728396	-2.479551	16141.594565
HLA B*2705	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.336818	1.857234	-2.479584	21717.910378
HLA A*3001	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.284622	1.804702	-2.479920	19258.474276
HLA A*2602	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.092855	1.612498	-2.480356	12383.818049
HLA A*0203	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.208933	1.728396	-2.480538	16178.312443
HLA A*6802	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.303526	1.822872	-2.480653	20115.268509
HLA A*2602	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.563217	2.082473	-2.480744	36577.730934

HLA A*6802	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.002329	1.521566	-2.480763	10053.769066
HLA B*1509	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.253205	1.772257	-2.480948	17914.494761
HLA B*1517	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.465436	1.984040	-2.481396	29203.566566
HLA A*3201	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.310269	1.828772	-2.481496	20430.023025
HLA A*2402	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-3.923062	1.440990	-2.482072	8376.488186
HLA B*0802	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.432050	1.949733	-2.482317	27042.678947
HLA A*8001	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.399993	1.917562	-2.482431	25118.479048
HLA B*4002	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.721739	1.239243	-2.482496	5269.134802
HLA B*1501	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.342896	1.859882	-2.483014	22023.997765
HLA A*2501	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.437959	1.954913	-2.483046	27413.132611
HLA A*2603	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.510903	2.027725	-2.483178	32426.727940
HLA A*0202	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.487580	2.004292	-2.483288	30731.219191
HLA A*3002	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.487582	2.004292	-2.483291	30731.385444
HLA B*4001	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.794451	1.311116	-2.483335	6229.471041
HLA B*0802	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.376926	1.893265	-2.483661	23819.140990
HLA B*5101	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.467764	1.984040	-2.483724	29360.553173
HLA A*3101	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-3.712177	1.228391	-2.483786	5154.385605
HLA A*0101	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.401403	1.917562	-2.483841	25200.144428
HLA A*2403	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.263204	1.779355	-2.483849	18331.751968
HLA B*1509	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.157061	1.673173	-2.483889	14356.920271
HLA B*0702	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.433715	1.949733	-2.483982	27146.603334
HLA A*0250	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.447240	0.962975	-2.484265	2800.525805
HLA A*3001	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.275727	1.791215	-2.484512	18868.037364
HLA A*0211	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.488952	2.004292	-2.484660	30828.464180
HLA B*5301	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.443771	1.958921	-2.484850	27782.498072
HLA A*0219	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.341891	1.856944	-2.484947	21973.061676
HLA A*3002	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.469416	1.984120	-2.485296	29472.428426
HLA B*0802	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.204046	1.718496	-2.485550	15997.285280
HLA B*1502	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.343148	1.856944	-2.486204	22036.750226
HLA A*2902	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.396199	1.909820	-2.486379	24899.975545
HLA A*0250	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.273871	1.787266	-2.486604	18787.570983
HLA A*2902	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.452662	1.965836	-2.486826	28357.095391
HLA B*5801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.346968	1.859882	-2.487085	22231.451139
HLA A*0101	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.345145	1.858036	-2.487109	22138.317490
HLA A*6901	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.344658	1.856944	-2.487714	22113.539837
HLA B*0801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.160929	1.673173	-2.487756	14485.334913
HLA B*5401	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.579520	1.091476	-2.488044	3797.696753
HLA A*6802	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.115109	1.627062	-2.488047	13034.935436
HLA A*0206	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.492359	2.004292	-2.488067	31071.244091
HLA B*4501	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-2.284146	-0.203931	-2.488077	192.373756
HLA A*0216	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.406107	1.917562	-2.488545	25474.560426
HLA B*1501	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.162028	1.673173	-2.488855	14522.055757
HLA A*0206	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.349010	1.859882	-2.489127	22336.211553
HLA A*2403	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.245477	1.756081	-2.489396	17598.558987
HLA B*1801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.382736	1.893265	-2.489472	24139.950293
HLA B*1517	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-3.846159	1.356576	-2.489582	7017.115698
HLA B*7301	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.399634	1.909820	-2.489814	25097.696757
HLA A*2501	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.455735	1.965836	-2.489899	28558.465648
HLA A*0219	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-3.967871	1.477798	-2.490074	9286.912598
HLA A*2301	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.474256	1.984120	-2.490135	29802.717133
HLA A*0216	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.474254	1.984040	-2.490214	29802.555904
HLA A*2603	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.117468	1.627062	-2.490406	13105.927686
HLA A*3002	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.043783	1.553110	-2.490674	11060.715424
HLA A*6802	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.246765	1.756081	-2.490683	17650.809427
HLA B*7301	1:31-39	9	ARRVREARV	0.936445	0.312607	-3.739741	1.249052	-2.490689	5492.133225
HLA A*6901	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.384355	1.893265	-2.491091	24230.097777
HLA B*0702	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.384583	1.893265	-2.491318	24242.816081
HLA B*4501	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.575460	2.084113	-2.491347	37623.563507
HLA B*3901	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.384632	1.893265	-2.491368	24245.570408
HLA B*1517	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.393337	1.901679	-2.491658	24736.442876
HLA A*1101	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.457826	1.965836	-2.491990	28696.300544
HLA A*2601	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.366770	0.874608	-2.492162	2326.857125
HLA B*4403	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.600884	2.108491	-2.492392	39891.806563
HLA A*8001	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.416520	1.924123	-2.492397	26092.735768
HLA A*2902	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.409960	1.917562	-2.492398	25701.581887

HLA A*2902	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.442425	1.949733	-2.492692	27696.509383
HLA B*0803	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.402590	1.909820	-2.492769	25269.085202
HLA A*3001	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.277472	1.784483	-2.492989	18944.030966
HLA A*0212	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.125700	1.632644	-2.493056	13356.736636
HLA B*4002	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.459879	1.966426	-2.493453	28832.304906
HLA A*0206	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.417781	1.924123	-2.493658	26168.648262
HLA A*2501	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.351735	1.858036	-2.493699	22476.822548
HLA A*0216	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.106801	1.612498	-2.494303	12787.955179
HLA A*2603	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.408884	1.914570	-2.494314	25637.979154
HLA B*5101	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.408898	1.914570	-2.494328	25638.811360
HLA A*3001	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.269562	1.775111	-2.494450	18602.087332
HLA A*2601	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.387903	1.893265	-2.494638	24428.842473
HLA A*6901	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.111655	1.617007	-2.494649	12931.685722
HLA A*0201	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.387959	1.893265	-2.494695	24432.014455
HLA A*0211	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.107233	1.612498	-2.494735	12800.690898
HLA A*3001	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.876862	1.381752	-2.495110	7531.157103
HLA A*3101	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.412718	1.917562	-2.495156	25865.337500
HLA A*0250	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.490604	1.995235	-2.495368	30945.932751
HLA B*3801	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.499698	2.004292	-2.495407	31600.825948
HLA B*1503	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.765036	1.269596	-2.495440	5821.509615
HLA B*4002	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.578110	2.082473	-2.495638	37853.857800
HLA B*1509	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.500053	2.004292	-2.495762	31626.650996
HLA B*0702	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.405764	1.909820	-2.495944	25454.447446
HLA A*3201	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.357585	1.861603	-2.495982	22781.647857
HLA B*4801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.324829	1.828772	-2.496056	21126.551596
HLA B*0803	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.420309	1.924123	-2.496186	26321.421246
HLA A*2902	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.785570	1.289353	-2.496217	6103.375893
HLA B*4002	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.514087	2.017754	-2.496333	32665.302174
HLA A*0212	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.420535	1.924123	-2.496412	26335.094810
HLA A*6802	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.132354	1.635727	-2.496627	13562.948238
HLA B*4402	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.245754	1.749103	-2.496651	17609.796912
HLA B*3501	1:36-44	9	EARVFSEVI	1.251732	0.243780	-3.992283	1.495512	-2.496771	9823.867753
HLA B*5701	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.420960	1.924123	-2.496837	26360.894499
HLA A*1101	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.479009	1.982154	-2.496854	30130.675549
HLA A*2902	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.421313	1.924123	-2.497190	26382.294608
HLA B*7301	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.595332	2.097879	-2.497453	39385.092646
HLA B*4001	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.415028	1.917562	-2.497466	26003.253711
HLA B*1517	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.407350	1.909820	-2.497530	25547.568741
HLA B*1502	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.815131	1.317518	-2.497613	6533.281007
HLA B*5301	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.320489	1.822872	-2.497617	20916.504862
HLA B*5701	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.407453	1.909820	-2.497633	25553.650683
HLA A*0212	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.282188	1.784483	-2.497704	19150.839271
HLA B*0801	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.135211	1.637421	-2.497790	13652.465196
HLA B*1509	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.216297	1.718496	-2.497800	16454.947631
HLA A*3002	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.354876	1.856944	-2.497932	22639.987271
HLA A*0212	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.957510	1.459325	-2.498185	9067.971143
HLA B*5801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.355506	1.857234	-2.498272	22672.835670
HLA A*8001	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.400026	1.901679	-2.498347	25120.381554
HLA A*0212	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.834726	1.336347	-2.498379	6834.803658
HLA A*2603	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.787873	1.289353	-2.498520	6135.820037
HLA B*3801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.464787	1.965836	-2.498952	29159.994399
HLA B*5301	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.596840	2.097879	-2.498961	39522.120756
HLA A*0206	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.792120	1.293038	-2.499082	6196.129445
HLA A*0219	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.409239	1.909820	-2.499419	25658.931203
HLA A*0203	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.359535	1.859882	-2.499653	22884.172200
HLA B*0702	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.417274	1.917562	-2.499712	26138.087112
HLA A*0202	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.218256	1.718496	-2.499760	16529.357583
HLA A*0202	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.284413	1.784483	-2.499929	19249.203935
HLA B*0702	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.322855	1.822872	-2.499983	21030.763871
HLA B*5701	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.328884	1.828772	-2.500111	21324.743977
HLA A*0202	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.780260	1.280105	-2.500156	6029.208210
HLA A*3001	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.194404	1.694140	-2.500264	15646.024401
HLA B*5301	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-3.248877	0.748391	-2.500486	1773.688127
HLA B*0803	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.287408	1.786784	-2.500625	19382.436375
HLA A*2902	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.358812	1.858036	-2.500776	22846.073293

HLA A*0101	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.394228	1.893265	-2.500963	24787.213223
HLA B*1501	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.168064	0.666703	-2.501361	1472.530750
HLA A*0202	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.506559	1.005151	-2.501409	3210.401695
HLA B*5401	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.529340	2.027725	-2.501614	33832.924272
HLA A*2603	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.411445	1.909820	-2.501625	25789.607275
HLA B*3501	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.791148	1.289353	-2.501795	6182.267540
HLA A*6802	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.419670	1.917562	-2.502108	26282.718025
HLA B*5401	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.790076	1.287816	-2.502260	6167.035242
HLA A*2402	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-3.531346	1.028966	-2.502381	3398.963045
HLA A*3301	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.461402	1.958921	-2.502481	28933.557041
HLA B*4403	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.614619	2.111966	-2.502653	41173.595519
HLA B*1501	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.359916	1.857234	-2.502682	22904.236726
HLA A*1101	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.360261	1.857234	-2.503027	22922.458650
HLA A*3001	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.282524	1.779355	-2.503169	19165.660363
HLA A*0201	1:291-299	9	TFLEALSGV	0.900311	0.134202	-3.537775	1.034513	-2.503261	3449.646821
HLA B*1502	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.450644	1.947300	-2.503344	28225.623000
HLA A*0301	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.361525	1.858036	-2.503489	22989.272116
HLA A*0250	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.332392	1.828772	-2.503619	21497.680638
HLA A*1101	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.308605	1.804702	-2.503903	20351.921588
HLA A*6801	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.486109	1.982154	-2.503955	30627.321162
HLA B*1509	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.057124	1.553110	-2.504014	11405.743339
HLA A*3101	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.276274	1.772257	-2.504018	18891.835599
HLA A*2301	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.198939	1.694140	-2.504799	15810.241699
HLA B*1509	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.284260	1.779355	-2.504905	19242.436281
HLA A*6901	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.364880	1.859882	-2.504998	23167.559415
HLA A*6901	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.134722	1.629570	-2.505153	13637.111305
HLA B*4002	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.487411	1.982154	-2.505256	30719.251342
HLA A*0201	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.117825	1.612498	-2.505327	13116.709164
HLA B*5701	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.407220	1.901679	-2.505541	25539.968348
HLA B*1502	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.464630	1.958921	-2.505709	29149.426908
HLA B*5101	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.258789	1.753043	-2.505746	18146.350296
HLA B*5701	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.932197	1.426359	-2.505838	8554.542298
HLA A*2603	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.531776	2.025736	-2.506040	34023.262243
HLA A*3101	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.334847	1.828772	-2.506074	21619.558393
HLA A*0202	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.469071	0.962975	-2.506096	2944.902992
HLA A*0301	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.366189	1.859882	-2.506307	23237.475700
HLA A*3201	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.420923	1.914570	-2.506353	26358.612845
HLA B*1801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.490613	1.984120	-2.506493	30946.602415
HLA B*7301	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.590631	2.084113	-2.506517	38961.040968
HLA A*3101	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.366546	1.859882	-2.506664	23256.591808
HLA A*0211	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.523899	1.017185	-2.506714	3341.170016
HLA B*4002	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.615396	2.108491	-2.506905	41247.390029
HLA B*7301	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.589388	2.082473	-2.506915	38849.700434
HLA A*3301	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.489370	1.982154	-2.507216	30858.165064
HLA A*1101	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.457067	1.949733	-2.507334	28646.200580
HLA B*0802	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.279594	1.772257	-2.507337	19036.801432
HLA B*1501	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-3.584891	1.077535	-2.507356	3844.954510
HLA A*6801	1:399-407	9	RQPFPGPGL	1.549104	0.615807	-4.672599	2.164911	-2.507688	47054.307327
HLA A*2902	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.422485	1.914570	-2.507915	26453.610744
HLA A*0301	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.364885	1.856944	-2.507941	23167.810085
HLA B*1801	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.369640	1.861603	-2.508037	23422.882624
HLA A*8001	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.417868	1.909820	-2.508048	26173.886857
HLA B*4402	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.295467	1.787266	-2.508201	19745.452946
HLA A*0203	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-2.941701	0.433361	-2.508340	874.381360
HLA B*1501	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.003875	1.495512	-2.508363	10089.621313
HLA A*2501	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.492441	1.984040	-2.508401	31077.127867
HLA B*4002	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.401960	1.893265	-2.508695	25232.475358
HLA B*1503	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-3.537244	1.028547	-2.508697	3445.431740
HLA B*1503	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.036866	1.528166	-2.508700	10885.949990
HLA A*2402	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.475158	1.966426	-2.508732	29864.693573
HLA B*2705	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.367096	1.858036	-2.509060	23286.051297
HLA A*0219	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.367373	1.858036	-2.509337	23300.921088
HLA B*5101	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.297062	1.787266	-2.509796	19818.117587
HLA A*0211	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.294631	1.784483	-2.510147	19707.461369
HLA B*5301	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.297833	1.787266	-2.510567	19853.314939

HLA B*5701	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.224125	1.713482	-2.510643	16754.249883
HLA B*0801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.428406	1.917562	-2.510844	26816.720218
HLA B*4402	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.368235	1.857234	-2.511001	23347.229375
HLA B*3501	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-3.223362	0.712255	-2.511107	1672.483538
HLA B*4601	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.340168	1.828772	-2.511396	21886.101159
HLA A*2603	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.529184	2.017754	-2.511431	33820.846292
HLA A*0250	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-2.802038	0.290570	-2.511468	633.925328
HLA B*5701	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.404899	1.893265	-2.511634	25403.822144
HLA B*0801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.240282	1.728396	-2.511887	17389.311886
HLA A*0203	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.429493	1.917562	-2.511932	26883.974360
HLA A*3001	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.233596	1.720897	-2.512698	17123.627134
HLA B*4601	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.406010	1.893265	-2.512746	25468.910656
HLA A*3002	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.130160	1.617007	-2.513153	13494.589726
HLA B*4002	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.625257	2.111966	-2.513292	42194.637668
HLA B*4501	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.824421	1.311116	-2.513305	6674.537877
HLA A*0212	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.431190	1.917562	-2.513628	26989.186893
HLA A*0203	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.209737	1.695841	-2.513896	16208.272975
HLA B*5401	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.539694	2.025736	-2.513957	34649.240309
HLA A*2601	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.336846	1.822872	-2.513974	21719.320322
HLA B*5801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.336860	1.822872	-2.513988	21720.025328
HLA B*0702	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.143777	1.629570	-2.514208	13924.425964
HLA A*6901	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.337286	1.822872	-2.514413	21741.303774
HLA B*5301	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.542168	2.027725	-2.514443	34847.186909
HLA A*0203	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.298980	1.784483	-2.514496	19905.797452
HLA B*4501	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.374494	1.859882	-2.514612	23686.144702
HLA B*4002	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.527754	2.013049	-2.514705	33709.602724
HLA B*5101	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.462086	1.947300	-2.514786	28979.142369
HLA A*0211	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.270880	1.756081	-2.514798	18658.629454
HLA A*0219	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.438969	1.924123	-2.514846	27476.976705
HLA B*1501	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.142260	1.627062	-2.515198	13875.847976
HLA B*5801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.344007	1.828772	-2.515235	22080.426645
HLA B*1501	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.154665	1.639403	-2.515261	14277.915714
HLA B*4001	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.264553	1.749103	-2.515449	18388.765600
HLA B*5801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.303009	1.787266	-2.515743	20091.342048
HLA A*0212	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.302579	1.786784	-2.515795	20071.461267
HLA A*3001	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.755097	1.239243	-2.515854	5689.803885
HLA A*0201	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.579069	1.062990	-2.516079	3793.754138
HLA B*4001	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.338970	1.822872	-2.516098	21825.799680
HLA A*0219	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.433845	1.917562	-2.516283	27154.681842
HLA A*3001	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.154613	1.638021	-2.516592	14276.216492
HLA A*3101	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.373599	1.856944	-2.516655	23637.373863
HLA A*0212	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.870377	1.353717	-2.516660	7419.542530
HLA B*7301	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.628763	2.111966	-2.516797	42536.592185
HLA B*0702	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.133806	1.617007	-2.516800	13608.369285
HLA A*2902	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.212833	1.695841	-2.516992	16324.254749
HLA A*3001	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-3.626317	1.109115	-2.517203	4229.775580
HLA B*1509	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.434902	1.917562	-2.517340	27220.869093
HLA A*0216	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.441678	1.924123	-2.517555	27648.902801
HLA A*3002	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.483764	1.965836	-2.517929	30462.407721
HLA B*5401	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.472884	1.954913	-2.517971	29708.707749
HLA B*1503	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.296393	0.778023	-2.518370	1978.760551
HLA A*0202	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.804643	1.286148	-2.518495	6377.393829
HLA A*0101	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.378712	1.859882	-2.518829	23917.275365
HLA A*2403	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.310337	1.791215	-2.519122	20433.228477
HLA A*2301	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.478165	1.958921	-2.519244	30072.214041
HLA A*3002	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.420955	1.901679	-2.519276	26360.609281
HLA B*5101	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.436944	1.917562	-2.519382	27349.140949
HLA B*4801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.379395	1.859882	-2.519513	23954.957453
HLA A*3001	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.268667	1.749103	-2.519563	18563.784797
HLA A*6901	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.376959	1.857234	-2.519725	23820.945083
HLA B*2705	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.291997	1.772257	-2.519740	19588.307419
HLA A*6802	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.429580	1.909820	-2.519760	26889.356153
HLA B*1503	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.135860	1.616065	-2.519795	13672.865319
HLA B*1503	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.149703	1.629570	-2.520133	14115.709159
HLA B*3801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.348995	1.828772	-2.520223	22335.486546

HLA B*1801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.380265	1.859882	-2.520382	24002.955130
HLA A*0206	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.305309	1.784483	-2.520826	20198.033736
HLA A*0212	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.414142	1.893265	-2.520877	25950.273387
HLA A*2501	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.445012	1.924123	-2.520889	27861.970045
HLA B*0803	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.414198	1.893265	-2.520934	25953.642921
HLA A*0201	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.380960	1.859882	-2.521078	24041.422506
HLA A*0202	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-3.542008	1.020890	-2.521119	3483.440572
HLA A*0212	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.133693	1.612498	-2.521195	13604.835995
HLA A*3201	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.307995	1.786784	-2.521211	20323.315284
HLA A*0211	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.662001	1.140721	-2.521280	4591.993914
HLA A*2403	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.199968	1.678625	-2.521343	15847.748984
HLA A*0206	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.414898	1.893265	-2.521634	25995.517752
HLA A*0250	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.433801	0.911989	-2.521811	2715.191869
HLA A*3101	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.309374	1.787266	-2.522107	20387.956688
HLA A*0211	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.471949	1.949733	-2.522215	29644.809680
HLA A*0216	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.424421	0.902116	-2.522305	2657.182480
HLA A*2301	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.446880	1.924123	-2.522757	27982.058586
HLA B*3901	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.351531	1.828772	-2.522758	22466.246088
HLA A*2301	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.251645	1.728396	-2.523249	17850.258358
HLA B*0801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.381035	1.857234	-2.523801	24045.584832
HLA A*0301	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.352959	1.828772	-2.524187	22540.264012
HLA B*5301	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.474000	1.949733	-2.524267	29785.148309
HLA B*4403	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.537692	2.013049	-2.524643	34489.901642
HLA B*4501	1:70-78	9	VYADGAPKL	1.519604	0.588887	-4.633213	2.108491	-2.524721	42974.676694
HLA B*3501	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.384921	1.859882	-2.525039	24261.709176
HLA B*7301	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.575629	2.050505	-2.525124	37638.221191
HLA A*0203	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.418409	1.893265	-2.525144	26206.474627
HLA A*1101	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.426869	1.901679	-2.525190	26722.008499
HLA B*4801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.382687	1.857234	-2.525453	24137.207965
HLA B*4002	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.623462	2.097879	-2.525583	42020.600586
HLA A*0202	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.192588	0.666703	-2.525885	1558.074778
HLA B*1517	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.254344	1.728396	-2.525949	17961.560464
HLA B*0802	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.305318	1.779355	-2.525963	20198.470817
HLA A*2601	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.383258	1.857234	-2.526024	24168.959679
HLA A*0203	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.138655	1.612498	-2.526157	13761.171999
HLA A*3001	1:203-211	9	GAQWTPANI	1.276445	0.182880	-3.985572	1.459325	-2.526247	9673.249248
HLA A*3001	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.282427	1.756081	-2.526346	19161.409787
HLA A*2603	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.609213	2.082473	-2.526740	40664.237087
HLA A*0101	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.384038	1.857234	-2.526804	24212.408148
HLA A*3001	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-3.370393	0.843518	-2.526875	2346.349070
HLA B*1501	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.162620	1.635727	-2.526893	14541.867061
HLA B*4001	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.419704	0.892605	-2.527098	2628.473570
HLA B*1517	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.451257	1.924123	-2.527134	28265.505195
HLA A*2501	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.437432	1.909820	-2.527612	27379.933081
HLA A*2601	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.299870	1.772257	-2.527613	19946.653133
HLA B*4601	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.387593	1.859882	-2.527710	24411.403933
HLA B*4501	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.421052	1.893265	-2.527787	26366.456857
HLA A*0206	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.356770	1.828772	-2.527997	22738.921545
HLA A*0216	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.256574	1.728396	-2.528178	18054.011961
HLA A*1101	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.452366	1.924123	-2.528243	28337.772476
HLA A*0250	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.533277	2.004292	-2.528986	34141.081439
HLA A*0206	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-2.995640	0.466612	-2.529028	990.011792
HLA A*0212	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.248085	1.718496	-2.529589	17704.555864
HLA A*6802	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.431667	1.901679	-2.529988	27018.842901
HLA A*0219	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.670868	1.140721	-2.530147	4686.711929
HLA A*0211	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.162855	1.632644	-2.530211	14549.736179
HLA B*4402	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.722491	1.191820	-2.530672	5278.264442
HLA A*0206	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.814300	1.283502	-2.530797	6520.781088
HLA A*3101	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.353676	1.822872	-2.530803	22577.486512
HLA A*3301	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.388074	1.857234	-2.530840	24438.491863
HLA B*1502	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.480649	1.949733	-2.530916	30244.667159
HLA B*3901	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.604655	1.072837	-2.531818	4023.973147
HLA A*0301	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.195809	1.663852	-2.531957	15696.723032
HLA B*0802	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.361135	1.828772	-2.532363	22968.636061
HLA A*2902	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.389414	1.856944	-2.532470	24513.967607

HLA A*0101	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.389595	1.856944	-2.532651	24524.181308
HLA B*4601	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.389604	1.856944	-2.532660	24524.712006
HLA B*1501	1:278-286	9	ATGANLVTV	1.225117	0.184937	-3.942934	1.410054	-2.532880	8768.674004
HLA A*2601	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.392795	1.859882	-2.532912	24705.549437
HLA A*3001	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.074919	1.541660	-2.533258	11882.794703
HLA A*2501	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.448137	1.914570	-2.533567	28063.164113
HLA B*0803	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.390924	1.857234	-2.533690	24599.389369
HLA A*3201	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.166398	1.632644	-2.533754	14668.920065
HLA A*3001	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.150943	1.617007	-2.533937	14156.087215
HLA B*1501	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.322954	1.788992	-2.533961	21035.542926
HLA A*3301	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.209008	1.675016	-2.533992	16181.113418
HLA B*1502	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.500455	1.966426	-2.534029	31655.922065
HLA A*3002	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.484255	1.949733	-2.534522	30496.870034
HLA A*0206	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-3.578825	1.044058	-2.534767	3791.620265
HLA A*0201	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.391742	1.856944	-2.534798	24645.744820
HLA B*0802	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.436589	1.901679	-2.534910	27326.808743
HLA A*0201	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.363703	1.828772	-2.534931	23104.852135
HLA A*0219	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.322247	1.787266	-2.534980	21001.317014
HLA A*6801	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.363816	1.828772	-2.535044	23110.852659
HLA B*4801	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.324523	1.788992	-2.535531	21111.698820
HLA B*1502	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.561471	2.025736	-2.535735	36431.000095
HLA A*0201	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.393175	1.857234	-2.535941	24727.210922
HLA B*1517	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-3.355013	0.819048	-2.535965	2264.711547
HLA B*0702	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.315419	1.779355	-2.536064	20673.734149
HLA B*7301	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.450726	1.914570	-2.536156	28230.967918
HLA A*2602	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.563896	2.027725	-2.536171	36634.963407
HLA B*0801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-3.910802	1.373907	-2.536895	8143.336246
HLA B*3501	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.663355	1.126421	-2.536934	4606.325326
HLA B*5701	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.397031	1.859882	-2.537148	24947.707198
HLA A*3301	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.564995	2.027725	-2.537270	36727.834354
HLA B*5401	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.541785	2.004292	-2.537493	34816.471788
HLA B*0702	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.394759	1.857234	-2.537524	24817.537470
HLA B*2705	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.455204	1.917562	-2.537642	28523.570406
HLA B*0801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.394646	1.856944	-2.537702	24811.093820
HLA B*1509	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.312917	1.775111	-2.537805	20554.964246
HLA A*0216	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.366790	1.828772	-2.538018	23269.680310
HLA B*4002	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.360947	1.822872	-2.538075	22958.697590
HLA B*4001	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.395132	1.856944	-2.538188	24838.894014
HLA B*4501	1:324-332	9	VLDGKTAEF	1.113241	0.998725	-4.650378	2.111966	-2.538412	44707.249881
HLA A*0101	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.367197	1.828772	-2.538424	23291.468850
HLA B*5701	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.395694	1.857234	-2.538460	24871.030568
HLA A*2301	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.504928	1.966426	-2.538502	31983.676749
HLA A*2603	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.636678	2.097879	-2.538799	43318.968670
HLA A*2602	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-3.594679	1.055834	-2.538845	3932.594437
HLA A*0216	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.398774	1.859882	-2.538892	25048.051995
HLA B*1509	1:45-53	9	PHTASIEEI	1.223034	0.013946	-3.776102	1.236980	-2.539121	5971.751034
HLA A*2501	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.413844	0.874608	-2.539236	2593.247685
HLA B*1501	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.288454	1.749103	-2.539351	19429.153876
HLA A*2403	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.368444	1.828772	-2.539672	23358.473309
HLA B*1502	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.523818	1.984120	-2.539698	33405.520801
HLA A*0206	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.328696	1.788992	-2.539704	21315.516814
HLA A*0211	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.524091	1.984040	-2.540051	33426.490919
HLA B*4402	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.401661	1.861603	-2.540058	25215.145190
HLA B*3501	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.329053	1.788992	-2.540061	21333.051839
HLA A*0250	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.487502	1.947300	-2.540202	30725.733348
HLA B*5301	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.522373	1.982154	-2.540219	33294.562586
HLA A*6801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-3.801251	1.260962	-2.540288	6327.768481
HLA B*4403	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.400397	1.859882	-2.540515	25141.862693
HLA A*6801	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.553762	2.013049	-2.540714	35790.060561
HLA A*2403	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.328012	1.787266	-2.540746	21281.986670
HLA A*8001	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.434127	1.893265	-2.540862	27172.316024
HLA B*5701	1:211-219	9	IANALIEQV	1.224006	0.188649	-3.953718	1.412655	-2.541063	8989.138267
HLA B*5801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.345981	1.804702	-2.541279	22180.995214
HLA A*0206	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.525674	1.984040	-2.541634	33548.595250
HLA A*2501	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.435381	1.893265	-2.542117	27250.927100

HLA B*7301	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.497145	1.954913	-2.542231	31415.541049
HLA B*5101	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.681516	1.139224	-2.542292	4803.039145
HLA B*4601	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.399993	1.857234	-2.542759	25118.479048
HLA B*4501	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.625438	2.082473	-2.542966	42212.217989
HLA A*2301	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.527244	1.984040	-2.543204	33670.052692
HLA B*1503	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.829510	1.286148	-2.543362	6753.208936
HLA A*2403	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.160487	1.617007	-2.543480	14470.609960
HLA B*1503	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.831568	1.287816	-2.543752	6785.288772
HLA B*1801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.493540	1.949733	-2.543807	31155.909502
HLA B*5401	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.556932	2.013049	-2.543883	36052.209702
HLA A*0301	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.366802	1.822872	-2.543930	23270.309751
HLA B*0801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.166807	1.622722	-2.544085	14682.734724
HLA A*0203	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.401370	1.857234	-2.544136	25198.235881
HLA B*0702	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.300439	1.756081	-2.544357	19972.784257
HLA A*1101	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.459259	1.914570	-2.544689	28791.155691
HLA B*1501	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.273262	1.728396	-2.544867	18761.264999
HLA A*2602	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.258388	1.713482	-2.544906	18129.571032
HLA B*1502	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.462574	1.917562	-2.545012	29011.769704
HLA A*0212	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.402143	1.856944	-2.545199	25243.124986
HLA A*2402	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.324716	1.779355	-2.545361	21121.066278
HLA B*0702	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.405407	1.859882	-2.545524	25433.524778
HLA A*0206	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.463413	1.917562	-2.545851	29067.855159
HLA A*3002	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.369175	1.822872	-2.546303	23397.806448
HLA B*3801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.369314	1.822872	-2.546441	23405.275833
HLA A*2902	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.240665	1.694140	-2.546526	17404.652752
HLA B*5101	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.470753	1.924123	-2.546630	29563.291025
HLA A*2501	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.318967	1.772257	-2.546710	20843.308166
HLA A*0301	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.162808	1.616065	-2.546743	14548.162015
HLA B*0801	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.335754	1.788992	-2.546761	21664.751898
HLA B*4402	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.370345	1.822872	-2.547473	23460.928049
HLA B*7301	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.529932	1.982154	-2.547777	33879.079884
HLA A*3002	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.457807	1.909820	-2.547987	28695.058620
HLA A*0250	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.160571	1.612498	-2.548073	14473.428472
HLA B*5401	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.532448	1.984040	-2.548408	34075.944743
HLA A*6802	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.406144	1.856944	-2.549200	25476.765554
HLA B*1509	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.442519	1.893265	-2.549254	27702.503434
HLA A*0202	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.473401	1.924123	-2.549278	29744.087379
HLA B*1503	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.406365	1.856944	-2.549421	25489.724538
HLA B*4001	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.268218	1.718496	-2.549722	18544.612952
HLA A*1101	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.467391	1.917562	-2.549829	29335.308895
HLA B*4501	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.647876	2.097879	-2.549997	44450.408244
HLA A*0219	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-3.331997	0.781791	-2.550207	2147.817316
HLA A*6901	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.329605	1.779355	-2.550250	21360.190306
HLA B*4001	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.407493	1.857234	-2.550259	25556.000913
HLA A*0212	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-3.206389	0.656026	-2.550363	1608.381882
HLA A*8001	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.408534	1.858036	-2.550498	25617.321386
HLA B*7301	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.443882	1.893265	-2.550617	27789.563081
HLA B*1517	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.444131	1.893265	-2.550866	27805.503528
HLA B*7301	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.546355	1.995235	-2.551119	35184.753037
HLA A*0212	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.463221	0.911989	-2.551231	2905.499304
HLA B*5801	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.330695	1.779355	-2.551340	21413.875763
HLA A*0219	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.380352	1.828772	-2.551579	24007.760184
HLA A*3002	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.475868	1.924123	-2.551745	29913.525987
HLA A*2602	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.556178	2.004292	-2.551886	35989.656687
HLA A*0203	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.338745	1.786784	-2.551961	21814.467408
HLA B*0802	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.237254	1.685162	-2.552092	17268.471998
HLA A*0206	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.717308	1.165167	-2.552141	5215.646886
HLA A*0250	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.565247	2.013049	-2.552198	36749.100715
HLA A*0206	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.832315	1.280105	-2.552211	6796.971855
HLA B*4801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.324678	1.772257	-2.552422	21119.238155
HLA A*6802	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.445895	1.893265	-2.552631	27918.702269
HLA B*4601	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.332004	1.779355	-2.552649	21478.499689
HLA A*6802	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.640156	1.087303	-2.552853	4366.724494
HLA A*3301	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.328130	1.775111	-2.553018	21287.744108
HLA B*1503	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-3.590234	1.036964	-2.553270	3892.547626

HLA B*0803	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.332751	1.779355	-2.553396	21515.481915
HLA B*0801	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.340415	1.786784	-2.553632	21898.536836
HLA A*8001	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.413526	1.859882	-2.553644	25913.517759
HLA A*2301	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.501092	1.947300	-2.553792	31702.366215
HLA A*0203	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.306888	1.753043	-2.553845	20271.596222
HLA B*1801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.501263	1.947300	-2.553963	31714.888646
HLA B*5101	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.935787	1.381752	-2.554035	8625.549882
HLA A*6901	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.338644	1.784483	-2.554160	21809.393403
HLA B*1502	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.538371	1.984040	-2.554331	34543.867329
HLA B*0803	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.341728	1.787266	-2.554462	21964.861051
HLA B*4801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.411419	1.856944	-2.554475	25788.072613
HLA A*2402	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.233215	1.678625	-2.554590	17108.626527
HLA A*0203	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.190363	1.635727	-2.554636	15501.113243
HLA A*6901	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.303749	1.749103	-2.554646	20125.609197
HLA B*1801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.177380	1.622722	-2.554658	15044.564995
HLA A*0219	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.377549	1.822872	-2.554676	23853.313090
HLA B*2705	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.383834	1.828772	-2.555061	24201.015009
HLA A*0212	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.383857	1.828772	-2.555085	24202.324292
HLA B*4402	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.413134	1.858036	-2.555098	25890.116726
HLA A*3201	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.981992	1.426359	-2.555633	9593.824356
HLA A*0301	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.330799	1.775111	-2.555687	21418.973624
HLA A*0202	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.485470	0.929716	-2.555755	3058.231792
HLA A*2601	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.228157	1.672339	-2.555818	16910.509968
HLA A*0203	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.143961	1.587869	-2.556092	13930.302913
HLA B*3801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.173282	1.617007	-2.556276	14903.289336
HLA B*4403	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.471068	1.914570	-2.556498	29584.729968
HLA B*3901	1:263-271	9	LRAGERAQV	0.865849	0.254971	-3.677545	1.120820	-2.556725	4759.326469
HLA A*2402	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.506552	1.949733	-2.556819	32103.462953
HLA A*6802	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.414109	1.857234	-2.556875	25948.308028
HLA B*0802	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.343773	1.786784	-2.556989	22068.484610
HLA A*6802	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-3.512635	0.955413	-2.557223	3255.630768
HLA B*5301	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.583039	2.025736	-2.557303	38285.944538
HLA B*4402	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.231007	1.673173	-2.557834	17021.844942
HLA A*0202	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.869226	1.311116	-2.558110	7399.900513
HLA A*6802	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.705448	1.147258	-2.558190	5075.139456
HLA B*4403	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.562488	2.004292	-2.558197	36516.439088
HLA B*2705	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.252469	1.694140	-2.558330	17884.185900
HLA A*2501	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.508199	1.949733	-2.558466	32225.441096
HLA A*0301	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.230985	1.672339	-2.558647	17021.016186
HLA A*0101	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.381569	1.822872	-2.558696	24075.132027
HLA A*2403	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.987071	1.428368	-2.558704	9706.694242
HLA B*4001	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.331012	1.772257	-2.558756	21429.520779
HLA B*0803	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.476319	1.917562	-2.558757	29944.613271
HLA A*3301	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.571964	2.013049	-2.558915	37321.912777
HLA A*1101	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.421101	1.861603	-2.559498	26369.452459
HLA A*0212	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.315616	1.756081	-2.559535	20683.131063
HLA A*0211	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.461675	0.902116	-2.559559	2895.174964
HLA A*0211	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.186707	1.627062	-2.559645	15371.175826
HLA A*3001	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.223538	1.663852	-2.559686	16731.605541
HLA B*1801	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.153100	1.593295	-2.559805	14226.565144
HLA B*1509	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.416914	1.856944	-2.559970	26116.461228
HLA B*5801	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.349195	1.788992	-2.560203	22345.759671
HLA A*0203	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.417375	1.856944	-2.560431	26144.168198
HLA B*7301	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-3.669896	1.109115	-2.560781	4676.226873
HLA A*6901	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.282707	1.721649	-2.561058	19173.749429
HLA A*2402	1:388-396	9	RELGLPEEI	1.155087	0.273281	-3.989571	1.428368	-2.561204	9762.728274
HLA B*5101	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.471314	1.909820	-2.561494	29601.540003
HLA B*5101	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.463180	1.901679	-2.561501	29052.291194
HLA A*0202	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-3.343425	0.781791	-2.561635	2205.084489
HLA B*1517	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.340993	1.779355	-2.561638	21927.699526
HLA B*4402	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.390445	1.828772	-2.561673	24572.256030
HLA B*0803	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.421693	1.859882	-2.561811	26405.426240
HLA B*7301	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.862976	1.301147	-2.561830	7294.176214
HLA A*0216	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.318175	1.756081	-2.562094	20805.342669
HLA B*1517	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.349602	1.787266	-2.562335	22366.683099

HLA B*5101	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.385276	1.822872	-2.562404	24281.536500
HLA B*0802	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.349855	1.787266	-2.562589	22379.755055
HLA B*5401	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.544938	1.982154	-2.562783	35070.161642
HLA B*7301	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.588638	2.025736	-2.562902	38782.713202
HLA A*6901	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.319049	1.756081	-2.562968	20847.255139
HLA A*2402	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.116166	1.553110	-2.563056	13066.706994
HLA A*3201	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.701990	1.138932	-2.563057	5034.884804
HLA B*4002	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.613590	2.050505	-2.563085	41076.148887
HLA B*1517	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.284746	1.721649	-2.563097	19263.996937
HLA B*5401	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.547308	1.984120	-2.563188	35262.118288
HLA B*5801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.347750	1.784483	-2.563267	22271.537041
HLA A*0216	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.456708	1.893265	-2.563443	28622.499556
HLA B*3501	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-3.736184	1.172675	-2.563509	5447.333230
HLA B*1503	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.190640	1.627062	-2.563578	15511.011800
HLA B*2705	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.386481	1.822872	-2.563609	24349.017992
HLA B*3501	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.456905	1.893265	-2.563640	28635.509454
HLA A*3001	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.179739	1.616065	-2.563674	15126.502303
HLA A*8001	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.420652	1.856944	-2.563708	26342.219271
HLA A*6802	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.285663	1.721649	-2.564014	19304.684118
HLA B*0702	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.249206	1.685162	-2.564044	17750.301773
HLA B*5301	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.529993	1.965836	-2.564157	33883.845552
HLA B*2705	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.343514	1.779355	-2.564159	22055.355831
HLA B*3501	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.320388	1.756081	-2.564307	20911.639721
HLA B*4002	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.530192	1.965836	-2.564357	33899.430302
HLA B*0801	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.249598	1.685162	-2.564437	17766.345555
HLA A*0301	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.337109	1.772257	-2.564853	21732.484210
HLA A*0211	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.424966	1.859882	-2.565084	26605.168568
HLA A*1101	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.425135	1.859882	-2.565253	26615.533620
HLA B*1503	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.086863	1.521566	-2.565297	12214.153558
HLA B*1502	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.793389	1.228069	-2.565320	6214.256912
HLA B*1501	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.261651	1.695841	-2.565810	18266.315850
HLA B*3901	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.198807	1.632644	-2.566163	15805.452652
HLA B*5701	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.251496	1.685162	-2.566335	17844.175616
HLA A*8001	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.423690	1.857234	-2.566456	26527.128709
HLA A*6801	1:194-202	9	RFLHDFAGL	1.457268	0.626845	-4.650773	2.084113	-2.566660	44747.901043
HLA B*4601	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.239951	1.673173	-2.566778	17376.052475
HLA B*4801	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.346787	1.779355	-2.567432	22222.192302
HLA A*1101	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.193149	1.625692	-2.567458	15600.890126
HLA A*3201	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.160806	1.593295	-2.567512	14481.260555
HLA B*5401	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.533987	1.966426	-2.567561	34196.906268
HLA A*0250	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.517533	1.949733	-2.567800	32925.575491
HLA A*0201	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.949611	1.381752	-2.567859	8904.533269
HLA B*5401	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.563221	1.995235	-2.567986	36578.126699
HLA B*5401	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.533937	1.965836	-2.568102	34193.021458
HLA B*0801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.317221	1.749103	-2.568118	20759.695651
HLA A*0216	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-2.867429	0.299099	-2.568330	736.934639
HLA B*1517	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.428239	1.859882	-2.568357	26806.421836
HLA A*0206	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-3.994905	1.426359	-2.568546	9883.358132
HLA B*3801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.428448	1.859882	-2.568566	26819.331704
HLA B*5301	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.563837	1.995235	-2.568602	36630.008965
HLA A*0219	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.287110	1.718496	-2.568614	19369.124131
HLA B*5301	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.573038	2.004292	-2.568746	37414.298620
HLA A*6802	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.348246	1.779355	-2.568891	22296.974218
HLA A*0250	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-3.475913	0.906788	-2.569125	2991.663161
HLA B*5701	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.356490	1.787266	-2.569224	22724.287466
HLA B*4403	1:504-512	9	VAEVNRVVL	1.751585	0.330888	-4.651785	2.082473	-2.569313	44852.359768
HLA B*5801	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.356333	1.786784	-2.569549	22716.052255
HLA A*0206	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.318715	1.749103	-2.569612	20831.246339
HLA A*2601	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.265535	1.695841	-2.569693	18430.395787
HLA B*4403	1:376-384	9	RLLFKDEVR	1.310157	0.787722	-4.667602	2.097879	-2.569723	46515.964465
HLA A*6901	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.374464	1.804702	-2.569762	23684.478948
HLA A*6901	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.356662	1.786784	-2.569878	22733.263557
HLA A*2601	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.374591	1.804702	-2.569888	23691.399000
HLA A*2902	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.463366	1.893265	-2.570101	29064.710252
HLA A*3301	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.283856	1.713482	-2.570374	19224.539504

HLA B*5101	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.427607	1.856944	-2.570663	26767.439889
HLA A*0301	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.265044	1.694140	-2.570904	18409.568926
HLA A*2402	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.786966	1.215498	-2.571468	6123.020480
HLA B*3801	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.526471	1.954913	-2.571558	33610.178230
HLA B*5801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.299964	1.728396	-2.571568	19950.969967
HLA A*2402	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.555931	1.984040	-2.571891	35969.218987
HLA A*0212	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.429557	1.857234	-2.572323	26887.901508
HLA A*2602	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.377044	1.804702	-2.572341	23825.584807
HLA A*8001	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.401166	1.828772	-2.572393	25186.378861
HLA A*3001	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-3.929011	1.356576	-2.572434	8492.017419
HLA A*0219	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.184987	1.612498	-2.572489	15310.425738
HLA A*0212	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.432468	1.859882	-2.572586	27068.732515
HLA A*0202	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.094222	1.521566	-2.572656	12422.870634
HLA A*2902	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.432646	1.859882	-2.572764	27079.864155
HLA B*1509	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.364147	1.791215	-2.572932	23128.488213
HLA A*1101	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.284495	1.711364	-2.573131	19252.849042
HLA A*3001	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.291722	1.718496	-2.573226	19575.912786
HLA A*0219	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.466766	1.893265	-2.573501	29293.124850
HLA B*4403	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.624097	2.050505	-2.573592	42082.023668
HLA A*0203	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.861458	1.287816	-2.573642	7268.729104
HLA A*2603	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.557999	1.984040	-2.573959	36140.865991
HLA B*5701	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.396911	1.822872	-2.574038	24940.824966
HLA B*1502	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.498228	1.924123	-2.574105	31493.987898
HLA A*0301	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.365447	1.791215	-2.574231	23197.784591
HLA B*4801	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.327336	1.753043	-2.574293	21248.854129
HLA A*2603	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.540629	1.965836	-2.574793	34723.925206
HLA B*5801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.330975	1.756081	-2.574894	21427.665958
HLA B*1502	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.468450	1.893265	-2.575186	29406.970328
HLA A*2403	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.362425	1.786784	-2.575642	23036.954984
HLA A*3002	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.559850	1.984040	-2.575810	36295.263100
HLA B*1501	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.192976	1.617007	-2.575969	15594.645844
HLA B*1509	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.198939	1.622722	-2.576217	15810.241699
HLA A*3301	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.252133	1.675762	-2.576371	17870.355791
HLA A*1101	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-3.563619	0.987241	-2.576378	3661.162192
HLA B*0702	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.433365	1.856944	-2.576421	27124.729994
HLA B*5301	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.500570	1.924123	-2.576447	31664.314673
HLA B*5801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.325813	1.749103	-2.576710	21174.494387
HLA A*0203	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-3.949503	1.372792	-2.576712	8902.317608
HLA A*3001	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.206400	1.629570	-2.576831	16084.237365
HLA B*3501	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.434103	1.857234	-2.576869	27170.846072
HLA A*0202	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-2.980881	0.403979	-2.576901	956.931614
HLA B*7301	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.364368	1.787266	-2.577102	23140.252724
HLA A*0301	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.363940	1.786784	-2.577157	23117.480048
HLA B*3901	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.434590	1.857234	-2.577355	27201.290307
HLA A*2403	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.055352	1.477798	-2.577554	11359.313428
HLA A*0301	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.365205	1.787266	-2.577938	23184.861955
HLA A*6901	1:481-489	9	MTADWTRVP	0.898983	0.129318	-3.606417	1.028301	-2.578116	4040.333250
HLA A*3001	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.813336	1.235042	-2.578294	6506.333669
HLA B*1509	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.194390	1.616065	-2.578325	15645.516549
HLA A*0101	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.365611	1.787266	-2.578345	23206.571076
HLA A*2301	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.211071	1.632644	-2.578427	16258.154631
HLA A*3101	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.307125	1.728396	-2.578730	20282.675625
HLA A*3001	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.216292	1.637421	-2.578871	16454.769593
HLA A*2403	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.436107	1.857234	-2.578873	27296.519366
HLA A*2403	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.368235	1.788992	-2.579243	23347.229375
HLA A*0216	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.211908	1.632644	-2.579263	16289.496717
HLA A*0301	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.368428	1.788992	-2.579436	23357.588759
HLA A*3001	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.293019	1.713482	-2.579537	19634.458901
HLA B*0702	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.351956	1.772257	-2.579699	22488.255584
HLA A*0203	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.212495	1.632644	-2.579851	16311.542715
HLA A*3002	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.258879	1.678625	-2.580254	18150.081129
HLA A*2601	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.367535	1.787266	-2.580269	23309.620534
HLA A*0203	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.336879	1.756081	-2.580798	21720.965371
HLA B*4601	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.372103	1.791215	-2.580887	23556.057317
HLA A*3002	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.197050	1.616065	-2.580985	15741.623586

HLA B*4002	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.439209	1.858036	-2.581173	27492.142924
HLA B*2705	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.441107	1.859882	-2.581225	27612.579349
HLA A*2501	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.404100	1.822872	-2.581228	25357.138259
HLA A*2603	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.576510	1.995235	-2.581275	37714.655673
HLA A*3001	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-3.813162	1.231855	-2.581307	6503.729498
HLA A*3201	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.707154	1.125828	-2.581326	5095.111666
HLA A*0101	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.372692	1.791215	-2.581477	23588.065394
HLA A*0219	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.441434	1.859882	-2.581551	27633.351116
HLA B*1503	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.474198	0.892605	-2.581592	2979.871727
HLA A*0301	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.366262	1.784483	-2.581778	23241.373104
HLA A*8001	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.361276	1.779355	-2.581921	22976.092737
HLA A*0201	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.338040	1.756081	-2.581958	21779.091967
HLA A*0201	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.255138	1.673173	-2.581966	17994.433987
HLA A*2902	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.410787	1.828772	-2.582014	25750.571551
HLA B*4002	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.506359	1.924123	-2.582236	32089.224665
HLA A*6802	1:291-299	9	TFLEALSGV	0.900311	0.134202	-3.616774	1.034513	-2.582260	4137.840228
HLA A*0250	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-3.904520	1.322138	-2.582382	8026.382358
HLA A*2902	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.405618	1.822872	-2.582746	25445.911122
HLA A*6901	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.335824	1.753043	-2.582781	21668.268300
HLA A*0203	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.722153	1.139224	-2.582928	5274.154148
HLA B*4403	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-2.844291	0.261282	-2.583009	698.700803
HLA A*2602	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.497586	1.914570	-2.583016	31447.508766
HLA B*1501	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.255467	1.672339	-2.583128	18008.067854
HLA B*2705	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.440247	1.856944	-2.583303	27557.959997
HLA A*0101	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.388100	1.804702	-2.583398	24439.946212
HLA B*5101	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.412229	1.828772	-2.583457	25836.248719
HLA A*2403	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.901362	1.317518	-2.583844	7968.235054
HLA A*8001	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.370770	1.786784	-2.583987	23483.912004
HLA B*3501	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-3.845031	1.260962	-2.584069	6998.917663
HLA B*1509	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.219844	1.635727	-2.584117	16589.917519
HLA B*4801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.885306	1.301147	-2.584159	7679.019251
HLA B*1501	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.966156	1.381752	-2.584404	9250.308871
HLA A*3301	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.602202	2.017754	-2.584448	40013.060020
HLA B*5301	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.568501	1.984040	-2.584461	37025.484709
HLA A*3101	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.371316	1.786784	-2.584532	23513.405033
HLA B*3801	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.477811	1.893265	-2.584546	30047.658283
HLA A*2301	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.013494	1.428368	-2.585126	10315.580156
HLA B*3901	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.360308	1.775111	-2.585197	22924.938943
HLA A*0201	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.369706	1.784483	-2.585223	23426.430919
HLA B*7301	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.598304	2.013049	-2.585255	39655.549293
HLA A*0202	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.569417	1.984040	-2.585377	37103.685646
HLA A*6802	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.724667	1.139224	-2.585442	5304.772552
HLA B*4601	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.341557	1.756081	-2.585476	21956.188359
HLA B*5801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.360893	1.775111	-2.585782	22955.841075
HLA B*4801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.390609	1.804702	-2.585907	24581.563115
HLA A*2603	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.796119	1.210159	-2.585960	6253.444584
HLA B*3801	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.495883	1.909820	-2.586063	31324.407872
HLA B*5101	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.259318	1.673173	-2.586145	18168.451937
HLA A*0101	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.203506	1.617007	-2.586499	15977.392644
HLA A*8001	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.409506	1.822872	-2.586634	25674.760649
HLA A*2902	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.444025	1.857234	-2.586791	27798.735241
HLA B*1503	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-3.968416	1.381432	-2.586985	9298.575866
HLA A*2603	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.591305	2.004292	-2.587013	39021.580353
HLA A*0301	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.367157	1.779355	-2.587802	23289.326876
HLA A*2902	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.392863	1.804702	-2.588160	24709.425716
HLA A*0216	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.217767	1.629570	-2.588198	16510.768269
HLA A*0216	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.215446	1.627062	-2.588384	16422.754127
HLA A*0211	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.851666	1.263068	-2.588598	7106.664776
HLA A*0216	1:428-436	9	SIVREELTA	1.468906	-0.179470	-3.878262	1.289436	-2.588826	7555.478956
HLA A*2902	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.211673	1.622722	-2.588951	16280.686663
HLA A*0101	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.338117	1.749103	-2.589014	21782.980456
HLA A*0206	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.491292	0.902116	-2.589176	3099.505580
HLA A*0250	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.513438	1.924123	-2.589315	32616.565045
HLA B*4402	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.317975	1.728396	-2.589580	20795.777728
HLA B*1503	1:99-107	9	MAQALGGIV	1.150311	0.231441	-3.971818	1.381752	-2.590067	9371.702487

HLA A*0219	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.447350	1.857234	-2.590115	28012.350938
HLA B*1501	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.395116	1.804702	-2.590413	24837.953402
HLA B*0802	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.413573	1.822872	-2.590701	25916.321696
HLA A*1101	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.178893	1.587869	-2.591024	15097.071199
HLA B*3901	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.782887	1.191820	-2.591068	6065.784907
HLA A*2602	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.146327	0.555251	-2.591076	1400.641331
HLA B*5301	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.264254	1.673173	-2.591082	18376.135829
HLA B*0803	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.319526	1.728396	-2.591130	20870.162327
HLA B*4501	1:415-423	9	VTAKRLDTL	1.681869	0.368636	-4.641643	2.050505	-2.591138	43816.993008
HLA A*0203	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.750610	1.159455	-2.591155	5631.314480
HLA A*3001	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.267083	1.675762	-2.591321	18496.219568
HLA A*3002	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.484840	1.893265	-2.591576	30537.978902
HLA A*0211	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.509214	1.917562	-2.591652	32300.842351
HLA B*4801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.231117	1.639403	-2.591714	17026.173548
HLA A*0203	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.018089	1.426359	-2.591730	10425.316553
HLA B*4403	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.830990	1.239243	-2.591747	6776.264694
HLA B*0802	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.380791	1.788992	-2.591799	24032.059906
HLA A*0211	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.258548	0.666703	-2.591845	1813.626025
HLA A*0206	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.204375	1.612498	-2.591877	16009.405965
HLA A*3201	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.596178	2.004292	-2.591886	39461.872223
HLA B*5101	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.451790	1.859882	-2.591908	28300.237825
HLA B*4403	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.485310	1.893265	-2.592046	30571.038200
HLA B*1501	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.004998	1.412655	-2.592343	10115.746101
HLA B*4002	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.576590	1.984120	-2.592470	37721.593403
HLA A*0101	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.348551	1.756081	-2.592470	22312.660874
HLA A*6801	1:330-338	9	AEFLVQGTL	1.554668	0.473057	-4.620276	2.027725	-2.592551	41713.473348
HLA B*3501	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.314592	1.721649	-2.592943	20634.403011
HLA A*2402	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.384184	1.791215	-2.592968	24220.530669
HLA A*2602	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.577069	1.984040	-2.593029	37763.246589
HLA B*1501	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-2.997092	0.403979	-2.593113	993.327249
HLA A*3201	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.517362	1.924123	-2.593239	32912.575027
HLA B*5301	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.450326	1.856944	-2.593382	28205.016365
HLA A*0216	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.382443	1.788992	-2.593450	24123.631504
HLA A*0101	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.372916	1.779355	-2.593560	23600.191347
HLA A*2301	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.053031	1.459325	-2.593705	11298.760205
HLA B*4002	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.577819	1.984040	-2.593779	37828.472953
HLA B*0702	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.381106	1.787266	-2.593839	24049.487667
HLA A*2902	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.312336	1.718496	-2.593840	20527.516169
HLA A*3201	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.599312	1.005151	-2.594162	3974.773127
HLA B*0702	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.557341	0.962975	-2.594367	3608.619943
HLA B*7301	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.322909	1.728396	-2.594514	21033.380838
HLA A*0212	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.499783	0.905240	-2.594543	3160.701345
HLA A*0201	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.895850	1.301147	-2.594704	7867.744445
HLA A*0201	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.399434	1.804702	-2.594732	25086.158471
HLA A*2603	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.561163	1.966426	-2.594737	36405.190757
HLA B*1503	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.379269	1.784483	-2.594785	23947.960417
HLA A*0250	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.578862	1.984040	-2.594822	37919.445811
HLA A*2902	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.273448	1.678625	-2.594823	18769.284926
HLA A*6901	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.369995	1.775111	-2.594884	23442.024437
HLA B*4403	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.561330	1.966426	-2.594904	36419.176754
HLA A*2601	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.379449	1.784483	-2.594966	23957.938292
HLA B*0802	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.351056	1.756081	-2.594975	22441.708438
HLA A*0206	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.182845	1.587869	-2.594976	15235.072912
HLA B*0802	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.452309	1.857234	-2.595075	28334.093414
HLA B*4403	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.379590	1.784483	-2.595107	23965.716142
HLA A*0201	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.908321	1.313175	-2.595146	8096.947277
HLA B*1509	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.207726	1.612498	-2.595227	16133.388174
HLA A*2501	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.148509	1.553110	-2.595399	14076.969290
HLA A*0219	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.658829	1.062990	-2.595839	4558.579142
HLA B*5401	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.554782	1.958921	-2.595861	35874.190479
HLA A*6802	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.913424	1.317518	-2.595906	8192.649833
HLA B*0801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.380467	1.784483	-2.595983	24014.125114
HLA B*0801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-3.831394	1.235408	-2.595986	6782.572949
HLA A*0201	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.735409	1.139224	-2.596184	5437.616981
HLA A*3201	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.324805	1.728396	-2.596410	21125.408704

HLA A*3101	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.385464	1.788992	-2.596472	24292.047608
HLA A*0301	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.307915	1.711364	-2.596551	20319.577434
HLA B*1501	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.318222	1.721649	-2.596573	20807.593883
HLA A*0101	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.381237	1.784483	-2.596754	24056.774654
HLA A*2501	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.310283	1.713482	-2.596801	20430.686181
HLA A*2501	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.498510	1.901679	-2.596830	31514.440014
HLA A*2301	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.352975	1.756081	-2.596894	22541.117610
HLA A*0211	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.566274	0.969193	-2.597080	3683.612066
HLA A*6802	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-3.518608	0.921448	-2.597160	3300.711263
HLA A*6901	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-3.329079	0.731526	-2.597553	2133.434329
HLA A*3101	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.377041	1.779355	-2.597686	23825.455913
HLA A*3001	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.220460	1.622722	-2.597738	16613.448590
HLA A*2602	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.593199	1.995235	-2.597963	39192.100402
HLA A*2601	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.389183	1.791215	-2.597968	24500.974502
HLA A*0211	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.511056	0.912830	-2.598227	3243.816588
HLA B*4801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.316758	1.718496	-2.598262	20737.582829
HLA B*4501	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.624090	2.025736	-2.598353	42081.340696
HLA B*3901	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.455347	1.856944	-2.598403	28532.984830
HLA B*3501	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.221357	1.622722	-2.598636	16647.817072
HLA A*8001	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.347842	1.749103	-2.598739	22276.236512
HLA B*1503	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-3.502401	0.903619	-2.598781	3179.807194
HLA B*4403	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.617086	2.017754	-2.599332	41408.142865
HLA A*0301	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.216348	1.617007	-2.599342	16456.906175
HLA A*0101	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.374490	1.775111	-2.599378	23685.888424
HLA B*5701	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.378799	1.779355	-2.599443	23922.063267
HLA A*0250	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.412801	0.813260	-2.599540	2587.026203
HLA A*0219	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.386956	1.786784	-2.600173	24375.641085
HLA A*0211	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.524396	1.924123	-2.600273	33450.007557
HLA A*8001	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.387844	1.787266	-2.600578	24425.538763
HLA A*2601	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.387391	1.786784	-2.600607	24400.049157
HLA B*1501	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.353795	1.753043	-2.600752	22583.716599
HLA B*0801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.392087	1.791215	-2.600872	24665.352235
HLA A*3201	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.392160	1.791215	-2.600945	24669.489123
HLA A*1101	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.295091	1.694140	-2.600952	19728.369027
HLA A*0202	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.888806	1.287816	-2.600990	7741.167934
HLA B*4001	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.405700	1.804702	-2.600998	25450.729663
HLA B*4403	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.388488	1.787266	-2.601222	24461.771822
HLA A*0201	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.319820	1.718496	-2.601323	20884.280258
HLA B*0802	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.458317	1.856944	-2.601373	28728.764849
HLA A*0201	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.388321	1.786784	-2.601538	24452.377808
HLA B*5701	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.388394	1.786784	-2.601610	24456.478976
HLA A*3001	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.241048	1.639403	-2.601645	17420.007151
HLA A*2501	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.274091	1.672339	-2.601753	18797.127448
HLA A*0202	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-3.885823	1.284024	-2.601799	7688.164073
HLA A*0202	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.388977	1.786784	-2.602193	24489.313093
HLA B*5301	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.549569	1.947300	-2.602269	35446.111766
HLA A*3301	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.597660	1.995235	-2.602425	39596.811036
HLA B*3901	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.938775	1.336347	-2.602428	8685.110254
HLA B*1501	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.232163	1.629570	-2.602593	17067.211748
HLA B*5801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.321490	1.718496	-2.602994	20964.764895
HLA B*5801	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.356147	1.753043	-2.603104	22706.345915
HLA A*2601	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.392139	1.788992	-2.603147	24668.288020
HLA A*2902	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.242679	1.639403	-2.603275	17485.532855
HLA A*0250	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.156436	1.553110	-2.603327	14336.275082
HLA A*0211	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.690670	1.087303	-2.603367	4905.346835
HLA A*0101	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.390459	1.786784	-2.603676	24573.053642
HLA B*4801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.388460	1.784483	-2.603976	24460.183848
HLA B*1503	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-3.897251	1.293038	-2.604212	7893.153307
HLA B*0702	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-3.943860	1.339557	-2.604303	8787.384334
HLA A*2501	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.461611	1.857234	-2.604377	28947.491329
HLA B*5401	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.554211	1.949733	-2.604478	35827.061143
HLA A*6802	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.839768	1.235042	-2.604726	6914.615542
HLA A*6901	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.396091	1.791215	-2.604876	24893.779835
HLA A*6901	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.393906	1.788992	-2.604914	24768.848867
HLA B*4002	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.333374	1.728396	-2.604978	21546.349074

HLA A*6901	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-3.979172	1.373907	-2.605265	9531.744251
HLA A*3301	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.467012	1.861603	-2.605409	29309.769195
HLA A*3101	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.358544	1.753043	-2.605501	22831.987838
HLA B*4601	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.410293	1.804702	-2.605591	25721.333538
HLA A*3301	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.463784	1.858036	-2.605748	29092.711893
HLA A*8001	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.397111	1.791215	-2.605895	24952.296407
HLA A*6901	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.693329	1.087303	-2.606027	4935.479323
HLA A*0211	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.321702	0.715584	-2.606118	2097.499645
HLA A*0201	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.397482	1.791215	-2.606267	24973.633812
HLA A*8001	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.362373	1.756081	-2.606292	23034.213344
HLA A*0301	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-3.683856	1.077535	-2.606321	4828.988968
HLA B*7301	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-3.635128	1.028547	-2.606581	4316.461725
HLA A*0211	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.955452	1.348830	-2.606622	9025.099125
HLA B*1501	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.381839	1.775111	-2.606727	24090.114723
HLA A*2501	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.233847	1.627062	-2.606785	17133.542154
HLA A*2601	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.320327	1.713482	-2.606845	20908.698557
HLA B*1509	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.320560	1.713482	-2.607078	20919.899816
HLA B*5401	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.516962	1.909820	-2.607142	32882.319866
HLA A*2301	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.396429	1.788992	-2.607437	24913.180244
HLA A*1101	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.292655	1.685162	-2.607493	19618.001664
HLA B*0801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.243222	1.635727	-2.607495	17507.397912
HLA A*3001	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.234726	1.627062	-2.607664	17168.243519
HLA B*3501	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.220399	1.612498	-2.607900	16611.111955
HLA B*1502	1:480-488	9	AMTADWTRV	0.947260	0.174566	-3.730432	1.121826	-2.608606	5375.667567
HLA A*0211	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.337123	1.728396	-2.608728	21733.189644
HLA A*2902	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.396241	1.787266	-2.608975	24902.400373
HLA A*0203	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-3.390937	0.781791	-2.609146	2460.008004
HLA B*3501	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.393713	1.784483	-2.609230	24757.863572
HLA B*5701	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.414046	1.804702	-2.609343	25944.518114
HLA A*0216	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-3.983885	1.374504	-2.609381	9635.748322
HLA B*3501	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.396201	1.786784	-2.609418	24900.110251
HLA A*0202	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.898966	1.289353	-2.609613	7924.386731
HLA A*0202	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.748866	1.139224	-2.609642	5608.754917
HLA A*2301	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.519547	1.909820	-2.609727	33078.581929
HLA B*1517	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.362841	1.753043	-2.609798	23059.024593
HLA A*0216	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.358917	1.749103	-2.609814	22851.635732
HLA B*4501	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.511674	1.901679	-2.609995	32484.318422
HLA B*4601	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.385123	1.775111	-2.610012	24272.999574
HLA A*0101	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.399049	1.788992	-2.610057	25063.911354
HLA B*4002	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.635846	2.025736	-2.610110	43236.087868
HLA B*1517	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.247836	1.637421	-2.610415	17694.406128
HLA A*0203	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.131997	1.521566	-2.610431	13551.799967
HLA A*6801	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.577081	1.966426	-2.610655	37764.268078
HLA B*4001	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.402063	1.791215	-2.610848	25238.482288
HLA A*0201	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.400040	1.788992	-2.611048	25121.196959
HLA A*3002	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.305215	1.694140	-2.611075	20193.663444
HLA A*0219	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.395560	1.784483	-2.611076	24863.362428
HLA B*2705	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.364923	1.753043	-2.611880	23169.815536
HLA A*0301	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.368256	1.756081	-2.612175	23348.366156
HLA A*0301	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.365249	1.753043	-2.612206	23187.245201
HLA A*0203	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.913575	1.301147	-2.612428	8195.486889
HLA A*3001	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.036749	1.424271	-2.612478	10883.005799
HLA B*2705	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.334227	1.721649	-2.612577	21588.703147
HLA B*4601	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.399425	1.786784	-2.612641	25085.615623
HLA A*6802	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.238447	1.625692	-2.612756	17315.994893
HLA B*5401	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.527451	1.914570	-2.612881	33686.085819
HLA B*3901	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.229905	1.617007	-2.612898	16978.711214
HLA A*0206	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.245545	1.632644	-2.612901	17601.320185
HLA A*0201	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.392496	1.779355	-2.613141	24688.581173
HLA A*0301	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.217824	1.604651	-2.613173	16512.912123
HLA A*0211	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.546482	0.933159	-2.613322	3519.506934
HLA B*1517	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.470663	1.857234	-2.613429	29557.214152
HLA B*4403	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.515264	1.901679	-2.613585	32753.956810
HLA A*0212	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.392952	1.779355	-2.613597	24714.505897
HLA B*4601	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.398217	1.784483	-2.613734	25015.957372

HLA B*4601	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.403139	1.788992	-2.614147	25301.093948
HLA B*5701	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.398640	1.784483	-2.614157	25040.329276
HLA A*3101	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.398821	1.784483	-2.614337	25050.762285
HLA B*5101	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.363701	1.749103	-2.614598	23104.727141
HLA A*8001	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.404037	1.788992	-2.615044	25353.434688
HLA B*5101	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.508556	1.893265	-2.615291	32251.951076
HLA B*5401	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.562601	1.947300	-2.615301	36525.922713
HLA A*3101	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.406558	1.791215	-2.615343	25501.034566
HLA B*1509	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.399993	1.784483	-2.615510	25118.479048
HLA A*3301	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.599707	1.984120	-2.615586	39783.832018
HLA A*2403	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.228091	1.612498	-2.615593	16907.948610
HLA A*0211	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.251346	1.635727	-2.615619	17837.998445
HLA B*4501	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.168752	1.553110	-2.615643	14748.651917
HLA A*0250	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.781017	1.165167	-2.615850	6039.720150
HLA A*0216	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.402714	1.786784	-2.615931	25276.331497
HLA A*0201	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.952398	1.336347	-2.616050	8961.849576
HLA A*6801	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.600193	1.984120	-2.616073	39828.408780
HLA B*5701	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.391187	1.775111	-2.616076	24614.298842
HLA A*0212	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.344647	1.728396	-2.616251	22112.941686
HLA A*2301	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.473281	1.856944	-2.616337	29735.881988
HLA B*1801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.473591	1.857234	-2.616357	29757.124124
HLA B*5701	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.405414	1.788992	-2.616421	25433.937559
HLA A*3002	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.474721	1.858036	-2.616685	29834.657657
HLA B*3501	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.970442	1.353717	-2.616725	9342.039406
HLA B*4501	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.634517	2.017754	-2.616763	43103.901566
HLA A*3201	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.474841	1.858036	-2.616805	29842.890304
HLA A*6901	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.851849	1.235042	-2.616807	7109.664217
HLA A*2602	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.232898	1.616065	-2.616833	17096.136059
HLA A*0211	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.255070	1.638021	-2.617049	17991.611120
HLA A*6901	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.330540	1.713482	-2.617059	21406.231246
HLA B*0702	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.408376	1.791215	-2.617161	25608.037749
HLA B*4501	1:289-297	9	AETFLEALS	0.785461	-0.921388	-2.481620	-0.135927	-2.617547	303.123801
HLA B*4501	1:187-195	9	HGQQVLSRF	1.146015	0.867034	-4.630645	2.013049	-2.617596	42721.316849
HLA B*7301	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.621919	2.004292	-2.617627	41871.511994
HLA B*1801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-3.517832	0.900174	-2.617658	3294.823881
HLA A*0211	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.511049	1.893265	-2.617784	32437.606115
HLA A*2403	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.339607	1.721649	-2.617958	21857.821515
HLA A*0301	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.367213	1.749103	-2.618110	23292.350897
HLA B*3901	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.230743	1.612498	-2.618245	17011.534401
HLA A*0202	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.150500	0.532233	-2.618266	1414.163497
HLA A*0216	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.475764	1.857234	-2.618530	29906.406365
HLA A*2403	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.403130	1.784483	-2.618646	25300.546450
HLA A*2601	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.394155	1.775111	-2.619043	24783.056593
HLA B*4402	1:51-59	9	EEIRARQPV	0.859860	0.021658	-3.500643	0.881518	-2.619126	3166.965795
HLA A*3201	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.584996	1.965836	-2.619161	38458.867100
HLA B*4001	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.372246	1.753043	-2.619203	23563.832175
HLA A*3201	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.603395	1.984040	-2.619355	40123.176102
HLA A*6801	1:53-61	9	IRARQPVAL	1.567292	0.450462	-4.637284	2.017754	-2.619531	43379.473396
HLA A*3201	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.235656	1.616065	-2.619591	17205.062749
HLA B*2705	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.424386	1.804702	-2.619683	26569.641350
HLA A*0203	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.531694	0.911989	-2.619705	3401.685561
HLA A*2501	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.479622	1.859882	-2.619740	30173.249543
HLA B*3501	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.424482	1.804702	-2.619780	26575.535295
HLA A*0203	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.394925	1.775111	-2.619814	24827.071770
HLA A*0216	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.637116	1.017185	-2.619931	4336.262439
HLA A*0201	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.395191	1.775111	-2.620080	24842.253633
HLA A*0206	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-3.729272	1.109115	-2.620157	5361.320355
HLA B*0802	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.404645	1.784483	-2.620162	25388.983839
HLA B*4403	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.604305	1.984120	-2.620184	40207.267067
HLA B*5801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.249798	1.629570	-2.620228	17774.517121
HLA A*2403	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.173371	1.553110	-2.620262	14906.353407
HLA B*1509	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.443367	1.822872	-2.620495	27756.658456
HLA A*0212	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.900822	1.280105	-2.620717	7958.326548
HLA A*1101	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.478812	1.858036	-2.620776	30116.986356
HLA B*1517	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.339280	1.718496	-2.620784	21841.391167

HLA A*6802	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.407695	1.786784	-2.620911	25567.893620
HLA A*6802	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.425873	1.804702	-2.621171	26660.783988
HLA A*0202	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.244103	1.622722	-2.621381	17542.951369
HLA A*2301	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.481302	1.859882	-2.621420	30290.187823
HLA A*2403	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.426202	1.804702	-2.621500	26680.984100
HLA A*2402	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.546145	1.924123	-2.622022	35167.816355
HLA B*0801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.397181	1.775111	-2.622070	24956.346410
HLA A*6802	1:480-488	9	AMTADWTRV	0.947260	0.174566	-3.743951	1.121826	-2.622125	5545.635749
HLA B*4403	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.569478	1.947300	-2.622178	37108.904911
HLA A*2902	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.401593	1.779355	-2.622238	25211.189577
HLA B*4403	1:307-315	9	KIIGRQFIR	1.192172	0.833564	-4.647984	2.025736	-2.622247	44461.471322
HLA B*7301	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.606445	1.984120	-2.622325	40405.914029
HLA A*2301	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.515658	1.893265	-2.622394	32783.739148
HLA B*5701	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.351014	1.728396	-2.622618	22439.523216
HLA A*0202	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.524909	0.902116	-2.622793	3348.951468
HLA A*0212	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.372107	1.749103	-2.623004	23556.312190
HLA A*0219	1:451-459	9	LADVRSVGV	1.034616	0.104608	-3.762315	1.139224	-2.623091	5785.153882
HLA B*5301	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.336823	1.713482	-2.623341	21718.145362
HLA B*4001	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.398501	1.775111	-2.623390	25032.338093
HLA B*1517	1:98-106	9	AMAQALGGI	0.985073	0.332445	-3.941275	1.317518	-2.623757	8735.246967
HLA B*7301	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.589728	1.965836	-2.623893	38880.187413
HLA B*1501	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.852014	1.228069	-2.623944	7112.357102
HLA B*4801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.399343	1.775111	-2.624231	25080.866209
HLA B*5701	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.250171	1.625692	-2.624480	17789.812847
HLA A*3201	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-3.978303	1.353717	-2.624586	9512.684032
HLA A*0219	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-3.661719	1.036964	-2.624756	4589.013820
HLA B*4402	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.377821	1.753043	-2.624778	23868.286867
HLA A*0206	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.404187	1.779355	-2.624832	25362.214401
HLA B*1503	1:45-53	9	PHTASIEEI	1.223034	0.013946	-3.862126	1.236980	-2.625145	7279.905424
HLA A*3101	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.381623	1.756081	-2.625541	24078.127821
HLA B*2705	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.300558	1.675016	-2.625542	19978.295595
HLA B*4002	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.630053	2.004292	-2.625761	42663.114898
HLA B*5801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.350884	1.725080	-2.625804	22432.847466
HLA A*0211	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.374969	1.749103	-2.625866	23712.043012
HLA A*3301	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.592411	1.966426	-2.625985	39121.136378
HLA A*6901	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.354453	1.728396	-2.626058	22617.951634
HLA B*3901	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.299348	1.673173	-2.626176	19922.711674
HLA B*5401	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.484220	1.858036	-2.626184	30494.395364
HLA A*0219	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.415427	1.788992	-2.626435	26027.179414
HLA A*0250	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.536362	1.909820	-2.626542	34384.455178
HLA A*6901	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.252443	1.625692	-2.626752	17883.121665
HLA A*6802	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.411332	1.784483	-2.626848	25782.911237
HLA A*0202	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.484030	1.856944	-2.627086	30481.035616
HLA B*4402	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.432132	1.804702	-2.627430	27047.799858
HLA A*6802	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.355839	1.728396	-2.627444	22690.259731
HLA B*3801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.356182	1.728396	-2.627787	22708.188572
HLA A*0219	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.180951	1.553110	-2.627841	15168.786968
HLA B*3801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.486078	1.858036	-2.628043	30625.167262
HLA A*8001	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.432952	1.804702	-2.628250	27098.915732
HLA B*1509	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.356669	1.728396	-2.628273	22733.632514
HLA A*2403	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.377570	1.749103	-2.628467	23854.474513
HLA A*3301	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.292441	1.663852	-2.628589	19608.346100
HLA B*4501	1:384-392	9	RAVGRELGL	1.384772	0.599348	-4.612904	1.984120	-2.628783	41011.312627
HLA A*3001	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.264672	1.635727	-2.628946	18393.839840
HLA B*1502	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.385135	1.756081	-2.629054	24273.656154
HLA B*3801	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.222382	1.593295	-2.629087	16687.130819
HLA B*4601	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.378444	1.749103	-2.629341	23902.529475
HLA A*0219	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.378467	1.749103	-2.629364	23903.822610
HLA A*3001	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.262227	1.632644	-2.629582	18290.542494
HLA A*0101	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.382863	1.753043	-2.629820	24147.003424
HLA B*4501	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.613902	1.984040	-2.629862	41105.714438
HLA B*0803	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.402543	1.772257	-2.630286	25266.351291
HLA B*4402	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.402580	1.772257	-2.630323	25268.538396
HLA B*5701	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.386622	1.756081	-2.630541	24356.922804
HLA A*0201	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.379764	1.749103	-2.630661	23975.312301

HLA B*0702	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.967082	1.336347	-2.630735	9270.046899
HLA A*2601	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.386918	1.756081	-2.630837	24373.531264
HLA B*7301	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.548474	1.917562	-2.630912	35356.864367
HLA B*5801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.352578	1.721649	-2.630929	22520.518332
HLA A*6901	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.269118	1.638021	-2.631097	18583.076994
HLA A*1101	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.403515	1.772257	-2.631259	25323.003607
HLA A*3201	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.410676	1.779355	-2.631321	25744.024920
HLA B*3901	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.005928	1.374504	-2.631424	10137.440456
HLA B*7301	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-3.915558	1.284024	-2.631534	8232.992603
HLA B*4403	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.381096	1.749103	-2.631993	24048.967252
HLA A*3201	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.299717	1.667650	-2.632067	19939.640269
HLA A*3101	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.350703	1.718496	-2.632207	22423.504752
HLA A*0212	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.421240	1.788992	-2.632247	26377.870495
HLA B*1501	1:497-505	9	STRITNEVA	1.301822	-0.192924	-3.741188	1.108898	-2.632290	5510.466243
HLA A*2501	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.421458	1.788992	-2.632466	26391.145060
HLA B*4601	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.354141	1.721649	-2.632492	22601.683526
HLA A*0211	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-3.895639	1.263086	-2.632552	7863.914651
HLA A*2603	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.556756	1.924123	-2.632633	36037.584785
HLA A*0219	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.388974	1.756081	-2.632893	24489.180609
HLA A*2501	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.389193	1.756081	-2.633111	24501.504698
HLA B*3901	1:62-70	9	VLSGGPASV	1.079564	0.190032	-3.902758	1.269596	-2.633162	7993.881958
HLA B*5801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.354089	1.720897	-2.633192	22598.993689
HLA B*4801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.424581	1.791215	-2.633365	26581.574351
HLA A*0203	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.438107	1.804702	-2.633404	27422.477230
HLA B*5701	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.386564	1.753043	-2.633521	24353.628821
HLA A*6901	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.269275	1.635727	-2.633548	18589.813885
HLA A*2402	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.421033	1.787266	-2.633767	26365.315765
HLA B*5301	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.493728	1.859882	-2.633846	31169.396422
HLA B*5101	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.425076	1.791215	-2.633861	26611.934186
HLA B*3901	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.418432	1.784483	-2.633949	26207.892406
HLA B*1801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.383333	1.749103	-2.634230	24173.144085
HLA A*0202	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-2.862260	0.227657	-2.634603	728.215811
HLA A*3101	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.274143	1.639403	-2.634740	18799.364769
HLA B*4801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.307985	1.673173	-2.634812	20322.875502
HLA A*2601	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.356638	1.721649	-2.634989	22732.033746
HLA A*0202	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.492251	1.857234	-2.635016	31063.512822
HLA A*0206	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.228373	1.593295	-2.635078	16918.928589
HLA A*2601	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.388178	1.753043	-2.635135	24444.309775
HLA B*4002	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.350765	0.715584	-2.635182	2242.668203
HLA A*2902	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.426402	1.791215	-2.635186	26693.255921
HLA A*0203	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.384348	1.749103	-2.635245	24229.704533
HLA A*3201	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.585051	1.949733	-2.635317	38463.652736
HLA B*5701	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.357061	1.721649	-2.635412	22754.180528
HLA B*4601	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.388488	1.753043	-2.635445	24461.771822
HLA A*0250	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-3.839331	1.203805	-2.635526	6907.661283
HLA A*3002	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.464332	1.828772	-2.635559	29129.406500
HLA B*2705	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.307999	1.672339	-2.635660	20323.535179
HLA B*4501	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.308977	1.673173	-2.635804	20369.325084
HLA B*7301	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.583234	1.947300	-2.635935	38303.139583
HLA B*5301	1:208-216	9	PANIANALI	0.995189	0.008861	-3.640015	1.004050	-2.635964	4365.307314
HLA A*6901	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.356951	1.720897	-2.636053	22748.395677
HLA B*5401	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.560357	1.924123	-2.636234	36337.700214
HLA A*3201	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.274312	1.638021	-2.636291	18806.688774
HLA A*0212	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.263519	1.627062	-2.636457	18345.045934
HLA A*0212	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.411628	1.775111	-2.636517	25800.492047
HLA A*0203	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.425589	1.788992	-2.636596	26643.337640
HLA A*0301	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.365007	1.728396	-2.636612	23174.328436
HLA A*0203	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.846915	1.210159	-2.636756	7029.350056
HLA A*6802	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.385892	1.749103	-2.636788	24315.977332
HLA A*3301	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.493742	1.856944	-2.636799	31170.408176
HLA A*0216	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.158405	1.521566	-2.636839	14401.415947
HLA A*0203	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.416285	1.779355	-2.636930	26078.623705
HLA A*2601	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.386265	1.749103	-2.637162	24336.902262
HLA A*0201	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.365667	1.728396	-2.637272	23209.584351
HLA B*4501	1:256-264	9	VFVDHGLLR	1.229734	0.774558	-4.641567	2.004292	-2.637276	43809.408222

HLA A*8001	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.365712	1.728396	-2.637316	23211.970138
HLA A*0201	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.390537	1.753043	-2.637494	24577.440971
HLA A*8001	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.422050	1.784483	-2.637567	26427.148435
HLA A*2601	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.230981	1.593295	-2.637686	17020.832023
HLA A*0202	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.555271	1.917562	-2.637709	35914.580881
HLA B*0801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.442425	1.804702	-2.637723	27696.509383
HLA A*2603	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.539463	1.901679	-2.637784	34630.875220
HLA A*0206	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-3.901047	1.263068	-2.637979	7962.460774
HLA A*3002	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.555673	1.917562	-2.638111	35947.820511
HLA A*2402	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.548095	1.909820	-2.638275	35326.082223
HLA B*5301	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.552989	1.914570	-2.638420	35726.416151
HLA B*0702	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.366988	1.728396	-2.638592	23280.257170
HLA B*0803	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.495730	1.856944	-2.638786	31313.394806
HLA B*1517	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.313882	1.675016	-2.638866	20600.718325
HLA B*1502	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.541069	0.902116	-2.638953	3475.910711
HLA A*0301	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.142546	1.503120	-2.639426	13885.009149
HLA B*0702	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.444265	1.804702	-2.639562	27814.079057
HLA A*2602	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.335531	1.695841	-2.639689	21653.620388
HLA A*0203	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.314723	1.675016	-2.639707	20640.655228
HLA A*3002	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.415004	1.775111	-2.639893	26001.847002
HLA A*0203	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.831733	1.191820	-2.639913	6787.858795
HLA B*4601	1:496-504	9	ISTRITNEV	1.144524	0.204306	-3.989233	1.348830	-2.640403	9755.125835
HLA A*0206	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.766567	1.125828	-2.640739	5842.079778
HLA B*4002	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.599714	1.958921	-2.640793	39784.477702
HLA B*1503	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.278365	1.637421	-2.640944	18983.015365
HLA A*0201	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.270541	1.629570	-2.640972	18644.099593
HLA B*4001	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.362785	1.721649	-2.641135	23056.030865
HLA A*0212	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.432402	1.791215	-2.641187	27064.632538
HLA A*0216	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.445914	1.804702	-2.641212	27919.910592
HLA A*3201	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.280637	1.639403	-2.641234	19082.582614
HLA B*0702	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.416632	1.775111	-2.641521	26099.512271
HLA A*0101	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.360151	1.718496	-2.641655	22916.631016
HLA A*3101	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.390964	1.749103	-2.641861	24601.651832
HLA A*0219	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.394937	1.753043	-2.641894	24827.743337
HLA A*1101	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.498928	1.856944	-2.641984	31544.801784
HLA B*4601	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.327155	1.685162	-2.641993	21240.004519
HLA B*1801	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.279479	1.637421	-2.642058	19031.755738
HLA A*0202	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.834012	1.191820	-2.642192	6823.572335
HLA B*5701	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.391526	1.749103	-2.642423	24633.481443
HLA A*1101	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.465323	1.822872	-2.642451	29195.984123
HLA B*1517	1:497-505	9	STRITNEVA	1.301822	-0.192924	-3.751592	1.108898	-2.642694	5644.063170
HLA A*2602	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.430135	1.787266	-2.642868	26923.708629
HLA B*1517	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.275551	1.632644	-2.642906	18860.383367
HLA B*4002	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.597820	1.954913	-2.642907	39611.380292
HLA A*0202	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.542746	0.899837	-2.642909	3489.362939
HLA A*0201	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.554916	0.911989	-2.642927	3588.529133
HLA A*0219	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.586724	0.943730	-2.642994	3861.213397
HLA B*5101	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.399138	1.756081	-2.643057	25069.064417
HLA B*2705	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.399197	1.756081	-2.643116	25072.455168
HLA A*0301	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.282564	1.639403	-2.643160	19167.423074
HLA B*5401	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.561004	1.917562	-2.643442	36391.800753
HLA B*1502	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.415704	1.772257	-2.643448	26043.799608
HLA B*4801	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.236749	1.593295	-2.643454	17248.398262
HLA B*1501	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.328717	1.685162	-2.643555	21316.554670
HLA A*0250	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-3.047620	0.403979	-2.643641	1115.887400
HLA B*1501	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.357205	1.713482	-2.643723	22761.690721
HLA A*0250	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.561370	1.917562	-2.643808	36422.526311
HLA B*1509	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.393025	1.749103	-2.643921	24718.651030
HLA B*2705	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.322547	1.678625	-2.643922	21015.864744
HLA B*1501	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.318971	1.675016	-2.643955	20843.533687
HLA A*3201	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.559178	0.915104	-2.644074	3623.918668
HLA B*4002	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-3.544287	0.900174	-2.644113	3501.768294
HLA A*3002	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.784856	1.140721	-2.644134	6093.346492
HLA B*0802	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.365790	1.721649	-2.644140	23216.114456
HLA A*8001	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.397251	1.753043	-2.644209	24960.397071

HLA B*1517	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.428948	1.784483	-2.644465	26850.253603
HLA A*2902	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.420504	1.775111	-2.645393	26333.242766
HLA B*0803	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.450183	1.804702	-2.645481	28195.710154
HLA A*3002	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.278126	1.632644	-2.645481	18972.543261
HLA A*0211	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.946731	1.301147	-2.645584	8845.669162
HLA B*2705	1:509-517	9	RVVLDITSK	0.817327	0.463904	-3.926873	1.281231	-2.645642	8450.313962
HLA A*0212	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.018573	1.372792	-2.645782	10436.941390
HLA A*0250	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.430452	1.784483	-2.645969	26943.379139
HLA B*5801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.357367	1.711364	-2.646003	22770.188844
HLA B*3801	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.425419	1.779355	-2.646064	26632.961761
HLA A*6901	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.371203	1.725080	-2.646122	23507.299989
HLA A*2403	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.319380	1.673173	-2.646207	20863.163375
HLA A*0216	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.437458	1.791215	-2.646243	27381.562476
HLA B*1503	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.234385	1.587869	-2.646516	17154.781447
HLA A*0211	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.284150	1.637421	-2.646729	19237.544229
HLA A*3001	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.272609	1.625692	-2.646917	18733.070217
HLA B*4001	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.367838	1.720897	-2.646941	23325.893429
HLA A*0219	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.451738	1.804702	-2.647036	28296.869800
HLA B*4402	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.368865	1.721649	-2.647216	23381.103913
HLA A*0201	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.020044	1.372792	-2.647252	10472.346955
HLA A*0212	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-3.668199	1.020890	-2.647309	4657.997437
HLA A*2403	1:291-299	9	TFLEALSGV	0.900311	0.134202	-3.682061	1.034513	-2.647548	4809.071197
HLA A*0212	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.452511	1.804702	-2.647809	28347.278931
HLA B*5101	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.505128	1.857234	-2.647894	31998.387524
HLA B*4402	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.320496	1.672339	-2.648157	20916.844332
HLA B*2705	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.076789	1.428368	-2.648421	11934.075581
HLA B*1801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.471321	1.822872	-2.648449	29602.020430
HLA A*0212	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.401542	1.753043	-2.648499	25208.189182
HLA A*0301	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.073077	1.424271	-2.648806	11832.502304
HLA A*3002	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.928987	1.280105	-2.648883	8491.558023
HLA A*6802	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.438027	1.788992	-2.649034	27417.433707
HLA A*0301	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.367613	1.718496	-2.649117	23313.782287
HLA A*3001	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.258284	1.608922	-2.649362	18125.256071
HLA A*6801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-3.636622	0.987241	-2.649381	4331.338909
HLA B*5701	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.322688	1.673173	-2.649516	21022.687461
HLA A*2602	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.573707	1.924123	-2.649584	37472.029168
HLA A*3101	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.062292	1.412655	-2.649638	11542.302751
HLA B*4801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.398795	1.749103	-2.649692	25049.271589
HLA A*2501	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.440943	1.791215	-2.649727	27602.124659
HLA B*1502	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.437073	1.787266	-2.649807	27357.279730
HLA A*6802	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.441697	1.791215	-2.650481	27650.099446
HLA B*1503	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.375641	1.725080	-2.650560	23748.759353
HLA B*4801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.372246	1.721649	-2.650597	23563.832175
HLA A*2402	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.473546	1.822872	-2.650674	29754.065609
HLA A*2902	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.371668	1.720897	-2.650770	23532.493514
HLA A*2601	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.379240	1.728396	-2.650845	23946.405798
HLA B*4501	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.508178	1.857234	-2.650943	32223.872110
HLA A*2601	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.372220	1.720897	-2.651323	23562.429962
HLA A*0301	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.364944	1.713482	-2.651462	23170.943679
HLA A*6802	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.370425	1.718496	-2.651929	23465.243760
HLA B*4001	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.325228	1.673173	-2.652055	21145.990224
HLA A*2402	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.545377	1.893265	-2.652113	35105.658297
HLA B*4801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.348110	1.695841	-2.652268	22289.979114
HLA B*5401	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.554004	1.901679	-2.652325	35810.009005
HLA B*5401	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.405446	1.753043	-2.652404	25435.863958
HLA A*2301	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.481372	1.828772	-2.652600	30295.104219
HLA A*2902	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.439500	1.786784	-2.652716	27510.591562
HLA B*0802	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.427962	1.775111	-2.652850	26789.314964
HLA A*6901	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.778700	1.125828	-2.652872	6007.589144
HLA A*3301	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.618744	1.965836	-2.652909	41566.598778
HLA A*0206	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-3.992508	1.339557	-2.652951	9828.971097
HLA A*2501	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.290982	1.638021	-2.652961	19542.581586
HLA B*5301	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.554770	1.901679	-2.653091	35873.220115
HLA B*0803	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.371823	1.718496	-2.653327	23540.897354
HLA B*5101	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.079726	1.426359	-2.653367	12015.051600

HLA A*0219	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.432766	1.779355	-2.653411	27087.336638
HLA A*6802	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.290940	1.637421	-2.653519	19540.678661
HLA A*6901	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.347701	1.694140	-2.653561	22269.006967
HLA B*3801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.510518	1.856944	-2.653574	32397.970998
HLA A*3002	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.513600	1.859882	-2.653718	32628.742506
HLA A*8001	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.428890	1.775111	-2.653778	26846.622426
HLA B*0803	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.410098	1.756081	-2.654017	25709.786717
HLA A*0203	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.869560	1.215498	-2.654061	7405.587332
HLA A*0212	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.066738	1.412655	-2.654083	11661.050796
HLA B*4501	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.609229	1.954913	-2.654316	40665.777040
HLA B*5401	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.327697	1.673173	-2.654525	21266.564413
HLA A*0212	1:26-34	9	YAQLIARRV	1.199062	0.114113	-3.967721	1.313175	-2.654545	9283.697719
HLA B*4801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.375714	1.720897	-2.654816	23752.742510
HLA A*0201	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.008602	1.353717	-2.654885	10200.043650
HLA A*2403	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.408029	1.753043	-2.654986	25587.542531
HLA A*0219	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.446266	1.791215	-2.655051	27942.576330
HLA A*0201	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.376733	1.721649	-2.655084	23808.576902
HLA A*6802	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.430227	1.775111	-2.655115	26929.389745
HLA B*1503	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.032562	1.377330	-2.655232	10778.593126
HLA A*0250	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.444225	1.788992	-2.655232	27811.521167
HLA A*6802	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.847084	1.191820	-2.655265	7032.088606
HLA B*4601	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.373902	1.718496	-2.655406	23653.875570
HLA B*2705	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.328792	1.673173	-2.655620	21320.245236
HLA A*2602	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.349940	1.694140	-2.655800	22384.114071
HLA B*0702	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.291607	1.635727	-2.655880	19570.724201
HLA B*1503	1:51-59	9	EEIRARQPV	0.859860	0.021658	-3.537399	0.881518	-2.655881	3446.662160
HLA B*0802	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.405280	1.749103	-2.656176	25426.095865
HLA A*2602	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.661353	1.005151	-2.656202	4585.142589
HLA A*2902	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.445207	1.788992	-2.656215	27874.483458
HLA A*3002	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.038018	1.381752	-2.656266	10914.845245
HLA B*3801	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.513577	1.857234	-2.656343	32626.977375
HLA B*0801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.378044	1.721649	-2.656395	23880.556874
HLA B*2705	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.447660	1.791215	-2.656444	28032.361852
HLA B*5101	1:9-17	9	VPETPARPV	0.601332	-0.092772	-3.165015	0.508560	-2.656455	1462.226806
HLA A*6801	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.603788	1.947300	-2.656488	40159.441825
HLA A*6802	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.409720	1.753043	-2.656677	25687.403443
HLA B*7301	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.513899	1.856944	-2.656955	32651.167979
HLA A*6901	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.720240	1.062990	-2.657250	5250.979684
HLA A*6801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.370766	1.713482	-2.657284	23483.657915
HLA B*2705	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.446285	1.788992	-2.657293	27943.785686
HLA B*4402	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.375848	1.718496	-2.657352	23760.068122
HLA A*3101	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.280158	1.622722	-2.657436	19061.534361
HLA A*3101	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.330615	1.673173	-2.657443	21409.937338
HLA B*0801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.179132	1.521566	-2.657566	15105.404193
HLA A*3002	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.430325	1.772257	-2.658069	26935.509211
HLA A*3201	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.517992	1.859882	-2.658109	32960.327942
HLA A*2402	1:42-50	9	EVIPHTASI	1.080334	0.256013	-3.994486	1.336347	-2.658139	9873.845432
HLA B*0803	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.447594	1.788992	-2.658602	28028.115919
HLA A*0203	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.330944	1.672339	-2.658605	21426.159034
HLA A*0202	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-3.849251	1.190433	-2.658818	7067.251708
HLA A*3201	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.552134	1.893265	-2.658870	35656.132928
HLA A*0101	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.387271	1.728396	-2.658875	24393.318006
HLA A*6801	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.515940	1.856944	-2.658996	32805.028825
HLA A*2403	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.434209	1.775111	-2.659098	27177.461484
HLA A*3301	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.583227	1.924123	-2.659104	38302.517941
HLA A*6901	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.326821	1.667650	-2.659171	21223.694122
HLA B*5801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.291825	1.632644	-2.659181	19580.573095
HLA A*0250	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.519084	1.859882	-2.659202	33043.347270
HLA A*0211	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.446245	1.786784	-2.659462	27941.215867
HLA B*0803	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.155069	1.495512	-2.659557	14291.207511
HLA A*0202	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.381656	1.721649	-2.660006	24079.951530
HLA A*2602	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.609887	1.949733	-2.660154	40727.422974
HLA A*0206	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.326871	0.666703	-2.660168	2122.612723
HLA A*2402	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.413348	1.753043	-2.660305	25902.865566
HLA B*4402	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.435637	1.775111	-2.660526	27267.001109

HLA B*7301	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.619463	1.958921	-2.660542	41635.466197
HLA A*2602	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.562714	1.901679	-2.661035	36535.408802
HLA A*0206	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-2.895679	0.234640	-2.661039	786.464599
HLA B*4403	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.643240	1.982154	-2.661086	43978.480511
HLA B*1517	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.436201	1.775111	-2.661090	27302.426851
HLA A*0203	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.452394	1.791215	-2.661179	28339.612186
HLA B*0802	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.372845	1.711364	-2.661481	23596.361426
HLA B*5801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.340114	1.678625	-2.661490	21883.378097
HLA B*5801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.357486	1.695841	-2.661645	22776.472105
HLA B*0803	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.484579	1.822872	-2.661707	30519.646421
HLA B*1801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.466458	1.804702	-2.661756	29272.372299
HLA B*1503	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.380502	1.718496	-2.662006	24016.073899
HLA B*2705	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.358147	1.695841	-2.662305	22811.122747
HLA B*4501	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.609809	1.947300	-2.662510	40720.152706
HLA A*2602	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-3.754468	1.091915	-2.662553	5681.560499
HLA A*2402	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.337697	1.675016	-2.662681	21761.896678
HLA B*2705	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.035682	1.372792	-2.662891	10856.308959
HLA B*4601	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.335249	1.672339	-2.662910	21639.567707
HLA B*2705	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.381557	1.718496	-2.663061	24074.480817
HLA A*2602	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.580652	1.917562	-2.663090	38076.085128
HLA B*1502	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.256398	1.593295	-2.663103	18046.688182
HLA B*1501	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.964606	1.301147	-2.663459	9217.339289
HLA A*0101	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.385347	1.721649	-2.663697	24285.477632
HLA B*7301	1:288-296	9	AAETFLEAL	1.587358	0.379068	-4.630389	1.966426	-2.663962	42696.132458
HLA B*4001	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.296618	1.632644	-2.663974	19797.864531
HLA B*4403	1:423-431	9	LRHADSIVR	1.231621	0.752419	-4.648014	1.984040	-2.663974	44464.598343
HLA A*0211	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.385800	1.721649	-2.664151	24310.847551
HLA B*0801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.360024	1.695841	-2.664183	22909.937267
HLA B*5801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.358407	1.694140	-2.664268	22824.824887
HLA A*2402	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.493115	1.828772	-2.664343	31125.416881
HLA A*3101	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.192703	1.528166	-2.664537	15584.862539
HLA B*4501	1:184-192	9	HTPHGQQVL	1.605375	0.376779	-4.646802	1.982154	-2.664648	44340.648376
HLA A*1101	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.493562	1.828772	-2.664789	31157.426489
HLA A*3002	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.338068	1.673173	-2.664895	21780.505883
HLA B*1801	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.417960	1.753043	-2.664917	26179.409755
HLA A*6901	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.566561	0.901531	-2.665030	3686.044076
HLA A*2902	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.418237	1.753043	-2.665194	26196.127159
HLA B*0802	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.469930	1.804702	-2.665228	29507.367042
HLA B*3901	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.469984	1.804702	-2.665282	29511.038797
HLA A*6802	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.672659	1.007289	-2.665369	4706.072005
HLA B*0702	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.361213	1.695841	-2.665372	22972.736933
HLA A*0250	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.598405	0.932998	-2.665408	3966.481598
HLA A*2902	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.106406	1.440990	-2.665417	12776.337980
HLA A*2402	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.414602	1.749103	-2.665499	25977.804049
HLA A*6901	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.338106	1.672339	-2.665767	21782.391246
HLA B*3501	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.441231	1.775111	-2.666120	27620.497677
HLA B*0802	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.457398	1.791215	-2.666183	28668.060076
HLA B*3801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.453477	1.787266	-2.666211	28410.378221
HLA A*6802	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.333938	1.667650	-2.666288	21574.342449
HLA A*3101	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-3.420878	0.754547	-2.666331	2635.593070
HLA B*4501	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.580981	1.914570	-2.666411	38104.934287
HLA A*0202	1:263-271	9	LRAGERAQV	0.865849	0.254971	-3.787248	1.120820	-2.666427	6126.996754
HLA A*6901	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.480005	0.813260	-2.666745	3019.989942
HLA A*0212	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-3.967895	1.301147	-2.666748	9287.415023
HLA B*3801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.441875	1.775111	-2.666764	27661.470166
HLA A*6901	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.378129	1.711364	-2.666765	23885.208209
HLA A*2601	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.392017	1.725080	-2.666936	24661.349455
HLA A*6901	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-3.622380	0.955413	-2.666967	4191.597655
HLA A*0301	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.342891	1.675762	-2.667129	22023.759472
HLA B*4002	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.220258	1.553110	-2.667148	16605.720973
HLA B*5301	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.525209	1.858036	-2.667173	33512.678641
HLA B*5801	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.283283	1.616065	-2.667218	19199.179604
HLA B*0803	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.416348	1.749103	-2.667245	26082.433210
HLA A*6802	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.580084	0.912830	-2.667254	3802.630784
HLA A*0206	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.524244	1.856944	-2.667300	33438.247171

HLA B*5401	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.560747	1.893265	-2.667483	36370.347637
HLA B*3501	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.306987	1.639403	-2.667583	20276.202763
HLA B*1517	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.294718	1.627062	-2.667656	19711.406525
HLA A*0250	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-3.468986	0.801202	-2.667784	2944.329511
HLA A*1101	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.454741	1.786784	-2.667958	28493.187656
HLA A*2602	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.261465	1.593295	-2.668170	18258.510838
HLA A*2501	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.362456	1.694140	-2.668316	23038.575196
HLA A*8001	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.343629	1.675016	-2.668613	22061.203140
HLA B*7301	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.618709	1.949733	-2.668976	41563.225855
HLA A*1101	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.444147	1.775111	-2.669036	27806.556521
HLA B*4601	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.382577	1.713482	-2.669095	24131.071503
HLA B*2705	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.380565	1.711364	-2.669202	24019.582112
HLA A*6802	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.342302	0.673013	-2.669289	2199.389668
HLA A*0202	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.043835	1.374504	-2.669331	11062.031921
HLA B*1501	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.387896	1.718496	-2.669400	24428.446004
HLA A*3201	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.341813	1.672339	-2.669474	21969.139256
HLA A*2501	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.456325	1.786784	-2.669541	28597.271020
HLA B*4002	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-3.343815	0.674222	-2.669594	2207.065636
HLA A*6901	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.365540	1.695841	-2.669699	23202.805032
HLA B*5301	1:24-32	9	AQYAQLIAR	1.102364	0.807456	-4.579670	1.909820	-2.669850	37990.079675
HLA B*1801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.461303	1.791215	-2.670088	28926.983640
HLA A*0219	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.006657	1.336347	-2.670309	10154.455873
HLA A*2402	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.530305	1.859882	-2.670423	33908.234269
HLA A*0201	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.811292	1.140721	-2.670571	6475.782887
HLA A*0201	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.019490	1.348830	-2.670660	10458.985087
HLA B*2705	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.308091	1.637421	-2.670670	20327.823607
HLA A*0212	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.343890	1.673173	-2.670717	22074.454820
HLA A*2603	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.458070	1.787266	-2.670804	28712.450442
HLA A*2402	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.528080	1.857234	-2.670846	33734.961022
HLA A*2501	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.424000	1.753043	-2.670957	26546.078639
HLA A*0250	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-2.768877	0.097746	-2.671131	587.323628
HLA A*2403	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.389688	1.718496	-2.671192	24529.488806
HLA B*5101	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.460262	1.788992	-2.671270	28857.740790
HLA A*0219	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.446534	1.775111	-2.671423	27959.814597
HLA B*3501	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.982560	1.311116	-2.671444	9606.392751
HLA A*2501	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.476429	1.804702	-2.671727	29952.228099
HLA B*5101	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.451290	1.779355	-2.671934	28267.646062
HLA A*0250	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.428272	1.756081	-2.672190	26808.452190
HLA B*2705	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.456691	1.784483	-2.672208	28621.415665
HLA A*0216	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.385692	1.713482	-2.672210	24304.798430
HLA B*1517	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.339865	1.667650	-2.672215	21870.832709
HLA B*3901	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.421470	1.749103	-2.672367	26391.858936
HLA B*0802	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.299442	1.627062	-2.672381	19927.023327
HLA B*0702	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.150299	1.477798	-2.672502	14135.119055
HLA A*0201	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.305201	1.632644	-2.672557	20193.007982
HLA B*2705	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.397700	1.725080	-2.672620	24986.201700
HLA B*4601	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.401027	1.728396	-2.672632	25178.341068
HLA A*2902	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.285355	1.612498	-2.672857	19291.007822
HLA A*1101	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.462013	1.788992	-2.673020	28974.282784
HLA A*0201	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.398161	1.725080	-2.673080	25012.709577
HLA B*4601	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.151042	1.477798	-2.673244	14159.304061
HLA A*0201	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.194846	1.521566	-2.673279	15661.945428
HLA A*2601	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.346582	1.673173	-2.673410	22211.735658
HLA B*4601	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.369321	1.695841	-2.673480	23405.655696
HLA B*3901	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.055338	1.381752	-2.673586	11358.944718
HLA A*6801	1:188-196	9	GQQVLSRFL	1.648333	0.346902	-4.668934	1.995235	-2.673699	46658.866924
HLA B*4001	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.385069	1.711364	-2.673706	24269.979534
HLA A*3301	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.575530	1.901679	-2.673851	37629.670181
HLA A*2301	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.461127	1.787266	-2.673861	28915.249138
HLA A*2601	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.392372	1.718496	-2.673876	24681.503376
HLA B*0803	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.311385	1.637421	-2.673964	20482.589512
HLA A*1101	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.465335	1.791215	-2.674120	29196.773869
HLA A*0202	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.402582	1.728396	-2.674187	25268.675097
HLA A*2902	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.402582	1.728396	-2.674187	25268.675097
HLA B*4601	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.399333	1.725080	-2.674253	25080.323476

HLA B*4001	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.370446	1.695841	-2.674605	23466.386288
HLA B*2705	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.314073	1.639403	-2.674669	20609.747559
HLA B*1801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.446967	1.772257	-2.674710	27987.660201
HLA A*2902	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.313076	1.638021	-2.675056	20562.527242
HLA A*0203	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.393654	1.718496	-2.675158	24754.515366
HLA B*3801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.424315	1.749103	-2.675212	26565.329536
HLA B*1501	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.396262	1.720897	-2.675365	24903.612875
HLA A*3001	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.287869	1.612498	-2.675371	19402.999214
HLA B*4001	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.268690	1.593295	-2.675395	18564.789104
HLA A*2501	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.462692	1.787266	-2.675425	29019.618288
HLA A*0201	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.135098	1.459325	-2.675773	13648.920457
HLA B*0803	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.305845	1.629570	-2.676275	20222.962467
HLA A*2902	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.343932	1.667650	-2.676282	22076.604491
HLA A*8001	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.394787	1.718496	-2.676291	24819.148644
HLA B*0702	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.460824	1.784483	-2.676340	28895.076928
HLA A*2301	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.467661	1.791215	-2.676446	29353.565162
HLA A*2501	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.404861	1.728396	-2.676466	25401.623330
HLA A*0206	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-2.904203	0.227657	-2.676546	802.053079
HLA A*2301	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.499440	1.822872	-2.676568	31582.026276
HLA B*4002	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.594134	1.917562	-2.676572	39276.577232
HLA A*6802	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.050493	1.373907	-2.676586	11232.937639
HLA A*3002	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-3.998781	1.322138	-2.676644	9971.975044
HLA A*3101	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.306315	1.629570	-2.676745	20244.855106
HLA B*1517	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.312520	1.635727	-2.676793	20536.180021
HLA B*5701	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.016468	1.339557	-2.676911	10386.473229
HLA A*3002	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.534191	1.857234	-2.676957	34213.005184
HLA B*5801	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.362310	1.685162	-2.677148	23030.849052
HLA A*0216	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.456585	1.779355	-2.677230	28614.448772
HLA B*1801	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.452544	1.775111	-2.677433	28349.425991
HLA B*0802	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.405886	1.728396	-2.677490	25461.609152
HLA A*0201	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.398842	1.720897	-2.677945	25051.982012
HLA A*0203	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.399791	1.721649	-2.678142	25106.795382
HLA B*1501	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.704696	1.026553	-2.678143	5066.361156
HLA A*0216	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.351479	1.673173	-2.678306	22463.572370
HLA B*5801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.350657	1.672339	-2.678318	22421.078710
HLA A*0203	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.271805	1.593295	-2.678511	18698.442670
HLA A*1101	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.463051	1.784483	-2.678568	29043.648148
HLA B*5401	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.465885	1.787266	-2.678618	29233.757880
HLA B*1801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.989830	1.311116	-2.678714	9768.539683
HLA A*2501	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.374595	1.695841	-2.678754	23691.655338
HLA B*3501	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.427945	1.749103	-2.678842	26788.300493
HLA A*0206	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-3.460768	0.781791	-2.678977	2889.135518
HLA A*2902	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.463552	1.784483	-2.679068	29077.134619
HLA B*4002	1:477-485	9	SEDAMTADW	0.981632	0.294154	-3.954874	1.275786	-2.679088	9013.096216
HLA B*2705	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.400160	1.720897	-2.679263	25128.128962
HLA B*1501	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.157075	1.477798	-2.679278	14357.386294
HLA B*1517	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.483983	1.804702	-2.679280	30477.737814
HLA A*2301	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.536581	1.857234	-2.679346	34401.759027
HLA A*0216	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.302302	1.622722	-2.679580	20058.652399
HLA A*0101	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.390948	1.711364	-2.679584	24600.720204
HLA B*1501	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.967510	1.287816	-2.679693	9279.178680
HLA A*1101	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.467036	1.787266	-2.679769	29311.354864
HLA A*6802	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.404925	1.725080	-2.679844	25405.333940
HLA B*1517	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.468953	1.788992	-2.679961	29441.034971
HLA A*3201	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.919209	1.239243	-2.679966	8302.498865
HLA B*5101	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.401690	1.721649	-2.680040	25216.782177
HLA B*5701	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.398584	1.718496	-2.680088	25037.078318
HLA A*6901	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.365249	1.685162	-2.680088	23187.245201
HLA A*0101	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.393659	1.713482	-2.680178	24754.783206
HLA A*2301	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.297335	1.617007	-2.680328	19830.558294
HLA A*3001	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.054873	1.374504	-2.680369	11346.784008
HLA B*4801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.393965	1.713482	-2.680483	24772.199011
HLA A*0101	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.348154	1.667650	-2.680504	22292.270372
HLA B*1503	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.485329	1.804702	-2.680627	30572.361316
HLA A*2902	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.429841	1.749103	-2.680738	26905.507999

HLA A*2902	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.233854	1.553110	-2.680745	17133.820228
HLA B*3801	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.433791	1.753043	-2.680748	27151.303265
HLA B*3901	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.472061	1.791215	-2.680846	29652.508686
HLA A*2601	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.348617	1.667650	-2.680967	22316.040982
HLA A*3101	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.394538	1.713482	-2.681056	24804.920226
HLA A*3301	1:355-363	9	KSHHNVGGL	1.450340	0.496960	-4.628549	1.947300	-2.681249	42515.656578
HLA B*0801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.392795	1.711364	-2.681431	24705.549437
HLA A*0206	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.538690	1.857234	-2.681456	34569.292155
HLA A*3201	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.269484	1.587869	-2.681615	18598.766666
HLA B*4403	1:255-263	9	CVFVDHGLL	1.443543	0.511370	-4.636554	1.954913	-2.681641	43306.549857
HLA A*0301	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.354956	1.673173	-2.681783	22644.151968
HLA A*0101	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.402712	1.720897	-2.681814	25276.194756
HLA A*0211	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.539182	1.857234	-2.681947	34608.400613
HLA A*2902	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.438081	1.756081	-2.682000	27420.845401
HLA A*0206	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.354444	1.672339	-2.682105	22617.462197
HLA A*0216	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.404027	1.721649	-2.682378	25352.886057
HLA A*6801	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.540495	1.858036	-2.682459	34713.219260
HLA A*0212	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.290153	0.607629	-2.682524	1950.531694
HLA B*1501	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-3.855481	1.172675	-2.682806	7169.376595
HLA A*0101	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.407911	1.725080	-2.682831	25580.622179
HLA B*1509	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.487744	1.804702	-2.683042	30742.859069
HLA A*0216	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.436119	1.753043	-2.683076	27297.257732
HLA A*2902	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.404735	1.721649	-2.683085	25394.203735
HLA B*4001	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.408167	1.725080	-2.683087	25595.710955
HLA A*0219	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.411647	1.728396	-2.683251	25801.608694
HLA B*5301	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.432459	1.749103	-2.683355	27068.146766
HLA B*4001	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.310476	1.627062	-2.683414	20439.751467
HLA B*4601	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.404361	1.720897	-2.683464	25372.369735
HLA A*2603	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.963755	1.280105	-2.683650	9199.305901
HLA A*2603	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.633441	1.949733	-2.683707	42997.233971
HLA B*3901	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.112369	1.428368	-2.684002	12952.970752
HLA B*1501	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.409288	1.725080	-2.684207	25661.846421
HLA A*0212	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.405869	1.721649	-2.684220	25460.644959
HLA A*3002	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.311516	1.627062	-2.684455	20488.795730
HLA B*4801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.409551	1.725080	-2.684471	25677.399839
HLA A*2601	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.310257	1.625692	-2.684565	20429.470412
HLA B*5701	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.409661	1.725080	-2.684581	25683.929528
HLA B*5801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.360346	1.675762	-2.684584	22926.923371
HLA B*3801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.469120	1.784483	-2.684636	29452.345508
HLA A*0219	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.357825	1.673173	-2.684652	22794.222437
HLA A*0201	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.398151	1.713482	-2.684670	25012.168319
HLA A*1101	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.440757	1.756081	-2.684676	27590.330549
HLA A*2501	1:421-429	9	DTLRHADSI	0.987060	0.113427	-3.785204	1.100487	-2.684716	6098.227166
HLA B*4403	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.643983	1.958921	-2.685061	44053.727121
HLA A*0211	1:91-99	9	GICYGFQAM	1.154925	0.134428	-3.974426	1.289353	-2.685073	9428.148654
HLA B*4801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-3.996216	1.311116	-2.685099	9913.238282
HLA B*4601	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.320994	1.635727	-2.685267	20940.847550
HLA B*4001	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.398866	1.713482	-2.685384	25053.337333
HLA B*5101	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.490261	1.804702	-2.685558	30921.499948
HLA A*2601	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.396988	1.711364	-2.685625	24945.277958
HLA B*3501	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.067076	1.381432	-2.685644	11670.138574
HLA B*5801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.349747	1.663852	-2.685896	22374.186436
HLA A*1101	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.438978	1.753043	-2.685935	27477.571301
HLA A*6801	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.610366	1.924123	-2.686243	40772.395278
HLA A*0216	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.324335	1.638021	-2.686314	21102.563841
HLA B*4002	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.636352	1.949733	-2.686618	43286.406151
HLA B*5801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.361657	1.675016	-2.686641	22996.237858
HLA B*2705	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.354402	1.667650	-2.686752	22615.259861
HLA B*5801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.354531	1.667650	-2.686881	22621.989895
HLA B*4501	1:285-293	9	TVDAAETFL	1.547755	0.411166	-4.645991	1.958921	-2.687070	44257.967651
HLA B*5701	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.408054	1.720897	-2.687157	25589.065260
HLA B*4801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.309881	1.622722	-2.687159	20411.794676
HLA A*2902	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.362430	1.675016	-2.687414	23037.204240
HLA B*3501	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.324852	1.637421	-2.687431	21127.694550
HLA A*0216	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.462562	1.775111	-2.687451	29010.984962

HLA A*0206	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.440531	1.753043	-2.687488	27576.005249
HLA B*0801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.069040	1.381432	-2.687609	11723.038262
HLA A*3301	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.637564	1.949733	-2.687831	43407.409086
HLA B*0802	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.382090	1.694140	-2.687951	24104.063519
HLA B*0803	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.463084	1.775111	-2.687973	29045.847952
HLA B*5801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.326062	1.638021	-2.688041	21186.640346
HLA B*4002	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.060873	1.372792	-2.688082	11504.648986
HLA B*4403	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.653956	1.965836	-2.688121	45077.126250
HLA B*5401	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.545614	1.857234	-2.688380	35124.845228
HLA B*5101	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.473015	1.784483	-2.688532	29717.709479
HLA A*6901	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.364584	1.675762	-2.688822	23151.772721
HLA A*0203	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.814676	1.125828	-2.688847	6526.427804
HLA A*0202	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.304959	1.616065	-2.688894	20181.759197
HLA A*0201	1:514-522	9	ITSKPPATI	1.110493	0.169612	-3.968999	1.280105	-2.688894	9311.059696
HLA B*0801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-3.916977	1.228069	-2.688908	8259.938508
HLA A*0211	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.513556	0.824605	-2.688951	3262.542234
HLA A*2601	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.363999	1.675016	-2.688983	23120.606835
HLA B*4501	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.654898	1.965836	-2.689063	45175.021161
HLA B*0702	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.410000	1.720897	-2.689102	25703.945722
HLA A*6901	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.305208	1.616065	-2.689143	20193.335710
HLA B*4501	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.613578	1.924123	-2.689455	41075.037815
HLA A*0201	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.401121	1.711364	-2.689757	25183.790139
HLA B*0802	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.414948	1.725080	-2.689867	25998.471210
HLA A*0202	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.583277	1.893265	-2.690012	38306.869648
HLA B*1501	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.401419	1.711364	-2.690056	25201.098756
HLA B*0801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.329683	1.639403	-2.690279	21364.004003
HLA A*0201	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.365562	1.675016	-2.690545	23203.934781
HLA B*1509	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.317719	1.627062	-2.690657	20783.518532
HLA B*5401	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.698024	1.007289	-2.690734	4989.116071
HLA A*0202	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.063561	1.372792	-2.690770	11576.071044
HLA B*4403	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.640510	1.949733	-2.690777	43702.886117
HLA A*1101	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.470497	1.779355	-2.691142	29545.863344
HLA A*3001	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.284991	1.593295	-2.691696	19274.838459
HLA B*1503	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.779297	1.087303	-2.691994	6015.849918
HLA A*2501	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.331438	1.639403	-2.692034	21450.514627
HLA A*0250	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.927164	1.235042	-2.692122	8455.984556
HLA A*0202	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.330451	1.638021	-2.692430	21401.831096
HLA B*5701	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.719098	1.026553	-2.692545	5237.191910
HLA A*3201	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.388662	1.695841	-2.692821	24471.566608
HLA A*2301	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.371447	1.678625	-2.692822	23520.529587
HLA A*0203	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.014988	1.322138	-2.692850	10351.133994
HLA B*4801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.404399	1.711364	-2.693035	25374.566017
HLA A*0202	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.121434	1.428368	-2.693066	13226.157742
HLA B*7301	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.551436	1.858036	-2.693401	35598.888898
HLA A*3002	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-3.512489	0.819048	-2.693442	3254.538970
HLA A*2601	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.387600	1.694140	-2.693460	24411.800125
HLA B*5801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.329248	1.635727	-2.693521	21342.632974
HLA A*0219	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.407244	1.713482	-2.693762	25541.350070
HLA A*0202	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.389712	1.695841	-2.693871	24530.815860
HLA A*0101	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.390048	1.695841	-2.694207	24549.800589
HLA B*4001	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.068801	1.374504	-2.694297	11716.571172
HLA B*2705	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.011929	1.317518	-2.694411	10278.480139
HLA B*4601	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.388641	1.694140	-2.694501	24470.375141
HLA B*5301	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.450714	1.756081	-2.694633	28230.204297
HLA A*1101	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.370472	1.675762	-2.694710	23467.782785
HLA B*1503	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.406109	1.711364	-2.694745	25474.698241
HLA A*8001	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.307309	1.612498	-2.694810	20291.236139
HLA B*4402	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.420060	1.725080	-2.694980	26306.331600
HLA A*0101	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.380258	1.685162	-2.695096	24002.565573
HLA A*2602	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.518003	1.822872	-2.695131	32961.219513
HLA B*1503	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.597362	0.902116	-2.695246	3956.965579
HLA A*2602	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.588598	1.893265	-2.695334	38779.146593
HLA B*4601	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.406718	1.711364	-2.695354	25510.417420
HLA A*6901	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.370402	1.675016	-2.695385	23463.974351
HLA B*5401	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.518478	1.822872	-2.695605	32997.259143

HLA B*1517	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-3.999416	1.303793	-2.695623	9986.551452
HLA A*2603	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.318363	1.622722	-2.695641	20814.348986
HLA B*0801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.416599	1.720897	-2.695702	26097.535609
HLA A*0211	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-3.979764	1.284024	-2.695741	9544.747664
HLA A*3301	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.610312	1.914570	-2.695742	40767.322388
HLA A*1101	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.414518	1.718496	-2.696022	25972.745208
HLA A*3001	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.283938	1.587869	-2.696069	19228.179940
HLA A*0301	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.237766	1.541660	-2.696106	17288.849685
HLA A*3002	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.487516	1.791215	-2.696301	30726.730701
HLA B*0801	1:492-500	9	VLERISTRI	1.151890	0.131612	-3.979882	1.283502	-2.696380	9547.329814
HLA A*0201	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.284709	1.587869	-2.696840	19262.329551
HLA B*1517	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.446029	1.749103	-2.696926	27927.312710
HLA B*0801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.391218	1.694140	-2.697078	24616.029991
HLA A*6801	1:115-123	9	YGRTELKVL	1.725445	0.240391	-4.663119	1.965836	-2.697284	46038.293014
HLA B*0801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.314296	1.617007	-2.697289	20620.342444
HLA B*5801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.336722	1.639403	-2.697318	21713.093761
HLA B*0803	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.391620	1.694140	-2.697480	24638.812596
HLA A*0250	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.590854	1.893265	-2.697589	38981.069731
HLA A*0201	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.641331	0.943730	-2.697601	4378.552231
HLA B*0801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.365364	1.667650	-2.697714	23193.392597
HLA B*3801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.470022	1.772257	-2.697765	29513.593330
HLA A*0203	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.828293	1.130410	-2.697883	6734.310758
HLA B*1502	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.520881	1.822872	-2.698009	33180.382686
HLA A*2603	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.336116	1.638021	-2.698095	21682.808820
HLA A*3002	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.365811	1.667650	-2.698161	23217.244853
HLA A*0203	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.336214	1.638021	-2.698193	21687.736047
HLA A*2603	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.485078	1.786784	-2.698294	30554.669377
HLA A*6801	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.477912	1.779355	-2.698557	30054.648939
HLA A*0216	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.158161	1.459325	-2.698835	14393.315579
HLA B*2705	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.303538	1.604651	-2.698887	20115.812623
HLA A*2403	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.328529	1.629570	-2.698959	21307.331050
HLA A*6901	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.829637	1.130410	-2.699227	6755.182067
HLA B*1517	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.420161	1.720897	-2.699264	26312.451829
HLA B*1517	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.384548	1.685162	-2.699386	24240.848897
HLA B*7301	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.455577	1.756081	-2.699496	28548.116148
HLA B*0801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.332199	1.632644	-2.699555	21488.146147
HLA A*0201	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.395433	1.695841	-2.699592	24856.100055
HLA A*0101	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.374715	1.675016	-2.699699	23698.192870
HLA B*5401	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.556779	1.856944	-2.699835	36039.534431
HLA B*0801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.413590	1.713482	-2.700108	25917.303146
HLA A*0101	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.373336	1.673173	-2.700163	23623.056137
HLA A*6802	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.394369	1.694140	-2.700229	24795.260293
HLA B*1502	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.396293	1.695841	-2.700452	24905.364372
HLA A*0201	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.394956	1.694140	-2.700816	24828.817883
HLA B*3501	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.429308	1.728396	-2.700912	26872.487108
HLA B*1501	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.395109	1.694140	-2.700969	24837.550293
HLA B*0801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.014443	1.313175	-2.701267	10338.150494
HLA B*5401	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.561159	1.859882	-2.701276	36404.796863
HLA B*1503	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.179264	1.477798	-2.701466	15109.981126
HLA B*2705	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.450648	1.749103	-2.701545	28225.928397
HLA B*0801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.848879	1.147258	-2.701621	7061.213468
HLA A*0219	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.334323	1.632644	-2.701679	21593.492170
HLA B*0801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.426822	1.725080	-2.701742	26719.117393
HLA A*0203	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.422692	1.720897	-2.701794	26466.207520
HLA B*1501	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.339424	1.637421	-2.702003	21848.600086
HLA A*0301	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.311025	1.608922	-2.702104	20465.642820
HLA A*6901	1:456-464	9	SVGVQGGDGR	0.950204	0.713648	-4.366008	1.663852	-2.702156	23227.797879
HLA B*5701	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.413649	1.711364	-2.702285	25920.808626
HLA A*2603	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.374706	1.672339	-2.702367	23697.680057
HLA A*6801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.311373	1.608922	-2.702451	20482.035477
HLA A*2601	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.318760	1.616065	-2.702695	20833.387649
HLA B*3801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.459182	1.756081	-2.703100	28786.016170
HLA A*3002	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.424022	1.720897	-2.703124	26547.371172
HLA B*0802	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.370803	1.667650	-2.703153	23485.690707
HLA B*1509	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.342570	1.639403	-2.703166	22007.442504

HLA B*5701	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.320242	1.617007	-2.703236	20904.626859
HLA B*1501	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.367129	1.663852	-2.703277	23287.815013
HLA A*3101	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.330545	1.627062	-2.703483	21406.462858
HLA B*4501	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.653381	1.949733	-2.703647	45017.419574
HLA B*2705	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.078274	1.374504	-2.703770	11974.948615
HLA A*0101	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.367730	1.663852	-2.703879	23320.089389
HLA A*0202	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-3.716664	1.012736	-2.703928	5207.921409
HLA B*3501	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.320040	1.616065	-2.703976	20894.903233
HLA B*4001	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.320990	1.617007	-2.703983	20940.620976
HLA A*2501	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.297304	1.593295	-2.704010	19829.163688
HLA B*5701	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.343528	1.639403	-2.704125	22056.071744
HLA B*5101	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.491081	1.786784	-2.704297	30979.936475
HLA A*0206	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.673504	0.969193	-2.704311	4715.246293
HLA A*2603	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.460481	1.756081	-2.704400	28872.263341
HLA B*5301	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.257584	1.553110	-2.704474	18096.059036
HLA A*2301	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.453794	1.749103	-2.704691	28431.134894
HLA A*2402	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.493968	1.788992	-2.704976	31186.600712
HLA A*8001	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.368846	1.663852	-2.704995	23380.092022
HLA B*0702	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.426773	1.721649	-2.705124	26716.082069
HLA B*1801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.338068	1.632644	-2.705424	21780.505883
HLA A*0212	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.373158	1.667650	-2.705508	23613.345477
HLA B*2705	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.390847	1.685162	-2.705685	24594.998122
HLA B*7301	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.494896	1.788992	-2.705904	31253.314808
HLA A*2402	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.424607	1.718496	-2.706111	26583.156235
HLA B*5701	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.310917	1.604651	-2.706267	20460.550478
HLA B*5401	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.511108	1.804702	-2.706405	32441.993508
HLA B*0803	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.497647	1.791215	-2.706432	31451.932393
HLA A*2402	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.511157	1.804702	-2.706455	32445.679376
HLA B*4402	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.417880	1.711364	-2.706516	26174.594856
HLA A*2601	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.385253	1.678625	-2.706628	24280.222931
HLA A*0101	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.400773	1.694140	-2.706634	25163.634465
HLA A*2403	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.370634	1.663852	-2.706783	23476.544529
HLA A*2501	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.491271	1.784483	-2.706787	30993.514889
HLA B*4001	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.379168	1.672339	-2.706829	23942.390165
HLA B*5101	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.435294	1.728396	-2.706899	27245.472940
HLA B*4801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.385542	1.678625	-2.706917	24296.384765
HLA A*0203	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.420417	1.713482	-2.706936	26327.972276
HLA B*1517	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.463467	1.756081	-2.707386	29071.472223
HLA A*0211	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-3.995440	1.287816	-2.707624	9895.556329
HLA A*0216	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.136156	1.428368	-2.707788	13682.188551
HLA A*2902	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.089241	1.381432	-2.707809	12281.207086
HLA A*2501	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.381038	1.673173	-2.707865	24045.714916
HLA B*3901	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.795367	1.087303	-2.708065	6242.628208
HLA A*2601	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.393394	1.685162	-2.708232	24739.654799
HLA A*0212	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.421775	1.713482	-2.708294	26410.426478
HLA A*0212	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.433518	1.725080	-2.708438	27134.269887
HLA A*0202	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.725790	1.017185	-2.708605	5318.508058
HLA A*3301	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.480966	1.772257	-2.708709	30266.763967
HLA B*5401	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.537506	1.828772	-2.708734	34475.164454
HLA B*4402	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.725945	1.017185	-2.708760	5320.407385
HLA B*4801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.381134	1.672339	-2.708795	24051.048978
HLA A*6802	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.429790	1.720897	-2.708892	26902.305961
HLA A*0211	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.641899	0.932998	-2.708901	4384.288356
HLA A*3001	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-3.995125	1.286148	-2.708977	9888.385391
HLA B*0803	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.493508	1.784483	-2.709024	31153.549891
HLA B*4403	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.262151	1.553110	-2.709042	18287.376375
HLA B*4001	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.387816	1.678625	-2.709191	24423.953141
HLA B*4501	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.626763	1.917562	-2.709201	42341.211649
HLA A*0211	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.498195	1.788992	-2.709202	31491.602682
HLA A*3001	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.262318	1.553110	-2.709209	18294.401944
HLA B*3501	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.394411	1.685162	-2.709249	24797.674924
HLA A*0101	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.338846	1.629570	-2.709276	21819.542594
HLA A*6802	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.422776	1.713482	-2.709295	26471.362474
HLA A*2403	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.430274	1.720897	-2.709376	26932.303603
HLA A*2501	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.325573	1.616065	-2.709509	21162.813340

HLA B*0802	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.423018	1.713482	-2.709537	26486.116920
HLA B*4001	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.394893	1.685162	-2.709731	24825.191477
HLA A*8001	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.342393	1.632644	-2.709749	21998.514978
HLA A*0219	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.431441	1.721649	-2.709792	27004.814326
HLA A*2301	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.428469	1.718496	-2.709973	26820.637542
HLA A*2402	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.485106	1.775111	-2.709994	30556.653010
HLA B*1503	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.404281	1.694140	-2.710141	25367.703266
HLA B*5701	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.326323	1.616065	-2.710258	21199.366695
HLA B*1503	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.406229	1.695841	-2.710388	25481.727791
HLA A*0101	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.383570	1.672339	-2.711232	24186.355871
HLA B*4403	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.568193	1.856944	-2.711249	36999.254211
HLA A*0201	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.383592	1.672339	-2.711253	24187.533510
HLA B*5801	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.336966	1.625692	-2.711274	21725.313603
HLA A*8001	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.424816	1.713482	-2.711334	26595.958578
HLA A*6802	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.728520	1.017185	-2.711335	5352.047056
HLA A*0101	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.390043	1.678625	-2.711418	24549.534967
HLA B*3901	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.433079	1.721649	-2.711430	27106.833403
HLA A*3002	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.498357	1.786784	-2.711573	31503.360136
HLA B*0801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.386834	1.675016	-2.711818	24368.784834
HLA B*4001	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.375885	1.663852	-2.712034	23762.124841
HLA A*0206	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-3.610012	0.897730	-2.712282	4073.914402
HLA A*6802	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.350424	1.638021	-2.712403	22409.073665
HLA B*5701	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.408393	1.695841	-2.712552	25609.007524
HLA A*2602	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.569871	1.857234	-2.712636	37142.446155
HLA A*0206	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.387722	1.675016	-2.712706	24418.668478
HLA A*8001	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.438017	1.725080	-2.712937	27416.840412
HLA A*6801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.139356	1.426359	-2.712997	13783.374923
HLA B*1801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.497640	1.784483	-2.713157	31451.421943
HLA B*4001	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-3.346696	0.633434	-2.713261	2221.752705
HLA B*5301	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.606783	1.893265	-2.713519	40437.403472
HLA B*1509	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.407681	1.694140	-2.713541	25567.063717
HLA B*5701	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.209107	1.495512	-2.713595	16184.790433
HLA A*2603	1:27-35	9	AQLIARRVR	1.168509	0.724756	-4.606917	1.893265	-2.713653	40449.874821
HLA B*4002	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.485912	1.772257	-2.713655	30613.406329
HLA A*0201	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.392303	1.678625	-2.713679	24677.631478
HLA B*4001	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.336421	1.622722	-2.713699	21698.063391
HLA A*0202	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.466824	1.753043	-2.713782	29297.086932
HLA B*1801	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.398943	1.685162	-2.713782	25057.810413
HLA B*4601	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.351921	1.638021	-2.713900	22486.430774
HLA B*4402	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.267034	1.553110	-2.713924	18494.118375
HLA A*0201	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.399183	1.685162	-2.714021	25071.641346
HLA B*5101	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.489133	1.775111	-2.714021	30841.308805
HLA B*2705	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.341150	1.627062	-2.714089	21935.648937
HLA A*0216	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.439216	1.725080	-2.714135	27492.589115
HLA A*6801	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.631751	1.917562	-2.714189	42830.312037
HLA B*7301	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.574250	1.859882	-2.714368	37518.886650
HLA A*0219	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.337112	1.622722	-2.714390	21732.601781
HLA A*0212	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.350187	1.635727	-2.714460	22396.832719
HLA B*5701	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.408630	1.694140	-2.714490	25623.004078
HLA A*0301	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.340335	1.625692	-2.714644	21894.509272
HLA A*2501	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.436382	1.721649	-2.714733	27313.802359
HLA B*5801	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.352170	1.637421	-2.714749	22499.329276
HLA B*4801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.389775	1.675016	-2.714759	24534.399265
HLA A*0202	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-3.621548	0.906788	-2.714760	4183.578005
HLA B*4601	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.354214	1.639403	-2.714810	22605.474295
HLA A*0211	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-3.487529	0.772641	-2.714888	3072.759341
HLA A*2403	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.426427	1.711364	-2.715064	26694.844451
HLA A*2601	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.353180	1.638021	-2.715159	22551.729318
HLA B*5701	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.382837	1.667650	-2.715187	24145.566508
HLA B*3501	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.387565	1.672339	-2.715226	24409.819228
HLA A*2601	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.391366	1.675762	-2.715604	24624.421130
HLA A*6802	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.391399	1.675762	-2.715637	24626.286216
HLA B*5101	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.175068	1.459325	-2.715742	14964.690585
HLA A*2501	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.491062	1.775111	-2.715950	30978.595719
HLA A*6802	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.027125	1.311116	-2.716009	10644.502542

HLA A*2601	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.348805	1.632644	-2.716161	22325.701257
HLA B*3501	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.412041	1.695841	-2.716200	25825.069439
HLA A*0202	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.521076	1.804702	-2.716374	33195.284714
HLA B*3801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.352191	1.635727	-2.716464	22500.424773
HLA B*4001	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.410646	1.694140	-2.716506	25742.214443
HLA B*5801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.329354	1.612498	-2.716856	21347.829364
HLA A*0212	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.098888	1.381752	-2.717136	12557.062039
HLA B*1503	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.176576	1.459325	-2.717251	15016.755545
HLA B*4001	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.392282	1.675016	-2.717266	24676.429978
HLA B*0802	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.390499	1.673173	-2.717326	24575.313683
HLA A*6901	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.396013	1.678625	-2.717388	24889.336036
HLA A*2601	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.381367	1.663852	-2.717515	24063.933666
HLA B*1501	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.350238	1.632644	-2.717594	22399.498494
HLA B*4801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.411896	1.694140	-2.717756	25816.408824
HLA B*5401	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.473920	1.756081	-2.717839	29779.670245
HLA A*2301	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.347431	1.629570	-2.717861	22255.156897
HLA A*3101	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.334927	1.617007	-2.717920	21623.535379
HLA A*0250	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.350626	1.632644	-2.717982	22419.501923
HLA B*1501	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-3.519251	0.801202	-2.718049	3305.607567
HLA B*1509	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.443182	1.725080	-2.718101	27744.798315
HLA A*0219	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.356279	1.638021	-2.718258	22713.225930
HLA A*2501	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.436760	1.718496	-2.718264	27337.602830
HLA A*0201	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.092864	1.374504	-2.718360	12384.086032
HLA A*2902	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.351011	1.632644	-2.718367	22439.401821
HLA B*4001	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.386082	1.667650	-2.718432	24326.634953
HLA A*0201	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.386153	1.667650	-2.718503	24330.583406
HLA B*4001	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.348220	1.629570	-2.718650	22295.647391
HLA B*4801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.386322	1.667650	-2.718672	24340.062306
HLA A*0201	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.250940	0.532233	-2.718707	1782.132978
HLA B*1517	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.414854	1.695841	-2.719013	25992.845865
HLA A*8001	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.392188	1.673173	-2.719016	24671.090686
HLA A*2402	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.358527	1.639403	-2.719124	22831.123225
HLA A*3201	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.437627	1.718496	-2.719131	27392.230001
HLA B*3501	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.346223	1.627062	-2.719161	22193.358321
HLA A*0250	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.178601	1.459325	-2.719276	15086.947084
HLA A*2403	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.358750	1.639403	-2.719347	22842.860056
HLA B*4403	1:112-120	9	TREYGRTEL	1.503201	0.420922	-4.643470	1.924123	-2.719347	44001.802725
HLA A*2402	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.392527	1.673173	-2.719354	24690.317546
HLA B*5801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.342335	1.622722	-2.719613	21995.539941
HLA A*3301	1:516-524	9	SKPPATIEW	1.492290	0.425272	-4.637273	1.917562	-2.719711	43378.300021
HLA A*2402	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.506627	1.786784	-2.719844	32109.021071
HLA B*1502	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.511070	1.791215	-2.719855	32439.185508
HLA B*1501	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.332413	1.612498	-2.719915	21498.727364
HLA B*1503	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.345685	1.625692	-2.719993	22165.880779
HLA B*4801	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.405280	1.685162	-2.720118	25426.095865
HLA A*2603	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.352832	1.632644	-2.720188	22533.680195
HLA B*7301	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.577565	1.857234	-2.720331	37806.377442
HLA A*2603	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.130531	1.410054	-2.720477	13506.129326
HLA A*3201	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.009880	1.289353	-2.720527	10230.106386
HLA B*4001	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.396333	1.675762	-2.720571	24907.654977
HLA A*0101	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.356406	1.635727	-2.720679	22719.862206
HLA B*0803	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.442383	1.721649	-2.720734	27693.812484
HLA A*0212	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.441713	1.720897	-2.720816	27651.146554
HLA A*0201	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.347936	1.627062	-2.720874	22281.057512
HLA B*1503	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-3.777493	1.056396	-2.721096	5990.907147
HLA A*2301	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.496437	1.775111	-2.721326	31364.426344
HLA A*6801	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.493639	1.772257	-2.721382	31162.989407
HLA A*2301	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.360858	1.639403	-2.721455	22953.978322
HLA A*0201	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.359500	1.638021	-2.721479	22882.315263
HLA A*0101	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.354171	1.632644	-2.721527	22603.273126
HLA A*1101	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.450014	1.728396	-2.721618	28184.729724
HLA A*3002	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.510645	1.788992	-2.721652	32407.436930
HLA B*1517	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.351284	1.629570	-2.721714	22453.488023
HLA B*1517	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.224844	1.503120	-2.721724	16782.008275
HLA B*5801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.058077	1.336347	-2.721730	11430.822617

HLA B*0702	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.470884	1.749103	-2.721781	29572.248693
HLA A*0301	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.351380	1.629570	-2.721810	22458.468881
HLA A*0216	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.070661	1.348830	-2.721832	11766.880071
HLA B*1501	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.389484	1.667650	-2.721834	24517.946465
HLA B*5701	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.394178	1.672339	-2.721839	24784.397365
HLA B*4801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.339137	1.617007	-2.722130	21834.184627
HLA A*0203	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.651964	0.929716	-2.722248	4487.085075
HLA B*0702	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.435811	1.713482	-2.722330	27277.919142
HLA B*4402	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.443231	1.720897	-2.722333	27747.950516
HLA A*0212	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.351939	1.629570	-2.722370	22487.403988
HLA A*6801	1:412-420	9	VGEVTAKRL	1.680818	0.268915	-4.672113	1.949733	-2.722380	47001.643193
HLA A*0219	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.349580	1.627062	-2.722519	22365.594114
HLA A*0212	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.394923	1.672339	-2.722584	24826.937458
HLA A*6802	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.433967	1.711364	-2.722603	27162.321916
HLA B*4501	1:493-501	9	LERISTRIT	1.013477	-0.322582	-3.413557	0.690895	-2.722662	2591.536689
HLA B*5701	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.360785	1.638021	-2.722764	22950.129112
HLA A*8001	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.390647	1.667650	-2.722997	24583.690943
HLA B*7301	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.625022	1.901679	-2.723343	42171.817010
HLA A*0201	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.399227	1.675762	-2.723465	25074.218540
HLA A*0212	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.419398	1.695841	-2.723557	26266.229554
HLA A*6801	1:113-121	9	REYGRTELK	0.904130	0.335113	-3.962806	1.239243	-2.723563	9179.221898
HLA B*3501	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.434933	1.711364	-2.723569	27222.783565
HLA A*8001	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.445322	1.721649	-2.723673	27881.873533
HLA A*3101	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.356361	1.632644	-2.723717	22717.526999
HLA B*1501	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.361955	1.638021	-2.723934	23012.042989
HLA A*0216	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.096830	1.372792	-2.724038	12497.694118
HLA A*1101	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.473152	1.749103	-2.724048	29727.035573
HLA B*0702	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.435614	1.711364	-2.724250	27265.526034
HLA B*4601	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.399335	1.675016	-2.724319	25080.459158
HLA A*3002	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.362350	1.638021	-2.724329	23032.967253
HLA B*0801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.013870	1.289353	-2.724516	10324.513005
HLA B*3501	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.183930	1.459325	-2.724605	15273.198603
HLA A*0216	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.388469	1.663852	-2.724617	24460.713161
HLA B*0802	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.445578	1.720897	-2.724681	27898.319707
HLA B*4501	1:490-498	9	YEVLERIST	1.211490	-0.403834	-3.532484	0.807656	-2.724828	3407.874505
HLA A*3002	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.446560	1.721649	-2.724911	27961.478501
HLA A*2301	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.529692	1.804702	-2.724990	33860.390270
HLA B*4801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.400752	1.675762	-2.724990	25162.409303
HLA A*2501	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.474157	1.749103	-2.725054	29795.946268
HLA B*5801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.352118	1.627062	-2.725056	22496.651620
HLA B*1517	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.073937	1.348830	-2.725107	11855.954098
HLA B*7301	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.586763	1.861603	-2.725160	38615.645561
HLA A*0219	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.354951	1.629570	-2.725382	22643.906965
HLA B*4601	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.138214	1.412655	-2.725559	13747.183188
HLA A*0212	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.363113	1.637421	-2.725693	23073.499760
HLA A*3201	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.582964	1.857234	-2.725730	38279.317185
HLA A*2403	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.358396	1.632644	-2.725751	22824.207497
HLA A*0301	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.361537	1.635727	-2.725810	22989.893972
HLA A*0203	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.420025	1.694140	-2.725885	26304.196972
HLA A*2902	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.355496	1.629570	-2.725927	22672.345045
HLA A*6801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-3.480536	0.754547	-2.725990	3023.684545
HLA A*0101	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.342203	1.616065	-2.726138	21988.877318
HLA A*8001	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.422022	1.695841	-2.726181	26425.432875
HLA B*3501	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.451306	1.725080	-2.726226	28268.716556
HLA B*5701	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.358880	1.632644	-2.726235	22849.657821
HLA B*4402	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.405017	1.678625	-2.726392	25410.694667
HLA A*3001	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.016087	1.289436	-2.726651	10377.374490
HLA B*1503	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-3.521511	0.794851	-2.726661	3322.855828
HLA A*0206	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.961894	1.235042	-2.726852	9159.974579
HLA A*6802	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.628709	0.901531	-2.727178	4253.134347
HLA A*0216	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.448132	1.720897	-2.727234	28062.860477
HLA B*4402	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.421399	1.694140	-2.727260	26387.575972
HLA A*2403	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.423521	1.695841	-2.727680	26516.798085
HLA B*5701	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.402705	1.675016	-2.727688	25275.784535
HLA A*6901	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-3.990845	1.263086	-2.727758	9791.396163

HLA B*4001	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.367368	1.639403	-2.727965	23300.668978
HLA A*2403	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.315870	1.587869	-2.728001	20695.219086
HLA A*0212	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.791143	1.062990	-2.728153	6182.200649
HLA A*0203	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.453275	1.725080	-2.728194	28397.163354
HLA B*2705	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.344339	1.616065	-2.728274	22097.275896
HLA B*2705	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.345539	1.617007	-2.728533	22158.447298
HLA A*6802	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-3.991808	1.263086	-2.728722	9813.138117
HLA B*5701	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.407387	1.678625	-2.728762	25549.780189
HLA B*4801	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.366276	1.637421	-2.728855	23242.127516
HLA B*0802	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.401220	1.672339	-2.728881	25189.512933
HLA A*0201	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.365002	1.635727	-2.729276	23174.077696
HLA A*0212	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.440649	1.711364	-2.729285	27583.465415
HLA B*4601	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.366739	1.637421	-2.729318	23266.910975
HLA B*5301	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.558330	1.828772	-2.729557	36168.444557
HLA A*2403	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.397228	1.667650	-2.729578	24959.046778
HLA A*0101	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.405397	1.675762	-2.729635	25432.974413
HLA B*2705	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-3.633314	0.903619	-2.729695	4298.471899
HLA B*2705	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.107158	1.377330	-2.729828	12798.475079
HLA A*0203	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.352851	1.622722	-2.730129	22534.655454
HLA A*2603	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.553034	1.822872	-2.730162	35730.088582
HLA B*0702	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.406135	1.675762	-2.730373	25476.214254
HLA A*8001	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.451323	1.720897	-2.730425	28269.787091
HLA A*2601	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.353175	1.622722	-2.730453	22551.485314
HLA B*3901	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.455775	1.725080	-2.730694	28561.092237
HLA B*4402	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.427015	1.695841	-2.731174	26730.972914
HLA A*0216	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.427097	1.695841	-2.731256	26736.034799
HLA B*4801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.343822	1.612498	-2.731324	22070.991902
HLA A*2601	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.319197	1.587869	-2.731328	20854.361574
HLA B*4601	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.360912	1.629570	-2.731342	22956.834605
HLA A*2301	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.518135	1.786784	-2.731351	32971.206752
HLA B*3901	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.425638	1.694140	-2.731498	26646.364700
HLA A*0301	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.358833	1.627062	-2.731771	22847.185672
HLA A*2402	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.488045	1.756081	-2.731964	30764.154820
HLA B*5401	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.453625	1.721649	-2.731976	28420.062782
HLA B*4002	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.589374	1.857234	-2.732139	38848.439419
HLA B*1501	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.325555	1.593295	-2.732260	21161.897452
HLA A*6802	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.428182	1.695841	-2.732341	26802.941588
HLA A*2301	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-3.761323	1.028966	-2.732358	5771.961595
HLA A*0203	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.443799	1.711364	-2.732436	27784.301734
HLA A*2602	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.400353	1.667650	-2.732703	25139.278547
HLA B*1501	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.411492	1.678625	-2.732867	25792.397804
HLA A*2603	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.524084	1.791215	-2.732869	33425.948423
HLA A*0203	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.370303	1.637421	-2.732882	23458.643582
HLA A*2602	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.524180	1.791215	-2.732965	33433.363303
HLA B*0702	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.370481	1.637421	-2.733061	23468.290623
HLA A*0216	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.368787	1.635727	-2.733061	23376.930143
HLA B*4801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.360268	1.627062	-2.733206	22922.830677
HLA B*0702	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.400872	1.667650	-2.733222	25169.352679
HLA A*2501	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.355985	1.622722	-2.733263	22697.871618
HLA B*0802	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.429162	1.695841	-2.733321	26863.475235
HLA B*4601	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.409180	1.675762	-2.733418	25655.461139
HLA A*0301	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.366083	1.632644	-2.733439	23231.819341
HLA A*2902	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.444930	1.711364	-2.733566	27856.694988
HLA A*2603	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.174574	1.440990	-2.733585	14947.699202
HLA A*0219	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.371323	1.637421	-2.733902	23513.786650
HLA A*2602	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.356645	1.622722	-2.733924	22732.402683
HLA A*0219	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.369795	1.635727	-2.734069	23431.247321
HLA A*6801	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.521398	1.787266	-2.734132	33219.896678
HLA A*0250	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.591385	1.857234	-2.734150	39028.758496
HLA B*2705	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.447643	1.713482	-2.734162	28031.300309
HLA B*5301	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.513520	1.779355	-2.734165	32622.741450
HLA B*1502	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-3.655625	0.921448	-2.734177	4525.064786
HLA A*0216	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.371713	1.637421	-2.734292	23534.912493
HLA A*2301	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.518927	1.784483	-2.734443	33031.372464
HLA B*1517	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-3.249234	0.514746	-2.734488	1775.147236

HLA A*2403	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.419661	1.685162	-2.734499	26282.149285
HLA A*6802	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.419736	1.685162	-2.734575	26286.699551
HLA A*2601	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.364429	1.629570	-2.734859	23143.507794
HLA A*6802	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.357714	1.622722	-2.734993	22788.427406
HLA A*3001	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.071399	1.336347	-2.735052	11786.885518
HLA B*0802	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.410888	1.675762	-2.735126	25756.562481
HLA B*3801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.526464	1.791215	-2.735249	33609.632752
HLA B*0801	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.360968	1.625692	-2.735277	22959.815453
HLA B*0802	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.328719	1.593295	-2.735424	21316.669991
HLA A*0219	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.460575	1.725080	-2.735494	28878.511846
HLA B*1501	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.351585	1.616065	-2.735520	22469.041680
HLA B*1801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.457267	1.721649	-2.735618	28659.376294
HLA B*0802	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.365205	1.629570	-2.735635	23184.861955
HLA A*2301	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-3.951270	1.215498	-2.735772	8938.608111
HLA B*1501	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.323668	1.587869	-2.735799	21070.166576
HLA A*3101	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.371595	1.635727	-2.735868	23528.547291
HLA B*0803	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.414619	1.678625	-2.735994	25978.787827
HLA B*4601	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.329295	1.593295	-2.736000	21344.942324
HLA B*4601	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.363179	1.627062	-2.736117	23076.995126
HLA A*3001	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.075840	1.339557	-2.736282	11908.021005
HLA B*1501	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-3.381308	0.644580	-2.736728	2406.070401
HLA B*1509	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.404450	1.667650	-2.736800	25377.586216
HLA A*2402	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.354054	1.617007	-2.737047	22597.159892
HLA A*0206	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.196378	1.459325	-2.737052	15717.286533
HLA B*5701	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.366718	1.629570	-2.737148	23265.778159
HLA B*0702	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.462231	1.725080	-2.737151	28988.863984
HLA B*4501	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.862990	1.125828	-2.737162	7294.412982
HLA A*3001	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.149848	1.412655	-2.737194	14120.444548
HLA B*0803	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.404899	1.667650	-2.737249	25403.822144
HLA B*4402	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.422565	1.685162	-2.737403	26458.476969
HLA B*1517	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.119169	1.381752	-2.737417	13157.361116
HLA A*0101	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.375448	1.638021	-2.737427	23738.226481
HLA A*0101	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.376912	1.639403	-2.737509	23818.367849
HLA A*2403	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.330839	1.593295	-2.737544	21420.943578
HLA B*1502	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.594881	1.857234	-2.737647	39344.204640
HLA A*0212	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.375789	1.638021	-2.737768	23756.854856
HLA A*6802	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.412859	1.675016	-2.737843	25873.734579
HLA A*2501	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.405578	1.667650	-2.737928	25443.571017
HLA B*0702	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.377365	1.639403	-2.737962	23843.249799
HLA A*3101	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.148096	1.410054	-2.738042	14063.572417
HLA A*0203	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.825408	1.087303	-2.738105	6689.720694
HLA B*0803	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.459137	1.720897	-2.738239	28783.057468
HLA A*3201	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.055845	1.317518	-2.738328	11372.225813
HLA B*7301	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.567115	1.828772	-2.738342	36907.493890
HLA B*1509	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.370996	1.632644	-2.738352	23496.111527
HLA B*4402	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.414177	1.675762	-2.738415	25952.379294
HLA A*8001	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.378054	1.639403	-2.738650	23881.073644
HLA A*2902	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.412013	1.673173	-2.738841	25823.392964
HLA B*1502	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.120696	1.381752	-2.738944	13203.709471
HLA A*0216	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.744177	1.005151	-2.739026	5548.516619
HLA A*3201	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.452596	1.713482	-2.739114	28352.800272
HLA A*2501	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.464282	1.725080	-2.739202	29126.097364
HLA B*0802	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.356227	1.617007	-2.739221	22710.522819
HLA B*0801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.351904	1.612498	-2.739406	22485.579246
HLA B*1517	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.025683	1.286148	-2.739534	10609.203655
HLA B*4601	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.418199	1.678625	-2.739575	26193.859767
HLA A*0211	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.544292	1.804702	-2.739589	35018.025869
HLA A*0216	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.414694	1.675016	-2.739678	25983.285572
HLA A*0206	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.544390	1.804702	-2.739688	35025.983406
HLA B*4001	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.377711	1.638021	-2.739690	23862.218773
HLA A*3001	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-3.865800	1.126026	-2.739775	7341.762509
HLA A*8001	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.424940	1.685162	-2.739779	26603.585374
HLA A*3002	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.412199	1.672339	-2.739860	25834.431757
HLA A*0216	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.905493	1.165167	-2.740326	8044.379146
HLA A*3002	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.150473	1.410054	-2.740419	14140.778926

HLA B*4402	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.349421	1.608922	-2.740499	22357.367941
HLA B*3801	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.545227	1.804702	-2.740524	35093.505667
HLA A*0101	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.366236	1.625692	-2.740544	23239.990079
HLA B*1502	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.600663	1.859882	-2.740781	39871.525557
HLA B*5301	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.469442	1.728396	-2.741046	29474.182346
HLA B*1502	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.527852	1.786784	-2.741069	33717.262934
HLA B*5701	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.416917	1.675762	-2.741155	26116.602515
HLA B*5101	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.376905	1.635727	-2.741178	23817.981288
HLA A*0301	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.363966	1.622722	-2.741245	23118.855782
HLA B*3901	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.437209	1.695841	-2.741368	27365.865068
HLA A*2501	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.353901	1.612498	-2.741403	22589.215161
HLA B*3901	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.413893	1.672339	-2.741554	25935.396515
HLA A*0206	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.516730	1.775111	-2.741618	32864.713501
HLA A*2602	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.601579	1.859882	-2.741697	39955.737571
HLA A*0206	1:210-218	9	NIANALIEQ	0.827718	0.099249	-3.668749	0.926967	-2.741782	4663.897795
HLA A*0219	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.462706	1.720897	-2.741808	29020.560261
HLA A*0203	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.123309	1.381432	-2.741877	13283.379703
HLA A*0216	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.420624	1.678625	-2.741999	26340.509224
HLA A*0212	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.417173	1.675016	-2.742157	26132.007441
HLA B*3501	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.436488	1.694140	-2.742348	27320.452577
HLA B*1801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.470776	1.728396	-2.742381	29564.890409
HLA B*1503	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.410242	1.667650	-2.742592	25718.272429
HLA B*0702	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.414999	1.672339	-2.742661	26001.565669
HLA A*0203	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.907908	1.165167	-2.742741	8089.241515
HLA B*4002	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.604565	1.861603	-2.742962	40231.418689
HLA A*0211	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.496144	1.753043	-2.743101	31343.223755
HLA A*3201	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-3.538047	0.794851	-2.743196	3451.812317
HLA B*4601	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.410888	1.667650	-2.743238	25756.562481
HLA B*3901	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.454675	1.711364	-2.743311	28488.871923
HLA B*5701	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.379128	1.635727	-2.743401	23940.188330
HLA B*4801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.407263	1.663852	-2.743411	25542.455501
HLA A*0250	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.530568	1.786784	-2.743785	33928.785751
HLA A*0219	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.369570	1.625692	-2.743878	23419.081477
HLA A*0203	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.429118	1.685162	-2.743956	26860.714137
HLA B*0803	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.469134	1.725080	-2.744054	29453.301527
HLA A*2403	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.371121	1.627062	-2.744059	23502.849395
HLA A*3002	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.469219	1.725080	-2.744138	29459.038293
HLA A*0212	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.438330	1.694140	-2.744190	27436.574346
HLA B*0802	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.369899	1.625692	-2.744207	23436.825444
HLA B*4501	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-3.979379	1.235042	-2.744337	9536.283111
HLA B*1501	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.420206	1.675762	-2.744444	26315.156569
HLA B*4601	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.408390	1.663852	-2.744539	25608.868982
HLA A*0216	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.412251	1.667650	-2.744601	25837.506691
HLA B*5401	1:9-17	9	VPETPARPV	0.601332	-0.092772	-3.253252	0.508560	-2.744692	1791.645157
HLA B*5101	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.374266	1.629570	-2.744697	23673.718439
HLA B*5801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.349383	1.604651	-2.744732	22355.432811
HLA B*4801	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.370491	1.625692	-2.744799	23468.798472
HLA A*0202	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.439018	1.694140	-2.744879	27480.098478
HLA A*0206	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.440762	1.695841	-2.744920	27590.629072
HLA A*3201	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.549961	1.804702	-2.745259	35478.150079
HLA A*3002	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.498319	1.753043	-2.745276	31500.633379
HLA B*3901	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.382805	1.637421	-2.745384	24143.737829
HLA A*3201	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.382906	1.637421	-2.745485	24149.354925
HLA A*0216	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.046922	1.301147	-2.745775	11140.947576
HLA B*5801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.354705	1.608922	-2.745783	22631.048009
HLA B*2705	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.375460	1.629570	-2.745890	23738.868595
HLA B*0803	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.457349	1.711364	-2.745985	28664.803350
HLA B*0803	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.431232	1.685162	-2.746071	26991.815174
HLA B*4801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.375646	1.629570	-2.746076	23749.016311
HLA B*3501	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.384240	1.638021	-2.746219	24223.675603
HLA A*0219	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.205635	1.459325	-2.746309	16055.895820
HLA B*4001	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.383751	1.637421	-2.746330	24196.433074
HLA A*2902	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.410284	1.663852	-2.746432	25720.776945
HLA A*2403	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.418933	1.672339	-2.746594	26238.109335
HLA A*2402	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.205949	1.459325	-2.746624	16067.539362

HLA A*0201	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.410510	1.663852	-2.746658	25734.138484
HLA A*6802	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.419017	1.672339	-2.746678	26243.219862
HLA A*2602	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.499926	1.753043	-2.746883	31617.413125
HLA A*0101	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.369638	1.622722	-2.746916	23422.755910
HLA A*3002	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.526316	1.779355	-2.746961	33598.179768
HLA B*3501	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.467868	1.720897	-2.746970	29367.542848
HLA B*4601	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.379621	1.632644	-2.746977	23967.401676
HLA B*5301	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.604305	1.857234	-2.747070	40207.267067
HLA A*2601	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.382873	1.635727	-2.747146	24147.525960
HLA B*1517	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.458789	1.711364	-2.747425	28760.021145
HLA A*3301	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.526807	1.779355	-2.747452	33636.189599
HLA A*3001	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.691281	0.943730	-2.747551	4912.251409
HLA A*0219	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.458972	1.711364	-2.747609	28772.159611
HLA B*5801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.269181	1.521566	-2.747615	18585.791567
HLA A*2301	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.360205	1.612498	-2.747707	22919.482652
HLA A*0211	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.539205	1.791215	-2.747990	34610.272939
HLA A*0101	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.375063	1.627062	-2.748001	23717.174748
HLA A*2301	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.501068	1.753043	-2.748025	31700.651198
HLA A*0250	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.497318	1.749103	-2.748215	31428.120207
HLA A*8001	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.383996	1.635727	-2.748269	24210.050507
HLA B*1503	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.088090	1.339557	-2.748533	12248.694613
HLA B*1501	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.371435	1.622722	-2.748714	23519.893378
HLA B*1517	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.473817	1.725080	-2.748736	29772.582481
HLA B*0801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.424541	1.675762	-2.748779	26579.129806
HLA A*2902	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.364984	1.616065	-2.748919	23173.074765
HLA B*3901	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.175345	1.426359	-2.748986	14974.246598
HLA A*3002	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.536343	1.787266	-2.749077	34382.967082
HLA B*3501	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.416806	1.667650	-2.749156	26109.962827
HLA B*4801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.382067	1.632644	-2.749422	24102.759551
HLA B*3501	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.424480	1.675016	-2.749463	26575.391525
HLA B*5401	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.540810	1.791215	-2.749595	34738.392869
HLA A*2602	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.376677	1.627062	-2.749615	23805.485860
HLA B*2705	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.375361	1.625692	-2.749670	23733.475373
HLA B*0802	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.387278	1.637421	-2.749857	24393.713905
HLA B*1517	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.387969	1.638021	-2.749948	24432.543159
HLA B*0702	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.428582	1.678625	-2.749957	26827.603087
HLA B*2705	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.209591	1.459325	-2.750266	16202.837419
HLA B*1503	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.426051	1.675762	-2.750289	26671.747865
HLA B*7301	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.529668	1.779355	-2.750313	33858.558510
HLA A*8001	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.388368	1.638021	-2.750347	24455.023644
HLA B*0702	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.444497	1.694140	-2.750358	27828.979685
HLA B*1801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.423664	1.673173	-2.750492	26525.550158
HLA B*0801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.429230	1.678625	-2.750605	26867.690090
HLA B*0801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.423068	1.672339	-2.750729	26489.126117
HLA B*5701	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.414609	1.663852	-2.750758	25978.225663
HLA A*8001	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.462135	1.711364	-2.750771	28982.434809
HLA B*4403	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.608024	1.857234	-2.750790	40553.074863
HLA A*0301	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.363308	1.612498	-2.750810	23083.862567
HLA A*0203	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.043934	1.293038	-2.750895	11064.545670
HLA A*6801	1:245-253	9	VQRAIGDRL	1.396629	0.517941	-4.665530	1.914570	-2.750960	46294.541190
HLA B*0803	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.387271	1.635727	-2.751544	24393.318006
HLA B*1801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.390948	1.639403	-2.751544	24600.720204
HLA A*2902	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.377267	1.625692	-2.751575	23837.832862
HLA A*0250	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.480188	1.728396	-2.751793	30212.614577
HLA B*1509	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.473748	1.721649	-2.752099	29767.911923
HLA A*3001	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.280536	1.528166	-2.752370	19078.144040
HLA A*0216	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.178780	1.426359	-2.752421	15093.151381
HLA B*4402	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.420175	1.667650	-2.752526	26313.305927
HLA A*2601	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.357505	1.604651	-2.752855	22777.457872
HLA B*3901	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.378578	1.625692	-2.752886	23909.901283
HLA B*0802	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.416809	1.663852	-2.752957	26110.104079
HLA A*3201	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.388758	1.635727	-2.753031	24476.995137
HLA A*3001	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.070610	1.317518	-2.753092	11765.479689
HLA A*6802	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-3.963276	1.210159	-2.753116	9189.158988
HLA A*2602	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.130451	1.377330	-2.753121	13503.645288

HLA A*0101	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.365923	1.612498	-2.753425	23223.274566
HLA A*0219	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.421204	1.667650	-2.753555	26375.730062
HLA A*0250	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.376327	1.622722	-2.753605	23786.304621
HLA A*6801	1:95-103	9	GFQAMAQAL	1.526780	0.374899	-4.655357	1.901679	-2.753677	45222.702719
HLA B*5401	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.438929	1.685162	-2.753767	27474.449815
HLA A*8001	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.432407	1.678625	-2.753782	27064.925373
HLA A*0212	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.697662	0.943730	-2.753932	4984.961255
HLA A*6802	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.417800	1.663852	-2.753948	26169.780842
HLA A*0101	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.391667	1.637421	-2.754246	24641.478605
HLA A*2602	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.543324	1.788992	-2.754331	34940.062009
HLA A*3001	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.257619	1.503120	-2.754499	18097.527560
HLA A*0211	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.377377	1.622722	-2.754655	23843.894754
HLA B*5401	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.232513	1.477798	-2.754715	17080.974721
HLA B*0802	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.392825	1.638021	-2.754804	24707.287004
HLA B*4402	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.380657	1.625692	-2.754965	24024.650434
HLA A*2403	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.393121	1.638021	-2.755100	24724.134370
HLA B*5401	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.167845	1.412655	-2.755191	14717.885663
HLA B*3901	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.476161	1.720897	-2.755264	29933.761436
HLA B*3801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.449415	1.694140	-2.755275	28145.875084
HLA A*6901	1:51-59	9	EEIRARQPV	0.859860	0.021658	-3.636805	0.881518	-2.755288	4333.166996
HLA B*1503	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-3.447865	0.692424	-2.755440	2804.558748
HLA B*0803	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.431796	1.675762	-2.756034	27026.883389
HLA B*4002	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.584858	1.828772	-2.756085	38446.593624
HLA B*4601	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.373252	1.617007	-2.756245	23618.455853
HLA B*4402	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.395684	1.639403	-2.756281	24870.492376
HLA A*0203	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.434998	1.678625	-2.756373	27226.907500
HLA B*5101	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.469886	1.713482	-2.756404	29504.334198
HLA A*0203	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.424087	1.667650	-2.756437	26551.392790
HLA A*2501	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.477543	1.720897	-2.756645	30029.132783
HLA B*0803	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.470208	1.713482	-2.756726	29526.209582
HLA B*0803	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.373757	1.617007	-2.756750	23645.943080
HLA B*1501	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.037059	1.280105	-2.756954	10890.780188
HLA A*0219	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.452796	1.695841	-2.756954	28365.841038
HLA A*0202	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.216452	1.459325	-2.757126	16460.823963
HLA A*0206	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.548500	1.791215	-2.757284	35358.968473
HLA B*5401	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.532547	1.775111	-2.757435	34083.688200
HLA B*2705	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.345335	1.587869	-2.757466	22148.020649
HLA B*1503	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.470948	1.713482	-2.757466	29576.568538
HLA B*4001	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.383159	1.625692	-2.757468	24163.468744
HLA A*0212	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.383171	1.625692	-2.757479	24164.122361
HLA A*0201	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.383232	1.625692	-2.757540	24167.521456
HLA A*0212	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.442705	1.685162	-2.757543	27714.345494
HLA B*4402	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.380488	1.622722	-2.757766	24015.294366
HLA A*6801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.045639	1.287816	-2.757823	11108.088005
HLA A*0212	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.380899	1.622722	-2.758177	24038.041146
HLA A*2501	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.383982	1.625692	-2.758290	24209.264677
HLA B*0802	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.394030	1.635727	-2.758304	24775.951711
HLA A*3002	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.454283	1.695841	-2.758442	28463.145233
HLA A*3002	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.394181	1.635727	-2.758454	24784.531446
HLA A*0216	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-3.191841	0.433361	-2.758480	1555.396656
HLA A*3001	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.280104	1.521566	-2.758537	19059.162730
HLA A*0211	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.688273	0.929716	-2.758557	4878.353249
HLA B*0802	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.433737	1.675016	-2.758720	27147.925108
HLA A*0212	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.434580	1.675762	-2.758818	27200.701689
HLA B*1517	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.452962	1.694140	-2.758823	28376.738510
HLA B*0801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.889234	1.130410	-2.758824	7748.793640
HLA B*1503	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.080990	1.322138	-2.758852	12050.072592
HLA B*1503	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.479794	1.720897	-2.758896	30185.167973
HLA A*2402	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.280651	1.521566	-2.759085	19083.202032
HLA A*2301	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.480740	1.721649	-2.759091	30251.049024
HLA B*0802	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.254682	1.495512	-2.759171	17975.558403
HLA A*3002	1:499-507	9	RITNEVAEV	0.947033	0.285622	-3.991827	1.232655	-2.759172	9813.562831
HLA A*8001	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.453477	1.694140	-2.759337	28410.378221
HLA A*2501	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.389066	1.629570	-2.759496	24494.348021
HLA A*1101	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.399267	1.639403	-2.759864	25076.524674

HLA A*2403	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.397320	1.637421	-2.759899	24964.313335
HLA A*0201	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.397595	1.637421	-2.760174	24980.119674
HLA B*5301	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.389759	1.629570	-2.760189	24533.470184
HLA B*3501	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.389900	1.629570	-2.760330	24541.434878
HLA B*5301	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.386197	1.625692	-2.760505	24333.084424
HLA A*0212	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.439331	1.678625	-2.760706	27499.877943
HLA B*5301	1:10-18 9		PETPARPVL	1.635476	0.153516	-4.549855	1.788992	-2.760863	35469.514151
HLA B*2705	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.399049	1.638021	-2.761028	25063.911354
HLA B*7301	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-3.039129	0.278063	-2.761066	1094.282200
HLA B*4601	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.373627	1.612498	-2.761129	23638.908420
HLA A*0212	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.425069	1.663852	-2.761218	26611.502287
HLA B*1801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.486351	1.725080	-2.761271	30644.392030
HLA A*0219	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.440031	1.678625	-2.761406	27544.247543
HLA A*0203	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.138975	1.377330	-2.761644	13771.300437
HLA A*6802	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.440306	1.678625	-2.761681	27561.687387
HLA B*2705	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.437479	1.675762	-2.761717	27382.895690
HLA A*2902	1:30-38 9		IARRVREAR	0.966536	0.718626	-4.446955	1.685162	-2.761793	27986.903160
HLA B*5801	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.355104	1.593295	-2.761809	22651.870932
HLA A*0212	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.136372	1.374504	-2.761868	13689.000005
HLA B*5401	1:10-18 9		PETPARPVL	1.635476	0.153516	-4.550952	1.788992	-2.761960	35559.238271
HLA B*3901	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.475522	1.713482	-2.762041	29889.746602
HLA A*0211	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.457948	1.695841	-2.762107	28704.374357
HLA A*2603	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.511291	1.749103	-2.762188	32455.685988
HLA A*0250	1:75-83 9		APKLDPALL	1.420023	0.333020	-4.515261	1.753043	-2.762219	32753.779615
HLA B*0803	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.458167	1.695841	-2.762325	28718.819727
HLA A*2603	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.484034	1.721649	-2.762385	30481.365416
HLA B*5401	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.534816	1.772257	-2.762560	34262.274184
HLA B*0801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.367265	1.604651	-2.762614	23295.123261
HLA B*0801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.426519	1.663852	-2.762667	26700.477275
HLA A*3001	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.240733	1.477798	-2.762936	17407.383526
HLA A*0212	1:19-27 9		VVDFGAQYA	1.013002	-0.199742	-3.576363	0.813260	-2.763102	3770.184255
HLA B*4801	1:46-54 9		HTASIEEIR	1.076887	0.539178	-4.379203	1.616065	-2.763138	23944.333129
HLA A*3301	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.623044	1.859882	-2.763162	41980.155894
HLA B*4001	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.375735	1.612498	-2.763237	23753.899035
HLA B*0802	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.367977	1.604651	-2.763326	23333.339857
HLA A*2501	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.438457	1.675016	-2.763441	27444.590673
HLA B*4402	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.400865	1.637421	-2.763444	25168.944192
HLA A*6801	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.356800	1.593295	-2.763506	22740.520797
HLA B*1509	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.427362	1.663852	-2.763511	26752.384001
HLA A*0203	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-3.784489	1.020890	-2.763600	6088.206226
HLA B*0702	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.376099	1.612498	-2.763601	23773.825813
HLA A*0212	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.296107	0.532233	-2.763873	1977.454987
HLA B*0801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.401943	1.638021	-2.763922	25231.519841
HLA A*0211	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.543399	1.779355	-2.764044	34946.111232
HLA B*3801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.475435	1.711364	-2.764072	29883.764292
HLA B*4402	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.439378	1.675016	-2.764362	27502.853529
HLA A*2603	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.624285	1.859882	-2.764402	42100.240336
HLA A*0211	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.539689	1.775111	-2.764578	34648.865414
HLA B*4801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.402726	1.638021	-2.764705	25277.015217
HLA B*4001	1:46-54 9		HTASIEEIR	1.076887	0.539178	-4.380840	1.616065	-2.764776	24034.790288
HLA B*7301	1:74-82 9		GAPKLDPAL	1.528258	0.294614	-4.587684	1.822872	-2.764812	38697.623749
HLA B*0802	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.397533	1.632644	-2.764889	24976.606290
HLA A*3001	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.068683	1.303793	-2.764890	11713.402333
HLA A*0211	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.139468	1.374504	-2.764964	13786.954581
HLA A*1101	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.438170	1.673173	-2.764997	27426.483042
HLA A*0211	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.137951	1.372792	-2.765159	13738.856189
HLA A*2403	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.401227	1.635727	-2.765500	25189.921753
HLA B*0702	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.392668	1.627062	-2.765606	24698.333160
HLA A*0201	1:21-29 9		DFGAQYAQL	1.321005	0.301717	-4.388422	1.622722	-2.765700	24458.066710
HLA B*5801	1:36-44 9		EARVFSEVI	1.251732	0.243780	-4.261479	1.495512	-2.765968	18259.103506
HLA B*4501	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.557444	1.791215	-2.766229	36094.753168
HLA A*0203	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.442023	1.675762	-2.766261	27670.899438
HLA B*1501	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.392071	1.625692	-2.766379	24664.418195
HLA A*3201	1:36-44 9		EARVFSEVI	1.251732	0.243780	-4.261905	1.495512	-2.766393	18276.991393
HLA A*0211	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.839397	1.072837	-2.766559	6908.707713

HLA B*1801	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.460826	1.694140	-2.766687	28895.233247
HLA B*5101	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.491821	1.725080	-2.766740	31032.774860
HLA B*1503	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.404869	1.638021	-2.766848	25402.035593
HLA B*5701	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.393925	1.627062	-2.766863	24769.920864
HLA A*0202	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.089058	1.322138	-2.766920	12276.025862
HLA B*4403	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.488637	1.721649	-2.766988	30806.123950
HLA A*0201	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.053167	1.286148	-2.767019	11302.306014
HLA B*4403	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.402991	1.635727	-2.767264	25292.472223
HLA A*0211	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.439648	1.672339	-2.767309	27519.969403
HLA B*0702	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.405587	1.638021	-2.767567	25444.121611
HLA A*6901	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.376536	1.608922	-2.767614	23797.760012
HLA B*4501	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.625664	1.858036	-2.767628	42234.146571
HLA A*2603	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.393342	1.625692	-2.767650	24736.710521
HLA A*2902	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.394853	1.627062	-2.767791	24822.908456
HLA B*1517	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.383874	1.616065	-2.767809	24203.240833
HLA B*4601	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.063129	1.295300	-2.767829	11564.553729
HLA A*0216	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.149646	1.381752	-2.767895	14113.876532
HLA A*2402	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.380636	1.612498	-2.768138	24023.480726
HLA B*1502	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.521260	1.753043	-2.768217	33209.295129
HLA B*1501	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.898660	1.130410	-2.768250	7918.815584
HLA B*1801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.440602	1.672339	-2.768263	27580.481106
HLA A*6801	1:426-434	9	ADSIVREEL	1.526192	0.333690	-4.628206	1.859882	-2.768324	42482.089108
HLA B*0803	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.373150	1.604651	-2.768500	23612.962243
HLA A*0206	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.405947	1.637421	-2.768526	25465.190760
HLA A*3002	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.487227	1.718496	-2.768731	30706.291433
HLA B*5801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.321854	1.553110	-2.768744	20982.351911
HLA B*1503	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.447521	1.678625	-2.768896	28023.415814
HLA A*3002	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.080205	1.311116	-2.769089	12028.318939
HLA A*0206	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-3.545025	0.775707	-2.769318	3507.721821
HLA A*2501	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.402051	1.632644	-2.769407	25237.799610
HLA A*0212	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.151009	1.381432	-2.769577	14158.231698
HLA A*3201	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.491518	1.721649	-2.769868	31011.125396
HLA A*6901	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.374600	1.604651	-2.769949	23691.911677
HLA B*5701	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.407399	1.637421	-2.769978	25550.471306
HLA B*5301	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.554561	1.784483	-2.770078	35855.952029
HLA A*0202	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.545349	1.775111	-2.770238	35103.379359
HLA B*5801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.358299	1.587869	-2.770430	22819.145525
HLA A*0301	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.363865	1.593295	-2.770570	23113.478379
HLA B*0702	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.434554	1.663852	-2.770703	27199.083057
HLA B*2705	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.434653	1.663852	-2.770801	27205.263808
HLA A*0202	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.559808	1.788992	-2.770815	36291.728912
HLA A*2902	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.443196	1.672339	-2.770857	27745.698907
HLA B*0802	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.449490	1.678625	-2.770865	28150.748020
HLA B*1509	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.491792	1.720897	-2.770895	31030.760319
HLA A*3201	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.052152	1.281231	-2.770921	11275.922552
HLA B*4002	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.627889	1.856944	-2.770945	42451.074277
HLA B*0702	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.396803	1.625692	-2.771111	24934.619092
HLA A*0219	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.465361	1.694140	-2.771221	29198.511385
HLA B*3501	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.449880	1.678625	-2.771255	28176.039917
HLA B*3901	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.400893	1.629570	-2.771323	25170.578179
HLA A*2601	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.388432	1.617007	-2.771425	24458.595977
HLA A*0216	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.482998	1.711364	-2.771635	30408.730838
HLA B*2705	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.313342	1.541660	-2.771682	20575.101317
HLA A*0203	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-3.815794	1.044058	-2.771736	6543.255713
HLA B*5101	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.456959	1.685162	-2.771797	28639.072719
HLA B*1502	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.492718	1.720897	-2.771821	31096.972811
HLA A*2902	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.407563	1.635727	-2.771837	25560.148903
HLA A*1101	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.407580	1.635727	-2.771853	25561.116864
HLA A*0219	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.444234	1.672339	-2.771895	27812.123002
HLA A*0101	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.365216	1.593295	-2.771921	23185.489101
HLA A*2402	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.397623	1.625692	-2.771931	24981.741403
HLA A*2403	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.388178	1.616065	-2.772113	24444.309775
HLA A*2403	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.447932	1.675762	-2.772170	28049.959002
HLA B*3501	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.448172	1.675762	-2.772410	28065.441484
HLA B*4601	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.398121	1.625692	-2.772429	25010.409311

HLA A*0202	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-3.672597	0.900138	-2.772460	4705.410109
HLA B*3501	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.436504	1.663852	-2.772653	27321.487201
HLA A*0201	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.388826	1.616065	-2.772761	24480.835555
HLA A*2902	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.042674	1.269596	-2.773079	11032.508273
HLA A*2601	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.385828	1.612498	-2.773330	24312.425830
HLA B*5301	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.578183	1.804702	-2.773481	37860.206672
HLA B*4601	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.389580	1.616065	-2.773516	24523.385282
HLA B*5401	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.560393	1.786784	-2.773609	36340.649077
HLA B*4501	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.502067	1.728396	-2.773671	31773.621281
HLA A*3301	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.485174	1.711364	-2.773810	30561.447321
HLA B*0803	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.447143	1.673173	-2.773970	27999.018265
HLA A*8001	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.396760	1.622722	-2.774039	24932.191127
HLA A*8001	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.446393	1.672339	-2.774054	27950.740500
HLA B*0702	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.091614	1.317518	-2.774096	12348.495118
HLA B*5101	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.087324	1.313175	-2.774148	12227.111561
HLA A*3002	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.367460	1.593295	-2.774165	23305.585604
HLA A*3002	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.578874	1.804702	-2.774171	37920.471525
HLA A*0202	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.565547	1.791215	-2.774332	36774.557023
HLA B*5401	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.553777	1.779355	-2.774421	35791.222301
HLA A*2501	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.391429	1.617007	-2.774423	24628.018208
HLA B*1509	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.229959	1.455494	-2.774464	16980.823963
HLA B*3901	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.449488	1.675016	-2.774471	28150.595728
HLA A*0250	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.558187	0.783681	-2.774506	3615.654795
HLA B*0802	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.390741	1.616065	-2.774676	24589.011321
HLA B*0803	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.070022	1.295300	-2.774723	11749.577960
HLA A*3101	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.368264	1.593295	-2.774969	23348.745096
HLA A*2402	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.559577	1.784483	-2.775094	36272.493257
HLA B*4402	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.439046	1.663852	-2.775195	27481.882507
HLA B*1801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.413371	1.638021	-2.775350	25904.266920
HLA A*2603	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.503784	1.728396	-2.775389	31899.522947
HLA B*0801	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.391587	1.616065	-2.775522	24636.946561
HLA A*2402	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.201946	1.426359	-2.775587	15920.102152
HLA A*0219	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.451050	1.675016	-2.776034	28252.052032
HLA B*4403	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.637651	1.861603	-2.776048	43416.098639
HLA A*2902	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.413540	1.637421	-2.776120	25914.358909
HLA A*3201	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.935613	1.159455	-2.776158	8622.097492
HLA A*0250	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.414205	1.638021	-2.776184	25954.064143
HLA A*3201	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.532838	1.756081	-2.776757	34106.560103
HLA A*8001	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.403933	1.627062	-2.776872	25347.400398
HLA B*1501	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.381644	1.604651	-2.776993	24079.300189
HLA B*4601	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.381855	1.604651	-2.777205	24091.027015
HLA A*2402	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.060897	1.283502	-2.777395	11505.271391
HLA B*1503	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.134003	1.356576	-2.777427	13614.554751
HLA B*5401	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.562223	1.784483	-2.777739	36494.122772
HLA B*1509	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.415206	1.637421	-2.777785	26013.947188
HLA A*3002	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.491391	1.713482	-2.777909	31002.067314
HLA B*3801	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.450308	1.672339	-2.777969	28203.795703
HLA B*5301	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.564772	1.786784	-2.777989	36708.963320
HLA A*3002	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.534840	1.756081	-2.778758	34264.127785
HLA A*0212	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.300469	1.521566	-2.778903	19974.188963
HLA B*1517	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.404674	1.625692	-2.778982	25390.632111
HLA A*2602	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.554223	1.775111	-2.779112	35828.030258
HLA A*0216	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.473307	1.694140	-2.779167	29737.651586
HLA A*0101	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.383836	1.604651	-2.779185	24201.145934
HLA B*1509	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.451604	1.672339	-2.779266	28288.145419
HLA B*1502	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.568287	1.788992	-2.779295	37007.261552
HLA A*0219	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.681549	0.902116	-2.779433	4803.402934
HLA A*1101	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.492939	1.713482	-2.779457	31112.790563
HLA B*0702	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.454696	1.675016	-2.779680	28490.259052
HLA A*8001	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.455451	1.675762	-2.779688	28539.777491
HLA A*2601	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.333012	1.553110	-2.779902	21528.405792
HLA B*5301	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.392449	1.612498	-2.779951	24685.910068
HLA B*2705	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.081126	1.301147	-2.779979	12053.854179
HLA A*6802	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.397275	1.617007	-2.780268	24961.747438
HLA B*4002	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.154881	1.374504	-2.780377	14285.023741

HLA A*3301	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.567728	1.787266	-2.780461	36959.643381
HLA A*3001	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.911141	1.130410	-2.780731	8149.682572
HLA B*1801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.302506	1.521566	-2.780940	20068.095434
HLA A*2902	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.456888	1.675762	-2.781126	28634.425070
HLA A*0203	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.444986	1.663852	-2.781134	27860.312062
HLA A*2602	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.567927	1.786784	-2.781144	36976.642833
HLA A*0216	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.094424	1.313175	-2.781249	12428.651725
HLA B*3501	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.309437	1.528166	-2.781271	20390.934913
HLA A*2501	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.445343	1.663852	-2.781491	27883.231107
HLA A*0216	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.941195	1.159455	-2.781740	8733.640386
HLA B*3501	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.259731	1.477798	-2.781934	18185.759093
HLA A*0203	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.398205	1.616065	-2.782141	25015.280713
HLA A*0211	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.104282	1.322138	-2.782145	12714.007331
HLA B*4601	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.277804	1.495512	-2.782292	18958.486879
HLA B*4501	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.611189	1.828772	-2.782416	40849.669361
HLA A*2603	1:212-220	9	ANALIEQVR	1.205252	0.651982	-4.639761	1.857234	-2.782526	43627.530700
HLA B*5701	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.395144	1.612498	-2.782646	24839.565901
HLA B*4402	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.310948	1.528166	-2.782782	20461.989490
HLA A*0212	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.376256	1.593295	-2.782962	23782.444497
HLA B*4601	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.405785	1.622722	-2.783063	25455.686828
HLA B*0801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.336271	1.553110	-2.783161	21690.552108
HLA A*2601	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.078466	1.295300	-2.783167	11980.262012
HLA B*1509	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.494534	1.711364	-2.783171	31227.287799
HLA A*6801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-3.955898	1.172675	-2.783223	9034.380603
HLA A*0202	1:210-218	9	NIANALIEQ	0.827718	0.099249	-3.710513	0.926967	-2.783547	5134.681030
HLA A*2301	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.119930	1.336347	-2.783583	13180.443616
HLA A*0206	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.421634	1.638021	-2.783614	26401.855221
HLA A*2601	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.392588	1.608922	-2.783666	24693.790660
HLA B*4501	1:275-283	9	FVAATGANL	1.478982	0.382621	-4.645298	1.861603	-2.783695	44187.391927
HLA B*3801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.423286	1.639403	-2.783883	26502.456671
HLA B*0702	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.137640	1.353717	-2.783923	13729.048700
HLA A*0219	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.377563	1.593295	-2.784268	23854.087366
HLA B*1509	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.469580	1.685162	-2.784419	29483.591519
HLA A*0206	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-3.944029	1.159455	-2.784574	8790.807792
HLA A*0202	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.280148	1.495512	-2.784637	19061.121882
HLA B*3901	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.460420	1.675762	-2.784658	28868.202537
HLA B*1503	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.389350	1.604651	-2.784700	24510.387186
HLA B*0803	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.424151	1.639403	-2.784747	26555.271356
HLA B*5101	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.505668	1.720897	-2.784771	32038.227082
HLA B*1501	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.158701	1.373907	-2.784794	14411.235961
HLA B*0802	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.407690	1.622722	-2.784969	25567.616983
HLA B*4402	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.417920	1.632644	-2.785276	26177.002195
HLA B*4601	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.373183	1.587869	-2.785314	23614.750720
HLA B*5101	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.424846	1.639403	-2.785443	26597.829099
HLA B*5701	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.408181	1.622722	-2.785460	25596.541788
HLA A*2501	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.496832	1.711364	-2.785468	31392.945218
HLA A*3002	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.460580	1.675016	-2.785563	28878.824307
HLA A*6901	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.107727	1.322138	-2.785589	12815.241728
HLA B*1517	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.449673	1.663852	-2.785822	28162.629335
HLA B*3801	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.510915	1.725080	-2.785834	32427.605077
HLA B*4501	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.061700	1.275786	-2.785914	11526.577943
HLA A*0250	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.590699	1.804702	-2.785996	38967.153920
HLA A*2902	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.390656	1.604651	-2.786006	24584.222929
HLA A*8001	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.402108	1.616065	-2.786043	25241.076632
HLA A*0201	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.395010	1.608922	-2.786088	24831.907462
HLA A*0211	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.511610	1.725080	-2.786530	32479.573881
HLA A*3002	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.425986	1.639403	-2.786582	26667.708017
HLA B*4403	1:382-390	9	EVRAVGREL	1.480172	0.348600	-4.615530	1.828772	-2.786758	41260.111187
HLA B*1509	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.462520	1.675762	-2.786758	29008.160068
HLA B*4801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.246215	1.459325	-2.786889	17628.479157
HLA A*3002	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.576461	0.789472	-2.786989	3771.040996
HLA B*4402	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.380450	1.593295	-2.787155	24013.215735
HLA A*0250	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.578394	1.791215	-2.787179	37878.644918
HLA B*1503	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.419969	1.632644	-2.787324	26300.781927
HLA A*0216	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.459738	1.672339	-2.787400	28822.947651

HLA B*1509	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.466084	1.678625	-2.787460	29247.203839
HLA A*3301	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.506110	1.718496	-2.787614	32070.828430
HLA B*1501	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.913514	1.125828	-2.787686	8194.334217
HLA B*4801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.392390	1.604651	-2.787740	24682.571593
HLA B*0802	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.396666	1.608922	-2.787745	24926.796495
HLA A*0201	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.381143	1.593295	-2.787849	24051.569438
HLA B*1517	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-3.770486	0.982586	-2.787900	5895.035493
HLA B*3901	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.455749	1.667650	-2.788099	28559.392651
HLA A*3201	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.572619	1.784483	-2.788136	37378.287479
HLA A*0101	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.397165	1.608922	-2.788243	24955.401351
HLA A*3001	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.183329	1.394918	-2.788410	15252.060907
HLA A*3001	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.077832	1.289353	-2.788479	11962.775575
HLA A*0206	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.721580	0.932998	-2.788582	5267.196789
HLA B*1801	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.500147	1.711364	-2.788783	31633.495604
HLA A*0202	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.502494	1.713482	-2.789013	31804.920989
HLA A*3201	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.311025	1.521566	-2.789459	20465.642820
HLA B*1502	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.412211	1.622722	-2.789489	25835.130573
HLA B*4601	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.342600	1.553110	-2.789490	22008.990310
HLA A*0211	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.024677	1.235042	-2.789635	10584.667177
HLA B*1801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.416834	1.627062	-2.789773	26111.657906
HLA B*4801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.377753	1.587869	-2.789884	23864.542542
HLA A*0219	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.453822	1.663852	-2.789971	28432.980666
HLA B*0803	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.399046	1.608922	-2.790125	25063.775762
HLA A*8001	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.383784	1.593295	-2.790489	24198.265744
HLA A*1101	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.407528	1.617007	-2.790522	25558.074824
HLA A*0201	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.938085	1.147258	-2.790827	8671.307501
HLA B*7301	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.563259	1.772257	-2.791002	36581.292973
HLA B*4402	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.403515	1.612498	-2.791017	25323.003607
HLA B*1503	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.054102	1.263068	-2.791034	11326.667632
HLA A*2602	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.519436	1.728396	-2.791041	33070.172279
HLA B*1501	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.054483	1.263068	-2.791415	11336.598698
HLA B*1517	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.470081	1.678625	-2.791456	29517.585232
HLA A*0219	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.467334	1.675762	-2.791572	29331.500324
HLA A*2602	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.466824	1.675016	-2.791808	29297.086932
HLA A*0202	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.466878	1.675016	-2.791862	29300.732520
HLA B*0801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.173700	1.381752	-2.791949	14917.647524
HLA A*0211	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.754999	0.962975	-2.792024	5688.511221
HLA B*3801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.487916	1.695841	-2.792075	30755.002495
HLA B*4002	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-3.999552	1.207422	-2.792130	9989.685460
HLA A*3001	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-3.713582	0.921448	-2.792134	5171.087631
HLA A*2603	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.517298	1.725080	-2.792218	32907.767937
HLA B*0702	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.424987	1.632644	-2.792343	26606.463979
HLA B*1502	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.577217	1.784483	-2.792734	37776.119367
HLA B*1801	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.810216	1.017185	-2.793031	6459.757512
HLA B*3801	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.430485	1.637421	-2.793064	26945.419866
HLA B*4001	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.402000	1.608922	-2.793078	25234.796048
HLA A*0250	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.800668	1.007289	-2.793379	6319.284507
HLA A*6901	1:480-488	9	AMTADWTRV	0.947260	0.174566	-3.915233	1.121826	-2.793407	8226.848435
HLA A*0202	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.573014	1.779355	-2.793659	37412.274603
HLA A*0206	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-3.420869	0.627189	-2.793680	2635.536038
HLA B*0802	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.406370	1.612498	-2.793872	25490.000333
HLA A*0219	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.479079	1.685162	-2.793918	30135.566055
HLA B*4801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.402869	1.608922	-2.793947	25285.358091
HLA B*3501	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.919838	1.125828	-2.794010	8314.544976
HLA A*0211	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.514928	1.720897	-2.794030	32728.627684
HLA A*3301	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.616973	1.822872	-2.794101	41397.391614
HLA B*2705	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.429949	1.635727	-2.794222	26912.204399
HLA B*3801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.470076	1.675762	-2.794314	29517.265860
HLA A*1101	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-3.821531	1.027198	-2.794333	6630.271850
HLA A*0203	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.289892	1.495512	-2.794380	19493.587539
HLA A*0201	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.399213	1.604651	-2.794563	25073.404660
HLA B*3901	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.479798	1.685162	-2.794637	30185.494572
HLA B*5101	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.506131	1.711364	-2.794768	32072.389965
HLA A*2403	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.420676	1.625692	-2.794984	26343.644394
HLA A*0101	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.382922	1.587869	-2.795053	24150.269460

HLA A*2902	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.388558	1.593295	-2.795264	24465.742209
HLA A*0250	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.619950	0.824605	-2.795345	4168.216047
HLA B*3901	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.418141	1.622722	-2.795419	26190.317360
HLA A*0216	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.421122	1.625692	-2.795431	26370.736392
HLA A*2402	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.432896	1.637421	-2.795475	27095.397509
HLA B*4402	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.425130	1.629570	-2.795561	26615.245647
HLA B*5701	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.144445	1.348830	-2.795615	13945.836014
HLA A*0250	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.433058	1.637421	-2.795637	27105.513631
HLA B*4402	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.422746	1.627062	-2.795684	26469.500847
HLA B*4402	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.433718	1.638021	-2.795697	27146.750195
HLA A*2603	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.600421	1.804702	-2.795719	39849.314591
HLA A*2501	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.471676	1.675762	-2.795914	29626.212001
HLA B*3901	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.474564	1.678625	-2.795939	29823.845670
HLA B*1801	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.491821	1.695841	-2.795979	31032.774860
HLA B*0702	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.177615	1.381432	-2.796183	15052.706140
HLA A*2501	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.481473	1.685162	-2.796312	30302.152444
HLA A*2402	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.434488	1.638021	-2.796468	27194.963336
HLA B*4403	1:485-493	9	WTRVPYEVL	1.502125	0.355911	-4.654614	1.858036	-2.796578	45145.459423
HLA B*0803	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.390024	1.593295	-2.796730	24548.472508
HLA A*8001	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.426338	1.629570	-2.796768	26689.357201
HLA B*2705	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.429602	1.632644	-2.796957	26890.665401
HLA B*4402	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.036251	1.239243	-2.797008	10870.531273
HLA B*4001	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-3.988956	1.191820	-2.797136	9748.900473
HLA A*2603	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.493338	1.695841	-2.797497	31141.417572
HLA B*1509	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.172004	1.374504	-2.797500	14859.493735
HLA A*2602	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.423234	1.625692	-2.797543	26499.302601
HLA B*2705	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.406537	1.608922	-2.797615	25499.792977
HLA B*4601	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.319406	1.521566	-2.797840	20864.404953
HLA B*1503	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.462147	1.663852	-2.798295	28983.218778
HLA B*4403	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.621270	1.822872	-2.798398	41809.039060
HLA B*1503	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.079712	1.281231	-2.798481	12014.661605
HLA A*2902	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.301620	1.503120	-2.798500	20027.207697
HLA A*1101	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-3.877830	1.079304	-2.798526	7547.961826
HLA A*2403	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.320343	1.521566	-2.798777	20909.490368
HLA A*3201	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.929194	1.130410	-2.798784	8495.601563
HLA B*1503	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.082357	1.283502	-2.798855	12088.072705
HLA A*0211	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.225413	1.426359	-2.799054	16803.993554
HLA B*4402	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.416085	1.617007	-2.799078	26066.634452
HLA B*1517	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.474888	1.675762	-2.799126	29846.119414
HLA B*5401	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.548246	1.749103	-2.799143	35338.315392
HLA A*6801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.431819	1.632644	-2.799175	27028.345553
HLA A*6802	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.403924	1.604651	-2.799273	25346.851898
HLA B*1501	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.176656	1.377330	-2.799325	15019.517924
HLA B*0803	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.415500	1.616065	-2.799435	26031.544709
HLA B*4501	1:130-138	9	DLPEVQPVW	1.585198	0.271746	-4.656423	1.856944	-2.799479	45333.910244
HLA B*1502	1:291-299	9	TFLEALSGV	0.900311	0.134202	-3.833993	1.034513	-2.799480	6823.277023
HLA B*1502	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.574645	1.775111	-2.799533	37553.001618
HLA B*5401	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.528111	1.728396	-2.799715	33737.333637
HLA A*6901	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.341376	1.541660	-2.799716	21947.044161
HLA A*2403	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.226211	1.426359	-2.799853	16834.930630
HLA B*1509	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.495730	1.695841	-2.799889	31313.394806
HLA B*1509	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.416896	1.617007	-2.799889	26115.330955
HLA B*0802	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.439448	1.639403	-2.800045	27507.317513
HLA A*2603	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.584675	1.784483	-2.800191	38430.373686
HLA A*0216	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.475962	1.675762	-2.800199	29919.999842
HLA B*1517	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-3.512466	0.712255	-2.800211	3254.362908
HLA A*2602	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.521892	1.721649	-2.800242	33257.658475
HLA B*3901	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.154181	1.353717	-2.800464	14262.012737
HLA B*3901	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.322136	1.521566	-2.800570	20995.977797
HLA B*4601	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.409532	1.608922	-2.800610	25676.288568
HLA B*0702	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.423629	1.622722	-2.800907	26523.397741
HLA B*7301	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.522646	1.721649	-2.800997	33315.463051
HLA A*3002	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.464898	1.663852	-2.801046	29167.409702
HLA B*5801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.229440	1.428368	-2.801072	16960.534067
HLA B*1801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.479740	1.678625	-2.801115	30181.412343

HLA A*3002	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.585614	1.784483	-2.801131	38513.625354
HLA A*0206	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.178568	1.377330	-2.801238	15085.804465
HLA B*4001	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.406097	1.604651	-2.801447	25474.009174
HLA B*5101	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.434366	1.632644	-2.801722	27187.314082
HLA A*0216	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.081901	1.280105	-2.801797	12075.392704
HLA A*2403	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.124065	1.322138	-2.801928	13306.539308
HLA A*6901	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.389940	1.587869	-2.802071	24543.692011
HLA A*3001	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.183554	1.381432	-2.802122	15259.984113
HLA A*0250	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.523947	1.721649	-2.802298	33415.461889
HLA B*3501	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.419384	1.617007	-2.802377	26265.376984
HLA B*0702	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.355534	1.553110	-2.802424	22674.307608
HLA A*3001	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.231002	1.428368	-2.802634	17021.660771
HLA B*5701	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.395978	1.593295	-2.802683	24887.316390
HLA B*2705	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.269332	0.466612	-2.802720	1859.224678
HLA B*1517	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.396220	1.593295	-2.802925	24901.187929
HLA B*3801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.478271	1.675016	-2.803255	30079.535862
HLA A*2603	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.467217	1.663852	-2.803365	29323.567389
HLA B*5701	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.412298	1.608922	-2.803376	25840.302403
HLA B*3801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.433006	1.629570	-2.803436	27102.287791
HLA B*0803	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.478638	1.675016	-2.803621	30104.931982
HLA B*1801	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.479100	1.675016	-2.804084	30137.033361
HLA B*1502	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.608832	1.804702	-2.804130	40628.614479
HLA B*7301	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.608968	1.804702	-2.804266	40641.364665
HLA B*1509	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.429961	1.625692	-2.804269	26912.932370
HLA B*1502	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.245425	1.440990	-2.804436	17596.464574
HLA B*3801	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.518182	1.713482	-2.804700	32974.774356
HLA B*4403	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.533200	1.728396	-2.804804	34134.986900
HLA A*6802	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-3.987043	1.182210	-2.804833	9706.064117
HLA A*2402	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.434533	1.629570	-2.804963	27197.758793
HLA B*1502	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.186444	1.381432	-2.805012	15361.865135
HLA A*0211	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.480261	1.675016	-2.805245	30217.681856
HLA B*3801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.478520	1.673173	-2.805348	30096.789866
HLA B*1501	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.768475	0.962975	-2.805501	5867.799491
HLA B*1801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.435158	1.629570	-2.805588	27236.925372
HLA B*1501	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.264957	1.459325	-2.805631	18405.884327
HLA B*3501	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.410390	1.604651	-2.805739	25727.039303
HLA B*4402	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.698517	0.892605	-2.805912	4994.787310
HLA B*1801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.526952	1.720897	-2.806055	33647.473511
HLA A*2603	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.595090	1.788992	-2.806098	39363.152654
HLA A*3101	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.359274	1.553110	-2.806165	22870.434432
HLA B*3801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.473972	1.667650	-2.806322	29783.214760
HLA B*1501	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.415690	1.608922	-2.806768	26042.954258
HLA A*2902	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.143157	1.336347	-2.806810	13904.553144
HLA B*4001	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.394684	1.587869	-2.806815	24813.241518
HLA A*0211	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.479916	0.673013	-2.806903	3019.369169
HLA A*2501	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.485674	1.678625	-2.807050	30596.683770
HLA B*3801	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.528715	1.721649	-2.807065	33784.272675
HLA A*2301	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.483071	1.675762	-2.807309	30413.831010
HLA A*3002	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.266949	1.459325	-2.807624	18490.516885
HLA A*3201	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.532774	1.725080	-2.807694	34101.578624
HLA A*2603	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.501848	1.694140	-2.807709	31757.639368
HLA B*3801	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.492925	1.685162	-2.807763	31111.780679
HLA B*3901	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.423874	1.616065	-2.807809	26538.324759
HLA A*3001	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-3.980695	1.172675	-2.808020	9565.217449
HLA B*5101	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.502285	1.694140	-2.808146	31789.611238
HLA A*0301	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.336353	1.528166	-2.808187	21694.659518
HLA A*2301	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.483247	1.675016	-2.808231	30426.173673
HLA A*0301	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.361417	1.553110	-2.808307	22983.551835
HLA A*2602	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.564518	1.756081	-2.808437	36687.521711
HLA A*0219	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.103911	1.295300	-2.808612	12703.144517
HLA B*1517	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.421204	1.612498	-2.808706	26375.730062
HLA B*1501	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-3.813867	1.005151	-2.808717	6514.293405
HLA A*0203	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.900197	1.091476	-2.808721	7946.882510
HLA A*2301	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.504599	1.695841	-2.808758	31959.461980
HLA B*0702	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.424910	1.616065	-2.808845	26601.714448

HLA B*1503	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.044295	1.235408	-2.808887	11073.767638
HLA A*6801	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.631855	1.822872	-2.808982	42840.508369
HLA B*3801	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.530270	1.720897	-2.809372	33905.482784
HLA A*0203	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.435109	1.625692	-2.809417	27233.831224
HLA B*0803	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.481826	1.672339	-2.809487	30326.752117
HLA A*2402	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.531189	1.721649	-2.809539	33977.277827
HLA B*4402	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.425610	1.616065	-2.809545	26644.634909
HLA B*4403	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.481995	1.672339	-2.809656	30338.567052
HLA B*2705	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.403041	1.593295	-2.809746	25295.345805
HLA A*2301	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.521347	1.711364	-2.809983	33215.943162
HLA B*3501	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-3.975150	1.165167	-2.809983	9443.871363
HLA B*1502	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.447472	1.637421	-2.810051	28020.232320
HLA A*3001	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.111209	1.301147	-2.810062	12918.400344
HLA B*4402	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.414859	1.604651	-2.810208	25993.127104
HLA A*0212	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.132551	1.322138	-2.810414	13569.113059
HLA A*3001	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-3.854518	1.044058	-2.810461	7153.492149
HLA A*0216	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.495707	1.685162	-2.810545	31311.700832
HLA B*5101	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.506416	1.695841	-2.810574	32093.391315
HLA B*4501	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.595144	1.784483	-2.810660	39368.050816
HLA B*3501	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.313864	1.503120	-2.810743	20599.826764
HLA A*3002	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.559862	1.749103	-2.810758	36296.244880
HLA B*0803	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.474719	1.663852	-2.810867	29834.496255
HLA A*0212	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.420032	1.608922	-2.811110	26304.623884
HLA B*1502	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.539604	1.728396	-2.811209	34642.117997
HLA B*0702	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.420211	1.608922	-2.811289	26315.441295
HLA B*7301	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.598088	1.786784	-2.811304	39635.817248
HLA B*4001	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.087197	1.275786	-2.811411	12223.540127
HLA B*1517	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.364573	1.553110	-2.811463	23151.146487
HLA A*8001	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.448912	1.637421	-2.811491	28113.309001
HLA A*0250	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.091619	1.280105	-2.811514	12348.628726
HLA A*3201	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.600747	1.788992	-2.811755	39879.291532
HLA B*1501	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.950701	1.138932	-2.811769	8926.913404
HLA A*2403	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.221907	1.410054	-2.811853	16668.905123
HLA A*0206	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.536961	1.725080	-2.811881	34431.922015
HLA A*3002	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.437665	1.625692	-2.811973	27394.601127
HLA B*0801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.400160	1.587869	-2.812291	25128.128962
HLA A*0211	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.525841	1.713482	-2.812360	33561.483812
HLA B*1502	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.187003	1.374504	-2.812499	15381.657099
HLA B*5701	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.365905	1.553110	-2.812795	23222.269505
HLA B*5101	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.450444	1.637421	-2.813023	28212.646697
HLA A*0206	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.885884	1.072837	-2.813046	7689.245544
HLA A*3101	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.272374	1.459325	-2.813049	18722.938575
HLA A*3002	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.316222	1.503120	-2.813102	20712.019728
HLA A*3001	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.239493	1.426359	-2.813134	17357.731649
HLA A*0212	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.241662	1.428368	-2.813294	17444.621245
HLA B*3901	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.477179	1.663852	-2.813327	30003.962924
HLA B*1801	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.481159	1.667650	-2.813509	30280.193612
HLA A*0203	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.418296	1.604651	-2.813645	26199.670352
HLA A*8001	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.439366	1.625692	-2.813674	27502.109603
HLA B*1503	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.954437	1.140721	-2.813716	9004.031445
HLA B*1517	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.103159	1.289353	-2.813806	12681.172308
HLA A*3301	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.440945	1.627062	-2.813883	27602.273984
HLA B*5401	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.162803	1.348830	-2.813974	14548.004608
HLA A*1101	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.443572	1.629570	-2.814002	27769.725489
HLA B*1509	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.443602	1.629570	-2.814032	27771.678563
HLA B*7301	1:494-502	9	ERISTRITN	1.065751	-0.517476	-3.362921	0.548275	-2.814647	2306.329006
HLA A*3101	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.427313	1.612498	-2.814815	26749.344898
HLA A*2301	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.098334	1.283502	-2.814831	12541.040243
HLA B*1501	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.168597	1.353717	-2.814880	14743.386811
HLA A*6802	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.274225	1.459325	-2.814900	18802.924693
HLA B*1509	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.452948	1.638021	-2.814927	28375.817435
HLA B*0801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.423895	1.608922	-2.814973	26539.616915
HLA B*5301	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.536745	1.721649	-2.815096	34414.789174
HLA A*0250	1:394-402	9	EEIVARQPF	0.860370	0.918985	-4.594923	1.779355	-2.815568	39348.036087
HLA A*0250	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.590931	1.775111	-2.815820	38988.029500

HLA A*3002	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.501120	1.685162	-2.815958	31704.424357
HLA A*0203	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-3.871820	1.055834	-2.815985	7444.228793
HLA A*0206	1:422-430	9	TLRHADSIV	1.051790	0.095468	-3.963318	1.147258	-2.816060	9190.053853
HLA B*1502	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.565470	1.749103	-2.816367	36767.992382
HLA B*1502	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.480341	1.663852	-2.816489	30223.240493
HLA B*5801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.358353	1.541660	-2.816693	22821.985029
HLA B*5301	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.153175	1.336347	-2.816828	14229.028210
HLA B*0801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-3.592551	0.775634	-2.816916	3913.366538
HLA B*4002	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.608270	1.791215	-2.817055	40576.117109
HLA B*7301	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.608287	1.791215	-2.817072	40577.653724
HLA A*0101	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.370324	1.553110	-2.817214	23459.785788
HLA A*6802	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.045512	1.228069	-2.817443	11104.843429
HLA A*0202	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.542628	1.725080	-2.817548	34884.156311
HLA B*4501	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.539210	1.721649	-2.817561	34610.647417
HLA B*1503	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.440311	1.622722	-2.817589	27561.985600
HLA B*3801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.444847	1.627062	-2.817785	27851.420931
HLA A*0250	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.491036	1.673173	-2.817863	30976.752276
HLA B*1517	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.140023	1.322138	-2.817885	13804.568094
HLA A*2501	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.227978	1.410054	-2.817924	16903.558614
HLA A*1101	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.228119	1.410054	-2.818065	16909.046287
HLA A*2403	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.154444	1.336347	-2.818097	14270.656817
HLA A*0212	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.434293	1.616065	-2.818229	27182.754973
HLA A*0216	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.411832	1.593295	-2.818538	25812.638174
HLA B*1502	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.537060	1.718496	-2.818564	34439.746365
HLA A*2602	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.491875	1.673173	-2.818702	31036.636429
HLA A*3101	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.167540	1.348830	-2.818710	14707.538425
HLA A*2301	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.503949	1.685162	-2.818787	31911.605337
HLA B*1503	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-3.760407	0.941565	-2.818842	5759.796421
HLA B*1509	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.172610	1.353717	-2.818893	14880.248375
HLA A*2301	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.456921	1.638021	-2.818900	28636.593879
HLA B*0803	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.441657	1.622722	-2.818935	27647.556636
HLA A*0219	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.406880	1.587869	-2.819011	25519.941786
HLA A*2602	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.457450	1.638021	-2.819429	28671.472282
HLA B*5301	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.594545	1.775111	-2.819433	39313.779177
HLA A*0211	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.513683	1.694140	-2.819543	32634.921217
HLA A*2601	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.108981	1.289353	-2.819628	12852.316961
HLA B*3801	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.452319	1.632644	-2.819674	28334.706558
HLA B*0803	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.457861	1.638021	-2.819840	28698.629295
HLA A*6901	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.107675	1.287816	-2.819859	12813.716580
HLA A*0202	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.054971	1.235042	-2.819929	11349.362464
HLA A*2301	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.540868	1.720897	-2.819971	34743.091458
HLA B*5801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.096064	1.275786	-2.820278	12475.672311
HLA B*1517	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.053040	1.232655	-2.820385	11299.004708
HLA A*0206	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.541515	1.720897	-2.820617	34794.817900
HLA B*1509	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.495636	1.675016	-2.820620	31306.619459
HLA B*1517	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.342908	1.521566	-2.821342	22024.593510
HLA B*1503	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.324486	1.503120	-2.821365	21109.871508
HLA A*3101	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.195471	1.373907	-2.821563	15684.499670
HLA B*4002	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-3.571955	0.750232	-2.821723	3732.114348
HLA A*0206	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.448980	1.627062	-2.821918	28117.719953
HLA B*1517	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.426714	1.604651	-2.822063	26712.469037
HLA B*1502	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.457838	1.635727	-2.822111	28697.076773
HLA A*6802	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.105885	1.283502	-2.822383	12761.002868
HLA B*3801	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.460427	1.638021	-2.822406	28868.671062
HLA B*3501	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.117975	1.295300	-2.822676	13121.251386
HLA B*1503	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.435348	1.612498	-2.822850	27248.863236
HLA B*3501	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.697732	0.874608	-2.823125	4985.770363
HLA A*0203	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.432247	1.608922	-2.823325	27054.970763
HLA B*1503	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.279025	1.455494	-2.823531	19011.894888
HLA B*1502	1:69-77	9	SVYADGAPK	0.472549	0.433678	-3.729803	0.906227	-2.823575	5367.879301
HLA B*5101	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.499391	1.675762	-2.823629	31578.438519
HLA A*3101	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-3.618616	0.794851	-2.823765	4155.427540
HLA B*1517	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.446560	1.622722	-2.823838	27961.478501
HLA A*3001	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.198140	1.373907	-2.824232	15781.187665
HLA A*6802	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.433241	1.608922	-2.824319	27116.953795

HLA B*1503	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-3.950753	1.126421	-2.824332	8927.975926
HLA B*4002	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.546498	1.721649	-2.824849	35196.366036
HLA B*4403	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.597338	1.772257	-2.825082	39567.474541
HLA B*5101	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.497589	1.672339	-2.825250	31447.678894
HLA B*4501	1:74-82	9	GAPKLDPAL	1.528258	0.294614	-4.648275	1.822872	-2.825403	44491.307251
HLA B*5101	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.500420	1.675016	-2.825404	31653.353343
HLA A*2501	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.461179	1.635727	-2.825452	28918.690765
HLA A*2402	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.458322	1.632644	-2.825677	28729.075689
HLA A*3001	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.198558	1.372792	-2.825766	15796.391641
HLA B*0801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.367561	1.541660	-2.825901	23311.007702
HLA B*5801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.354127	1.528166	-2.825961	22600.949902
HLA A*6801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.174978	1.348830	-2.826149	14961.614523
HLA B*1501	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.499210	0.673013	-2.826197	3156.531931
HLA A*0201	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-3.125313	0.299099	-2.826214	1334.483301
HLA A*3201	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.601426	1.775111	-2.826315	39941.689894
HLA B*1501	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-3.054067	0.227657	-2.826410	1132.576016
HLA A*0211	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.267583	1.440990	-2.826594	18517.545164
HLA B*5401	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.540159	1.713482	-2.826677	34686.375007
HLA B*5301	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-3.920736	1.094025	-2.826711	8331.745396
HLA B*1501	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.059652	1.232655	-2.826997	11472.330250
HLA A*0219	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.348706	1.521566	-2.827140	22320.629092
HLA A*3301	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.466672	1.639403	-2.827268	29286.786633
HLA B*1517	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.103174	1.275786	-2.827387	12681.583937
HLA B*1502	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.128600	1.301147	-2.827453	13446.201875
HLA A*0206	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.512740	1.685162	-2.827579	32564.200880
HLA B*3901	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.454772	1.627062	-2.827710	28495.191612
HLA A*0202	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.500081	1.672339	-2.827743	31628.704223
HLA B*5401	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.553509	1.725080	-2.828428	35769.155680
HLA B*5801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.915797	1.087303	-2.828495	8237.536893
HLA A*0216	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.269578	1.440990	-2.828588	18602.791792
HLA B*2705	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.441119	1.612498	-2.828621	27613.326264
HLA A*3201	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.581679	1.753043	-2.828636	38166.208110
HLA A*0250	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.524551	1.695841	-2.828710	33461.953104
HLA A*0219	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.445555	1.616065	-2.829490	27896.810479
HLA B*0802	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.382758	1.553110	-2.829648	24141.125672
HLA B*5701	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.417842	1.587869	-2.829973	26172.329327
HLA B*5101	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.508735	1.678625	-2.830110	32265.214243
HLA A*6801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-3.858526	1.028301	-2.830225	7219.819271
HLA B*4801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.371922	1.541660	-2.830262	23546.246815
HLA A*0206	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.524575	1.694140	-2.830435	33463.763408
HLA A*1101	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.439491	1.608922	-2.830569	27509.996251
HLA A*0211	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.542125	1.711364	-2.830762	34843.793724
HLA A*0202	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.903754	1.072837	-2.830917	8012.239314
HLA A*2602	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.551819	1.720897	-2.830922	35630.294267
HLA A*3002	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.308721	1.477798	-2.830923	20357.317283
HLA B*4001	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.372627	1.541660	-2.830966	23584.492618
HLA B*4501	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-3.649535	0.818458	-2.831077	4462.055177
HLA B*0702	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.120461	1.289353	-2.831108	13196.568342
HLA A*2602	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.615624	1.784483	-2.831141	41269.040658
HLA A*2902	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.257525	1.426359	-2.831166	18093.611759
HLA B*3901	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.132368	1.301147	-2.831222	13563.388489
HLA B*5101	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.469442	1.638021	-2.831421	29474.182346
HLA A*3001	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.272529	1.440990	-2.831539	18729.624844
HLA B*2705	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.454452	1.622722	-2.831730	28474.234130
HLA B*1502	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.444246	1.612498	-2.831748	27812.875315
HLA B*1801	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.507955	1.675762	-2.832192	32207.315245
HLA B*1801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.444829	1.612498	-2.832330	27850.215572
HLA A*0206	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.455223	1.622722	-2.832501	28524.804907
HLA A*2501	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.437207	1.604651	-2.832556	27365.717023
HLA A*2403	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.437327	1.604651	-2.832676	27373.268384
HLA B*0702	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.292112	1.459325	-2.832787	19593.500666
HLA A*3002	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.048346	1.215498	-2.832848	11177.531915
HLA A*0211	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-3.695040	0.862117	-2.832923	4954.955539
HLA B*0803	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.445425	1.612498	-2.832927	27888.511188
HLA B*1502	1:164-172	9	AAFEAFDRR	0.923160	0.798489	-4.554662	1.721649	-2.833013	35864.293999

HLA A*2501	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.328618	1.495512	-2.833107	21311.711772
HLA A*1101	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.386265	1.553110	-2.833156	24336.902262
HLA A*2402	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.426500	1.593295	-2.833205	26699.321727
HLA A*3201	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.246017	1.412655	-2.833363	17620.470055
HLA B*1503	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-3.959517	1.125828	-2.833689	9109.962507
HLA A*0201	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.123139	1.289436	-2.833703	13278.206674
HLA A*0206	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.545208	1.711364	-2.833844	35091.986884
HLA B*1501	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.260206	1.426359	-2.833847	18205.643310
HLA B*0801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.096980	1.263068	-2.833912	12502.021980
HLA B*0801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.123482	1.289436	-2.834046	13288.698527
HLA B*1509	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.355816	1.521566	-2.834250	22689.032246
HLA B*5101	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.461334	1.627062	-2.834272	28929.018105
HLA B*5101	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.446894	1.612498	-2.834396	27982.966880
HLA A*0250	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.559718	1.725080	-2.834638	36284.268978
HLA A*8001	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.388053	1.553110	-2.834944	24437.302007
HLA A*0101	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.245042	1.410054	-2.834988	17580.954642
HLA A*0212	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.051034	1.215498	-2.835536	11246.923196
HLA B*1801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.363823	1.528166	-2.835657	23111.227744
HLA A*0212	1:276-284	9	VAATGANLV	0.993882	0.146839	-3.976569	1.140721	-2.835848	9474.780373
HLA B*1517	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.105608	1.269596	-2.836012	12752.859265
HLA A*3001	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.105612	1.269596	-2.836017	12752.997249
HLA B*4601	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.364453	1.528166	-2.836287	23144.759866
HLA A*0101	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.378007	1.541660	-2.836347	23878.489905
HLA A*3201	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.530505	1.694140	-2.836365	33923.830237
HLA B*4501	1:367-375	9	LKFTLVEPL	1.359064	0.428202	-4.623671	1.787266	-2.836405	42040.837542
HLA A*0202	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.125893	1.289436	-2.836457	13362.663145
HLA B*0803	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.469127	1.632644	-2.836483	29452.823513
HLA B*1517	1:421-429	9	DTLRHADSI	0.987060	0.113427	-3.937051	1.100487	-2.836564	8650.691290
HLA A*8001	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.441309	1.604651	-2.836658	27625.429103
HLA B*1503	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.445705	1.608922	-2.836783	27906.470945
HLA A*6802	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.863357	1.026553	-2.836804	7300.571647
HLA A*2602	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.586357	1.749103	-2.837254	38579.521668
HLA B*1502	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.454330	1.617007	-2.837323	28466.225049
HLA A*6802	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.425227	1.587869	-2.837358	26621.149709
HLA B*0801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-3.881626	1.044058	-2.837569	7614.238268
HLA A*2402	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.505382	1.667650	-2.837732	32017.088621
HLA B*3801	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.454219	1.616065	-2.838155	28458.988010
HLA A*3301	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.627200	1.788992	-2.838208	42383.838486
HLA B*3901	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.476291	1.638021	-2.838270	29942.669369
HLA A*2402	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.534123	1.695841	-2.838282	34207.638037
HLA A*2602	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.563398	1.725080	-2.838317	36592.970981
HLA B*5401	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.559241	1.720897	-2.838344	36244.443194
HLA B*3501	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.426491	1.587869	-2.838622	26698.743972
HLA A*0202	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.131884	1.293038	-2.838846	13548.281365
HLA B*1517	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.447770	1.608922	-2.838848	28039.490401
HLA B*5701	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.360616	1.521566	-2.839050	22941.191502
HLA B*5101	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.464841	1.625692	-2.839150	29163.622929
HLA A*3001	1:208-216	9	PANIANALI	0.995189	0.008861	-3.843217	1.004050	-2.839167	6969.748098
HLA B*3801	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.517921	1.678625	-2.839296	32954.979025
HLA A*0212	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.128745	1.289436	-2.839309	13450.712664
HLA B*5701	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.127223	1.287816	-2.839406	13403.642290
HLA A*0202	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.560440	1.720897	-2.839542	36344.581268
HLA A*2601	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.335082	1.495512	-2.839570	21631.257499
HLA A*3002	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.469407	1.629570	-2.839837	29471.790663
HLA B*0803	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.465659	1.625692	-2.839967	29218.579289
HLA A*3101	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-3.978923	1.138932	-2.839991	9526.279855
HLA A*3001	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.295528	1.455494	-2.840034	19748.230480
HLA A*3101	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.362211	1.521566	-2.840645	23025.616684
HLA A*0211	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.508417	1.667650	-2.840767	32241.658430
HLA A*6801	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.596901	1.756081	-2.840820	39527.680215
HLA B*5801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.343989	1.503120	-2.840868	22079.471045
HLA A*3301	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.594014	1.753043	-2.840971	39265.742149
HLA A*3002	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-3.595633	0.754547	-2.841086	3941.241539
HLA A*3002	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.552644	1.711364	-2.841280	35698.015880
HLA B*4002	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.646010	1.804702	-2.841308	44259.883138

HLA B*5101	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.464273	1.622722	-2.841551	29125.467095
HLA B*7301	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.626044	1.784483	-2.841561	42271.176888
HLA A*0250	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.562488	1.720897	-2.841591	36516.439088
HLA A*2301	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.477536	1.635727	-2.841809	30028.645424
HLA B*5101	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.505685	1.663852	-2.841833	32039.440368
HLA B*1501	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.734718	0.892605	-2.842113	5428.975285
HLA B*0802	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.363689	1.521566	-2.842123	23104.102179
HLA A*2603	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.459179	1.617007	-2.842173	28785.860441
HLA A*0211	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-3.973233	1.131046	-2.842187	9402.273564
HLA B*1502	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.567291	1.725080	-2.842210	36922.471837
HLA A*0301	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.364044	1.521566	-2.842478	23122.983476
HLA B*1501	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.905478	1.062990	-2.842488	8044.118035
HLA B*0801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-3.943019	1.100487	-2.842531	8770.381922
HLA B*4601	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.384242	1.541660	-2.842582	24223.806651
HLA A*1101	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.436025	1.593295	-2.842730	27291.351365
HLA A*2403	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.451745	1.608922	-2.842824	28297.329053
HLA A*2602	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.506676	1.663852	-2.842825	32112.669110
HLA B*3501	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-3.071120	0.228245	-2.842875	1177.931193
HLA B*5301	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.478666	1.635727	-2.842939	30106.886418
HLA A*2603	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.561577	1.718496	-2.843081	36439.870120
HLA A*3201	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.592329	1.749103	-2.843226	39113.729644
HLA A*6901	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.869813	1.026553	-2.843260	7409.915445
HLA B*1501	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.147165	1.303793	-2.843373	14033.476049
HLA B*1801	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.459506	1.616065	-2.843441	28807.514818
HLA B*3501	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.930815	1.087303	-2.843512	8527.373407
HLA A*0211	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.507478	1.663852	-2.843626	32171.964345
HLA B*1501	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.272109	1.428368	-2.843741	18711.496413
HLA A*0201	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.270116	1.426359	-2.843757	18625.852414
HLA B*5101	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.173461	1.329702	-2.843759	14909.418107
HLA B*1517	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.008940	1.165167	-2.843774	10207.992825
HLA B*5401	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.555435	1.711364	-2.844072	35928.184030
HLA B*3901	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.432057	1.587869	-2.844188	27043.117845
HLA A*0250	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.479963	1.635727	-2.844236	30196.927749
HLA A*3101	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.077198	1.232655	-2.844542	11945.314663
HLA A*0206	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.128586	1.284024	-2.844562	13445.765428
HLA A*8001	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.453519	1.608922	-2.844597	28413.144902
HLA A*6901	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.372807	1.528166	-2.844641	23594.319055
HLA A*0203	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.852023	1.007289	-2.844734	7112.511012
HLA A*0211	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.226178	1.381432	-2.844747	16833.655627
HLA A*0212	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.449485	1.604651	-2.844835	28150.443436
HLA A*1101	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.386554	1.541660	-2.844894	24353.101825
HLA A*0250	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.271324	1.426359	-2.844965	18677.717082
HLA A*6801	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.474944	1.629570	-2.845375	29849.994806
HLA B*5101	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.513391	1.667650	-2.845741	32613.036196
HLA B*3901	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.129821	1.284024	-2.845797	13484.081210
HLA A*3301	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.637143	1.791215	-2.845928	43365.394993
HLA B*1801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.509895	1.663852	-2.846044	32351.557876
HLA B*3901	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.218919	1.372792	-2.846127	16554.593830
HLA A*2301	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.519516	1.673173	-2.846344	33076.255642
HLA B*5801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.256461	1.410054	-2.846407	18049.324400
HLA B*1517	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-3.192212	0.345470	-2.846743	1556.726719
HLA A*0202	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.514683	1.667650	-2.847034	32710.218805
HLA A*0202	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.228472	1.381432	-2.847040	16922.773266
HLA B*4402	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.434944	1.587869	-2.847075	27223.519936
HLA A*0201	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.388772	1.541660	-2.847112	24477.789657
HLA A*0211	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.532399	1.685162	-2.847237	34072.073674
HLA A*2902	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.435358	1.587869	-2.847489	27249.452895
HLA B*5801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.229393	1.381752	-2.847641	16958.699075
HLA A*0211	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.526675	1.678625	-2.848050	33626.000932
HLA A*0203	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.134215	1.286148	-2.848067	13621.185156
HLA A*6802	1:497-505	9	STRITNEVA	1.301822	-0.192924	-3.957101	1.108898	-2.848203	9059.439290
HLA A*0216	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.380510	0.532233	-2.848276	2401.648834
HLA A*6802	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.351458	1.503120	-2.848337	22462.478667
HLA A*3001	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.086290	1.237896	-2.848394	12198.041353
HLA A*0211	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.441995	1.593295	-2.848700	27669.103139

HLA A*3301	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.635654	1.786784	-2.848870	43216.912122
HLA A*6901	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.352247	1.503120	-2.849127	22503.346358
HLA B*1501	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.135296	1.286148	-2.849147	13655.124354
HLA B*4001	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.370827	1.521566	-2.849261	23486.961291
HLA B*3501	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-2.886469	0.037065	-2.849404	769.961832
HLA A*0206	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.563017	1.713482	-2.849535	36560.914875
HLA A*0212	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.138994	1.289353	-2.849641	13771.896460
HLA B*0702	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.391328	1.541660	-2.849668	24622.289776
HLA A*2402	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.345274	1.495512	-2.849762	22144.905592
HLA A*3301	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.378042	1.528166	-2.849876	23880.427683
HLA B*4501	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.654647	1.804702	-2.849945	45148.878799
HLA B*0803	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.371680	1.521566	-2.850113	23533.130063
HLA B*3901	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.459243	1.608922	-2.850321	28790.065413
HLA A*0202	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.528971	1.678625	-2.850346	33804.200390
HLA A*3301	1:317-325	9	FEGAVRDVL	1.443258	0.312823	-4.606696	1.756081	-2.850615	40429.310092
HLA A*2301	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.523151	1.672339	-2.850812	33354.235682
HLA A*2902	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.459762	1.608922	-2.850840	28824.506983
HLA A*2402	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.536024	1.685162	-2.850862	34357.679292
HLA A*0101	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.372589	1.521566	-2.851023	23582.451274
HLA B*3901	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.310363	1.459325	-2.851037	20434.444470
HLA B*5101	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.404147	1.553110	-2.851038	25359.881994
HLA A*3101	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.207627	1.356576	-2.851051	16129.722837
HLA B*1501	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.372619	1.521566	-2.851053	23584.109852
HLA A*2601	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.392954	1.541660	-2.851294	24714.639600
HLA A*0216	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.173696	1.322138	-2.851558	14917.486119
HLA A*2402	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.572622	1.720897	-2.851724	37378.489692
HLA B*1502	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.481333	1.629570	-2.851763	30292.318163
HLA B*5801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.233537	1.381432	-2.852105	17121.311368
HLA A*3301	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.636709	1.784483	-2.852225	43322.015338
HLA A*2601	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.330190	1.477798	-2.852393	21388.983203
HLA B*1501	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.380572	1.528166	-2.852406	24019.971945
HLA B*5101	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.469442	1.617007	-2.852435	29474.182346
HLA A*0206	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.516305	1.663852	-2.852453	32832.548455
HLA A*6901	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.145666	1.293038	-2.852628	13985.122870
HLA B*7301	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.405750	1.553110	-2.852640	25453.621225
HLA B*5301	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.234571	1.381752	-2.852819	17162.114646
HLA A*1101	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.485517	1.632644	-2.852873	30585.595627
HLA A*2603	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.446172	1.593295	-2.852878	27936.530335
HLA A*0216	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.468979	1.616065	-2.852914	29442.787023
HLA B*0702	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.440874	1.587869	-2.853005	27597.794590
HLA B*3801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.462238	1.608922	-2.853316	28989.334467
HLA A*2402	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.489044	1.635727	-2.853317	30834.969231
HLA B*1501	1:35-43	9	REARVFSEV	0.807139	0.210046	-3.870584	1.017185	-2.853399	7423.075594
HLA B*3901	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.142936	1.289353	-2.853583	13897.484065
HLA A*0202	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.258177	0.404390	-2.853787	1812.076468
HLA B*1801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.470819	1.617007	-2.853812	29567.769519
HLA A*0203	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.085914	1.231855	-2.854059	12187.487513
HLA A*0219	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.134469	1.280105	-2.854364	13629.145904
HLA B*0801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.228251	1.372792	-2.855459	16914.169723
HLA A*0219	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.464433	1.608922	-2.855511	29136.183523
HLA A*2402	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.471688	1.616065	-2.855623	29627.013384
HLA A*3101	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.237531	1.381752	-2.855779	17279.499138
HLA A*6901	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.947262	1.091476	-2.855786	8856.490800
HLA B*4002	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.528968	1.673173	-2.855796	33804.017513
HLA A*6801	1:436-444	9	AAGLDNQIW	1.388926	0.402289	-4.647241	1.791215	-2.856026	44385.528258
HLA A*2301	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.493500	1.637421	-2.856080	31153.044284
HLA B*5801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.149454	1.293038	-2.856415	14107.616851
HLA A*1101	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.483623	1.627062	-2.856561	30452.521430
HLA B*4002	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.632106	1.775111	-2.856995	42865.314124
HLA B*3501	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.398685	1.541660	-2.857025	25042.903251
HLA B*0803	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.193427	1.336347	-2.857079	15610.852398
HLA B*7301	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.610202	1.753043	-2.857159	40756.958011
HLA A*2402	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.568574	1.711364	-2.857210	37031.694647
HLA A*2301	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.450564	1.593295	-2.857269	28220.431763
HLA B*7301	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-3.799178	0.941565	-2.857613	6297.647312

HLA B*7301	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.606743	1.749103	-2.857640	40433.684691
HLA B*0702	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.462344	1.604651	-2.857693	28996.392635
HLA A*0202	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.039986	1.182210	-2.857777	10964.439889
HLA A*2403	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.317113	1.459325	-2.857787	20754.530142
HLA A*0202	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.017305	1.159455	-2.857850	10406.496026
HLA B*0702	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.353434	1.495512	-2.857922	22564.909422
HLA B*3801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.470457	1.612498	-2.857959	29543.146191
HLA A*2501	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.284406	1.426359	-2.858047	19248.891529
HLA A*0219	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.286466	1.428368	-2.858099	19340.434361
HLA B*4403	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.231359	1.372792	-2.858567	17035.663492
HLA A*0201	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.147997	1.289353	-2.858644	14060.377320
HLA A*6801	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.498352	1.639403	-2.858949	31503.019279
HLA A*3101	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.314756	1.455494	-2.859262	20642.218579
HLA A*0206	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-3.950875	1.091476	-2.859399	8930.487846
HLA B*1503	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.098658	1.239243	-2.859415	12550.406437
HLA A*2301	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.485204	1.625692	-2.859513	30563.596739
HLA A*0202	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.236852	1.377330	-2.859522	17252.504476
HLA B*4403	1:447-455	9	PVVLLADVR	1.278528	0.526174	-4.664242	1.804702	-2.859540	46157.498741
HLA B*4501	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.612814	1.753043	-2.859771	41002.882560
HLA A*0101	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.388042	1.528166	-2.859875	24436.641000
HLA B*5401	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.554044	1.694140	-2.859905	35813.302535
HLA A*3101	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.355431	1.495512	-2.859919	22668.910969
HLA A*2501	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.155238	1.295300	-2.859938	14296.775192
HLA A*0101	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.209069	1.348830	-2.860240	16183.389567
HLA A*0206	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.539073	1.678625	-2.860449	34599.789214
HLA A*3301	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.121659	1.260962	-2.860697	13233.028522
HLA A*2601	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.388897	1.528166	-2.860731	24484.809036
HLA B*3801	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.524753	1.663852	-2.860902	33477.524916
HLA B*5701	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.364363	1.503120	-2.861243	23140.002353
HLA B*1509	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.356934	1.495512	-2.861423	22747.534229
HLA B*5401	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.557444	1.695841	-2.861603	36094.753168
HLA A*2501	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.449610	1.587869	-2.861741	28158.516005
HLA B*1501	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.328473	0.466612	-2.861861	2130.458662
HLA B*5301	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.138021	1.275786	-2.862235	13741.086140
HLA A*3201	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.489405	1.627062	-2.862343	30860.669255
HLA A*2603	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.478440	1.616065	-2.862375	30091.254485
HLA A*6801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.022191	1.159455	-2.862737	10524.257160
HLA A*0250	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.556979	1.694140	-2.862839	36056.110682
HLA A*3301	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.492427	1.629570	-2.862857	31076.119141
HLA B*4002	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.616068	1.753043	-2.863026	41311.258555
HLA A*2402	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.490138	1.627062	-2.863076	30912.802513
HLA B*1502	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.536271	1.673173	-2.863098	34377.201316
HLA A*2602	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.548279	1.685162	-2.863117	35340.991963
HLA A*0201	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.244744	1.381432	-2.863312	17568.879691
HLA A*0216	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.199949	1.336347	-2.863601	15847.063122
HLA A*0250	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.653369	0.789472	-2.863897	4501.624812
HLA B*0801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.259184	1.394918	-2.864266	18162.850310
HLA B*4801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.392473	1.528166	-2.864307	24687.245584
HLA B*4801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.385918	1.521566	-2.864351	24317.424390
HLA B*3501	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.473384	1.608922	-2.864462	29742.961014
HLA B*1801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.469228	1.604651	-2.864577	29459.675780
HLA A*0201	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.392900	1.528166	-2.864734	24711.564612
HLA A*2601	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.386486	1.521566	-2.864920	24349.281444
HLA B*5301	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.497574	1.632644	-2.864930	31446.658140
HLA A*2301	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.532652	1.667650	-2.865002	34091.986714
HLA B*1509	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.246518	1.381432	-2.865086	17640.785938
HLA B*1501	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.406917	1.541660	-2.865257	25522.150843
HLA A*0101	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.343110	1.477798	-2.865312	22034.842847
HLA B*4501	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.640428	1.775111	-2.865317	43694.611929
HLA A*0250	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.578822	1.713482	-2.865340	37915.958591
HLA B*0802	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.453237	1.587869	-2.865368	28394.705452
HLA B*3501	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.278257	1.412655	-2.865602	18978.291936
HLA B*5401	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.544449	1.678625	-2.865824	35030.720894
HLA A*2902	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.394094	1.528166	-2.865928	24779.570925
HLA B*5101	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.953281	1.087303	-2.865978	8980.097592

HLA B*1503	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.292472	1.426359	-2.866113	19609.725175
HLA B*4501	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.276175	1.410054	-2.866121	18887.543572
HLA B*0801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.188507	1.322138	-2.866369	15435.005759
HLA B*3901	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.159571	1.293038	-2.866532	14440.111231
HLA A*0212	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-3.997085	1.130410	-2.866675	9933.101077
HLA A*3001	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.180091	1.313175	-2.866915	15138.782190
HLA A*0250	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.578347	1.711364	-2.866984	37874.546754
HLA A*2603	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.620100	1.753043	-2.867057	41696.551887
HLA B*4501	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.616228	1.749103	-2.867125	41326.458625
HLA B*3901	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.007939	1.140721	-2.867218	10184.494442
HLA B*3501	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.206875	1.339557	-2.867318	16101.823789
HLA A*3201	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.552480	1.685162	-2.867318	35684.499878
HLA A*0206	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.535728	1.667650	-2.868078	34334.267497
HLA B*1502	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.553358	1.685162	-2.868197	35756.773365
HLA B*1517	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-3.644498	0.775707	-2.868791	4410.599669
HLA A*2403	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.364321	1.495512	-2.868810	23137.749136
HLA B*1501	1:480-488	9	AMTADWTRV	0.947260	0.174566	-3.991972	1.121826	-2.870146	9816.854980
HLA B*4403	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.623293	1.753043	-2.870250	42004.236244
HLA B*4501	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.542713	1.672339	-2.870374	34890.950872
HLA A*3002	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.171548	1.301147	-2.870402	14843.906602
HLA A*1101	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.493477	1.622722	-2.870755	31151.358984
HLA A*0201	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.299135	1.428368	-2.870767	19912.906139
HLA A*0101	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.252570	1.381752	-2.870818	17888.346697
HLA A*3101	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.348676	1.477798	-2.870878	22319.059369
HLA A*0202	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.582306	1.711364	-2.870943	38221.376757
HLA B*4402	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.330308	1.459325	-2.870982	21394.769587
HLA A*0301	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.366508	1.495512	-2.870997	23254.578846
HLA B*3801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-3.943864	1.072837	-2.871027	8787.479412
HLA B*4001	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.348932	1.477798	-2.871134	22332.224307
HLA A*8001	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.392830	1.521566	-2.871263	24707.554333
HLA B*4501	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.507043	1.635727	-2.871316	32139.781802
HLA A*3301	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.599956	1.728396	-2.871560	39806.652530
HLA B*5301	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.596772	1.725080	-2.871692	39515.920744
HLA B*0801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-3.959145	1.087303	-2.871843	9102.178980
HLA A*2603	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.647091	1.775111	-2.871980	44370.163188
HLA A*6801	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.284659	1.412655	-2.872005	19260.141327
HLA A*2603	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.593137	1.720897	-2.872240	39186.588142
HLA A*0216	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.481333	1.608922	-2.872411	30292.318163
HLA A*2501	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.350570	1.477798	-2.872772	22416.591223
HLA B*3901	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.477463	1.604651	-2.872812	30023.609845
HLA B*1502	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.506042	1.632644	-2.873398	32065.797335
HLA B*7301	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.558856	1.685162	-2.873695	36212.300595
HLA A*0206	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.499515	1.625692	-2.873823	31587.494117
HLA A*6802	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-3.771774	0.897730	-2.874044	5912.537960
HLA A*0202	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-2.925565	0.051389	-2.874176	842.489754
HLA A*3201	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.595095	1.720897	-2.874197	39363.578557
HLA A*0250	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.549263	1.675016	-2.874247	35421.191790
HLA A*0203	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.302657	1.428368	-2.874289	20075.044872
HLA B*7301	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.248950	1.374504	-2.874446	17739.837897
HLA B*1501	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.214149	1.339557	-2.874592	16373.784687
HLA B*4601	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.284744	1.410054	-2.874690	19263.892721
HLA A*0101	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.377835	1.503120	-2.874715	23869.061628
HLA B*5701	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.416433	1.541660	-2.874773	26087.513415
HLA A*3301	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.507445	1.632644	-2.874800	32169.527783
HLA A*0206	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.550682	1.675762	-2.874920	35537.122425
HLA A*6801	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.624176	1.749103	-2.875073	42089.764789
HLA B*1517	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.016050	1.140721	-2.875328	10376.476282
HLA B*1517	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-3.888177	1.012736	-2.875441	7729.952532
HLA A*3301	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.750083	0.874608	-2.875476	5624.494501
HLA B*4001	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.334974	1.459325	-2.875648	21625.875124
HLA A*0219	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.480322	1.604651	-2.875672	30221.932487
HLA A*0203	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.110800	1.235042	-2.875758	12906.245707
HLA A*1101	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.249960	1.373907	-2.876053	17781.153273
HLA A*8001	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.464127	1.587869	-2.876258	29115.699669
HLA B*5101	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.156662	1.280105	-2.876557	14343.722551

HLA B*1503	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-3.162003	0.285427	-2.876576	1452.120650
HLA B*5101	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.481311	1.604651	-2.876661	30290.843296
HLA B*4402	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.249640	1.372792	-2.876849	17768.075691
HLA A*0301	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-3.956486	1.079304	-2.877182	9046.607619
HLA B*5401	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.549663	1.672339	-2.877324	35453.782977
HLA A*0101	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.372850	1.495512	-2.877338	23596.616734
HLA A*0250	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.810512	0.933159	-2.877353	6464.162281
HLA A*3002	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.163546	1.286148	-2.877398	14572.896055
HLA B*1501	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.112867	1.235408	-2.877459	12967.834991
HLA B*2705	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.258895	1.381432	-2.877463	18150.768472
HLA B*5101	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.494133	1.616065	-2.878068	31198.413072
HLA A*3002	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.500986	1.622722	-2.878264	31694.649371
HLA B*7301	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.551460	1.673173	-2.878287	35600.814810
HLA A*0201	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.791232	0.912830	-2.878403	6183.471691
HLA A*0203	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.420309	1.541660	-2.878649	26321.421246
HLA B*5801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.356526	1.477798	-2.878728	22726.131579
HLA A*6802	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-3.610289	0.731526	-2.878763	4076.515884
HLA B*4601	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.382133	1.503120	-2.879012	24106.410839
HLA B*0803	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.432332	1.553110	-2.879222	27060.240394
HLA B*3901	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.167126	1.287816	-2.879310	14693.541447
HLA A*3301	1:325-333	9	LDGKTAEFL	1.514727	0.234376	-4.628554	1.749103	-2.879450	42516.116591
HLA B*0801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.357350	1.477798	-2.879553	22769.326571
HLA B*4501	1:369-377	9	FTLVEPLRL	1.354455	0.417802	-4.651825	1.772257	-2.879569	44856.484944
HLA A*2301	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.320564	1.440990	-2.879575	20920.126166
HLA B*5301	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.600496	1.720897	-2.879599	39856.213760
HLA A*2301	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.543495	1.663852	-2.879644	34953.863330
HLA B*1502	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.573820	1.694140	-2.879680	37481.760969
HLA A*6901	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.308053	1.428368	-2.879686	20326.064142
HLA B*7301	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.593182	1.713482	-2.879700	39190.616256
HLA B*3801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.502523	1.622722	-2.879801	31806.985790
HLA A*0250	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.169180	1.289353	-2.879827	14763.180588
HLA B*7301	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.604946	1.725080	-2.879865	40266.693042
HLA A*2403	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.421559	1.541660	-2.879899	26397.285021
HLA B*5701	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.202195	1.322138	-2.880057	15929.234124
HLA B*5401	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.772855	0.892605	-2.880249	5927.269924
HLA A*2601	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.039784	1.159455	-2.880330	10959.339864
HLA B*4801	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.375909	1.495512	-2.880397	23763.410380
HLA B*1509	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.307074	1.426359	-2.880715	20280.261774
HLA A*0219	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.307123	1.426359	-2.880764	20282.565898
HLA B*1509	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.485458	1.604651	-2.880808	30581.459289
HLA A*6801	1:10-18	9	PETPARPVL	1.635476	0.153516	-4.669940	1.788992	-2.880947	46767.027555
HLA A*2301	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.497173	1.616065	-2.881108	31417.580570
HLA B*4601	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.262894	1.381752	-2.881142	18318.665839
HLA B*5401	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-3.017984	0.136752	-2.881232	1042.278957
HLA B*4001	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.254083	1.372792	-2.881292	17950.777826
HLA A*3002	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.518816	1.637421	-2.881395	33022.974816
HLA B*3501	1:277-285	9	AATGANLVT	1.269350	-0.216786	-3.934109	1.052564	-2.881546	8592.296573
HLA A*3101	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-3.573985	0.692424	-2.881561	3749.599621
HLA A*0211	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.557334	1.675762	-2.881572	36085.576710
HLA A*0202	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.519117	1.637421	-2.881696	33045.850017
HLA B*4403	1:314-322	9	IRAFEGAVR	1.069912	0.705199	-4.656893	1.775111	-2.881782	45382.987075
HLA B*5301	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.566962	1.685162	-2.881800	36894.517917
HLA B*2705	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.194977	1.313175	-2.881802	15666.690993
HLA B*1517	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.359636	1.477798	-2.881839	22889.496255
HLA B*1517	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.008123	1.125828	-2.882295	10188.792914
HLA A*2402	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.554662	1.672339	-2.882323	35864.293999
HLA B*4001	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.377908	1.495512	-2.882397	23873.064962
HLA A*0212	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.797693	0.915104	-2.882589	6276.152109
HLA A*6801	1:224-232	9	GDGHAICGL	1.646336	0.138147	-4.667106	1.784483	-2.882623	46462.897407
HLA A*6901	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.555908	0.673013	-2.882895	3596.731008
HLA B*5401	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.550588	1.667650	-2.882938	35529.433181
HLA B*1501	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-3.692371	0.809432	-2.882938	4924.597575
HLA A*2301	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.510219	1.627062	-2.883158	32375.719426
HLA A*3201	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.184362	1.301147	-2.883216	15288.409413
HLA B*1801	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.378740	1.495512	-2.883228	23918.828093

HLA A*8001	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.425011	1.541660	-2.883350	26607.903398
HLA A*0216	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.488289	1.604651	-2.883639	30781.468479
HLA B*7301	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.602145	1.718496	-2.883649	40007.865168
HLA B*4002	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.602448	1.718496	-2.883952	40035.795430
HLA B*4801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-3.975874	1.091915	-2.883959	9459.620291
HLA A*0201	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.387125	1.503120	-2.884005	24385.137539
HLA B*4501	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.379595	1.495512	-2.884084	23965.975447
HLA B*3901	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.425972	1.541660	-2.884311	26666.842415
HLA A*0206	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.500464	1.616065	-2.884400	31656.607092
HLA A*0202	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.548800	1.663852	-2.884949	35383.461829
HLA A*3001	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-3.030638	0.145582	-2.885056	1073.095308
HLA A*6801	1:431-439	9	REELTAAGL	1.365493	0.421291	-4.672129	1.786784	-2.885346	47003.423142
HLA B*5401	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.515243	1.629570	-2.885673	32752.362091
HLA B*0702	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.198906	1.313175	-2.885730	15809.044301
HLA A*2601	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.388906	1.503120	-2.885786	24485.338882
HLA B*1502	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.381345	1.495512	-2.885834	24062.762045
HLA A*6802	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.427496	1.541660	-2.885836	26760.634737
HLA A*0206	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-3.521277	0.635184	-2.886093	3321.058686
HLA B*4402	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.427924	1.541660	-2.886264	26786.996229
HLA A*3201	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.597778	1.711364	-2.886414	39607.523202
HLA B*4601	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.312987	1.426359	-2.886628	20558.300519
HLA A*3201	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.096872	1.210159	-2.886713	12498.911178
HLA A*2902	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.428511	1.541660	-2.886851	26823.249409
HLA A*0211	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.264231	1.377330	-2.886900	18375.141727
HLA B*5401	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.562669	1.675762	-2.886907	36531.653598
HLA B*0801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.313288	1.426359	-2.886929	20572.541369
HLA B*1801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.474874	1.587869	-2.887005	29845.150644
HLA A*6901	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.268570	1.381432	-2.887139	18559.667705
HLA A*3201	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.565909	1.678625	-2.887284	36805.207516
HLA A*0201	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.382920	1.495512	-2.887408	24150.138810
HLA A*0212	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.429376	1.541660	-2.887716	26876.703377
HLA A*3002	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.500603	1.612498	-2.888105	31666.712970
HLA B*4402	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.409929	1.521566	-2.888363	25699.774396
HLA A*2602	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.599812	1.711364	-2.888449	39793.518373
HLA A*2603	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.383979	1.495512	-2.888468	24209.133708
HLA A*0301	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.343965	1.455494	-2.888471	22078.276602
HLA B*5701	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.416799	1.528166	-2.888633	26109.539075
HLA A*6801	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.607622	1.718496	-2.889126	40515.576924
HLA A*3201	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.514822	1.625692	-2.889130	32720.661033
HLA A*0301	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.367246	1.477798	-2.889449	23294.115090
HLA B*1502	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.601290	1.711364	-2.889926	39929.159213
HLA A*2602	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.608510	1.718496	-2.890014	40598.513542
HLA A*2501	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.411872	1.521566	-2.890306	25815.012223
HLA A*2501	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.418491	1.528166	-2.890325	26211.437191
HLA A*2603	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.526114	1.635727	-2.890387	33582.551835
HLA B*1517	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.271848	1.381432	-2.890416	18700.263576
HLA A*0211	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.016365	1.125828	-2.890537	10384.001178
HLA B*5301	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.601950	1.711364	-2.890587	39989.904837
HLA B*0803	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.478490	1.587869	-2.890621	30094.673277
HLA B*5801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.208313	1.317518	-2.890795	16155.222896
HLA B*5701	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.350257	1.459325	-2.890932	22400.467945
HLA A*0219	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.265467	1.374504	-2.890963	18427.504528
HLA A*0219	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.272726	1.381752	-2.890975	18738.138094
HLA A*1101	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.503660	1.612498	-2.891161	31890.377896
HLA B*3501	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.264038	1.372792	-2.891246	18366.992122
HLA A*3001	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.860580	0.969193	-2.891386	7254.037163
HLA A*0250	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.555320	1.663852	-2.891469	35918.661285
HLA B*5401	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.531191	1.639403	-2.891787	33977.461641
HLA B*5401	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.566807	1.675016	-2.891791	36881.346982
HLA A*8001	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.394947	1.503120	-2.891826	24828.280605
HLA B*5301	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.129182	1.236980	-2.892202	13464.254113
HLA B*4801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.395393	1.503120	-2.892273	24853.814192
HLA B*1517	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.434077	1.541660	-2.892417	27169.229216
HLA B*4001	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.395661	1.503120	-2.892541	24869.146947
HLA A*2601	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.488257	0.595350	-2.892907	3077.916883

HLA A*2501	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.210554	1.317518	-2.893036	16238.816083
HLA A*2902	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.414645	1.521566	-2.893078	25980.333839
HLA B*0801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.352642	1.459325	-2.893316	22523.808077
HLA B*1502	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.108981	1.215498	-2.893483	12852.316961
HLA A*3301	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.502450	1.608922	-2.893528	31801.651997
HLA A*2902	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.352889	1.459325	-2.893563	22536.606099
HLA A*0211	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.519279	1.625692	-2.893587	33058.187752
HLA B*5401	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.529384	1.635727	-2.893657	33836.402065
HLA A*0219	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.389181	1.495512	-2.893669	24500.841955
HLA A*0201	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.215813	1.322138	-2.893675	16436.619840
HLA A*6901	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.900982	1.007289	-2.893692	7961.254736
HLA A*2301	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.173870	1.280105	-2.893765	14923.459259
HLA B*0702	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.268408	1.374504	-2.893904	18552.741001
HLA B*4002	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.205254	1.311116	-2.894138	16041.830564
HLA B*4001	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.422358	1.528166	-2.894192	26445.883874
HLA A*2402	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.569964	1.675762	-2.894202	37150.484485
HLA A*0250	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.579539	1.685162	-2.894377	37978.572179
HLA A*2501	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.503841	1.608922	-2.894919	31903.664965
HLA A*0203	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.423171	1.528166	-2.895005	26495.432210
HLA B*5701	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.251656	1.356576	-2.895080	17850.741204
HLA B*3901	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.373176	1.477798	-2.895379	23614.367464
HLA B*5301	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.570437	1.675016	-2.895421	37190.903437
HLA B*5801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.217739	1.322138	-2.895602	16509.696447
HLA A*6901	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.336682	1.440990	-2.895692	21711.096941
HLA A*0206	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-3.194881	0.299099	-2.895783	1566.323250
HLA A*2602	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.417396	1.521566	-2.895830	26145.441162
HLA A*0201	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.111434	1.215498	-2.895936	12925.111249
HLA B*7301	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.617039	1.720897	-2.896141	41403.662838
HLA A*2602	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.374149	1.477798	-2.896351	23667.315695
HLA A*0301	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.355795	1.459325	-2.896469	22687.927567
HLA B*1501	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.399834	1.503120	-2.896713	25109.240350
HLA B*4002	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-3.530355	0.633434	-2.896921	3391.212155
HLA A*3301	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.233845	1.336347	-2.897498	17133.449464
HLA B*5401	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.561659	1.663852	-2.897807	36446.770521
HLA A*3001	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-3.699114	0.801202	-2.897912	5001.655424
HLA B*5801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.338907	1.440990	-2.897917	21822.611884
HLA B*0803	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.181595	1.283502	-2.898092	15191.288479
HLA B*2705	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.220347	1.322138	-2.898209	16609.135058
HLA A*8001	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.426481	1.528166	-2.898315	26698.166229
HLA B*3501	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.247307	1.348830	-2.898478	17672.881157
HLA B*0802	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.426672	1.528166	-2.898506	26709.867957
HLA A*0206	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.179903	1.281231	-2.898672	15132.231676
HLA B*5101	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.209821	1.311116	-2.898705	16211.429941
HLA B*5801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.354214	1.455494	-2.898719	22605.474295
HLA B*0803	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.440480	1.541660	-2.898820	27572.723415
HLA B*5401	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-3.508138	0.609194	-2.898945	3222.094176
HLA A*2902	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.309059	1.410054	-2.899005	20373.182301
HLA B*1501	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-3.718131	0.819048	-2.899083	5225.531866
HLA A*0212	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.427370	1.528166	-2.899203	26752.818187
HLA A*6802	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.427562	1.528166	-2.899396	26764.688662
HLA A*0250	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.420984	1.521566	-2.899417	26362.320633
HLA A*2603	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.574527	1.675016	-2.899511	37542.845113
HLA B*1509	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.327913	1.428368	-2.899546	21277.151625
HLA B*2705	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.421353	1.521566	-2.899786	26384.721050
HLA B*1509	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.441455	1.541660	-2.899795	27634.696589
HLA B*4601	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.359213	1.459325	-2.899888	22867.217769
HLA A*0202	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.585072	1.685162	-2.899910	38465.525539
HLA B*1501	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.189926	1.289436	-2.900490	15485.523257
HLA A*0219	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.249462	1.348830	-2.900632	17760.771820
HLA B*4402	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.396248	1.495512	-2.900737	24902.804534
HLA B*5401	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.526461	1.625692	-2.900770	33609.450928
HLA B*5101	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.509869	1.608922	-2.900947	32349.632732
HLA B*5301	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.595153	1.694140	-2.901014	39368.902732
HLA B*4002	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.429291	1.528166	-2.901125	26871.469487
HLA B*4403	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.619698	1.718496	-2.901202	41657.996616

HLA A*0201	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.831066	0.929716	-2.901350	6777.437879
HLA B*3901	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.282829	1.381432	-2.901398	19179.144037
HLA B*5301	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.574020	1.672339	-2.901681	37499.000567
HLA B*1502	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.539924	1.638021	-2.901903	34667.615138
HLA A*3201	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.177718	1.275786	-2.901932	15056.289639
HLA A*0212	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.831676	0.929716	-2.901961	6786.977535
HLA A*2902	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.219656	1.317518	-2.902138	16582.739103
HLA B*4801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-3.979717	1.077535	-2.902182	9543.714999
HLA B*0801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.405458	1.503120	-2.902338	25436.551994
HLA A*0203	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.715922	0.813260	-2.902662	5199.025943
HLA A*0203	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.405989	1.503120	-2.902869	25467.670631
HLA B*3901	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.398412	1.495512	-2.902901	25027.192579
HLA A*6801	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.398504	1.495512	-2.902992	25032.473515
HLA B*4001	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.284892	1.381752	-2.903140	19270.459418
HLA B*1501	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.327843	1.424271	-2.903572	21273.698694
HLA B*5401	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.456757	1.553110	-2.903647	28625.751476
HLA B*0801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.042980	1.139224	-2.903755	11040.270006
HLA A*0250	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.576125	1.672339	-2.903786	37681.209247
HLA B*5301	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.599676	1.695841	-2.903835	39781.034177
HLA A*2601	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.330209	1.426359	-2.903850	21389.908920
HLA B*4002	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.576266	1.672339	-2.903927	37693.442302
HLA A*0250	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.582908	1.678625	-2.904283	38274.347423
HLA A*0211	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.520353	1.616065	-2.904288	33140.019264
HLA A*0202	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.580159	1.675762	-2.904397	38032.852336
HLA A*3201	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.568299	1.663852	-2.904447	37008.262592
HLA B*0801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.030889	1.126421	-2.904468	10737.155555
HLA B*0801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.314679	1.410054	-2.904625	20638.533728
HLA B*5401	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.045404	1.140721	-2.904683	11102.080278
HLA B*0801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.258526	1.353717	-2.904809	18135.358615
HLA B*5301	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.184983	1.280105	-2.904878	15310.260084
HLA A*2402	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.568769	1.663852	-2.904917	37048.326382
HLA B*3501	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-3.834698	0.929716	-2.904982	6834.359966
HLA A*0250	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.572636	1.667650	-2.904986	37379.702992
HLA B*0802	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.446788	1.541660	-2.905128	27976.155396
HLA B*5101	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.254001	1.348830	-2.905171	17947.379237
HLA B*3801	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.530897	1.625692	-2.905206	33954.492621
HLA B*0801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.209074	1.303793	-2.905282	16183.564668
HLA A*2501	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-3.961321	1.055834	-2.905487	9147.891271
HLA B*1801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.447319	1.541660	-2.905659	28010.380939
HLA B*3801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.458827	1.553110	-2.905717	28762.510670
HLA A*2603	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.591178	1.685162	-2.906016	39010.182487
HLA B*4501	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.617471	1.711364	-2.906107	41444.897375
HLA B*1517	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.434308	1.528166	-2.906141	27183.637322
HLA A*3001	1:228-236	9	AICGLSGGV	0.815527	0.247463	-3.969258	1.062990	-2.906267	9316.602244
HLA B*0702	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.316892	1.410054	-2.906838	20743.978532
HLA B*3801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.435015	1.528166	-2.906849	27227.938581
HLA B*5401	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.544931	1.638021	-2.906910	35069.592470
HLA B*0801	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.319688	1.412655	-2.907033	20877.954245
HLA B*7301	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.428775	1.521566	-2.907208	26839.506744
HLA B*7301	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.601699	1.694140	-2.907559	39966.763054
HLA B*5301	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.547285	1.639403	-2.907881	35260.210698
HLA A*0202	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.209116	1.301147	-2.907970	16185.140668
HLA A*3101	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.289431	1.381432	-2.908000	19472.928696
HLA A*3101	1:33-41	9	RVREARVFS	1.063374	-0.731690	-3.239705	0.331684	-2.908021	1736.620285
HLA B*7301	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.619452	1.711364	-2.908088	41634.339996
HLA B*0702	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.334537	1.426359	-2.908178	21604.125262
HLA A*3002	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.203482	1.295300	-2.908183	15976.528308
HLA B*5401	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.545607	1.637421	-2.908186	35124.275169
HLA A*0212	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.411400	1.503120	-2.908280	25786.956552
HLA A*6801	1:75-83	9	APKLDPALL	1.420023	0.333020	-4.661397	1.753043	-2.908354	45856.092016
HLA A*3201	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.282470	1.373907	-2.908562	19163.275777
HLA A*8001	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.404088	1.495512	-2.908577	25356.452372
HLA A*0212	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.257666	1.348830	-2.908836	18099.485779
HLA B*4403	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.582198	1.673173	-2.909026	38211.866364
HLA B*1503	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.283038	1.373907	-2.909131	19188.380637

HLA A*1101	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.437303	1.528166	-2.909137	27371.787561
HLA B*1502	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.581538	1.672339	-2.909199	38153.821623
HLA B*4501	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.634300	1.725080	-2.909220	43082.453670
HLA B*1503	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.018390	1.108898	-2.909492	10432.538228
HLA B*5401	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.525977	1.616065	-2.909913	33572.016171
HLA B*1502	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.497809	1.587869	-2.909941	31463.675036
HLA A*0219	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.211123	1.301147	-2.909976	16260.089753
HLA B*3501	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.284692	1.374504	-2.910188	19261.600116
HLA A*3001	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.263937	1.353717	-2.910220	18362.719993
HLA B*3801	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.514895	1.604651	-2.910244	32726.148962
HLA A*0250	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-3.685651	0.775312	-2.910339	4848.989233
HLA A*0101	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.365942	1.455494	-2.910448	23224.279671
HLA B*4501	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.040875	1.130410	-2.910464	10986.884431
HLA B*1509	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.519570	1.608922	-2.910648	33080.371492
HLA B*1801	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.519772	1.608922	-2.910851	33095.765731
HLA B*4402	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.414203	1.503120	-2.911083	25953.923735
HLA A*8001	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.339572	1.428368	-2.911204	21856.047861
HLA A*0101	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.323879	1.412655	-2.911225	21080.427928
HLA A*2402	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.228885	1.317518	-2.911367	16938.893797
HLA B*3801	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.499499	1.587869	-2.911630	31586.297946
HLA B*1503	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.076911	1.165167	-2.911744	11937.433279
HLA B*5301	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.549707	1.637421	-2.912286	35457.427384
HLA A*2402	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.415408	1.503120	-2.912288	26026.053005
HLA B*3901	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.440618	1.528166	-2.912452	27581.525577
HLA B*3501	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-3.123758	0.210953	-2.912804	1329.712602
HLA B*0702	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.234973	1.322138	-2.912835	17177.998510
HLA B*4403	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.638057	1.725080	-2.912977	43456.751256
HLA B*1503	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.454645	1.541660	-2.912985	28486.868413
HLA B*1517	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.500873	1.587869	-2.913004	31686.420142
HLA B*5101	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.501092	1.587869	-2.913223	31702.366215
HLA A*0216	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.197247	1.284024	-2.913223	15748.778688
HLA B*5301	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.589421	1.675762	-2.913658	38852.642961
HLA B*5401	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.546470	1.632644	-2.913825	35194.081209
HLA A*6802	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.034742	1.120820	-2.913922	10832.841788
HLA A*2403	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.442204	1.528166	-2.914038	27682.428470
HLA B*4801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.296040	1.381752	-2.914289	19771.534410
HLA B*4002	1:465-473	9	TYGHPIVLR	0.988791	0.736289	-4.639580	1.725080	-2.914499	43609.360937
HLA A*3002	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.590337	1.675762	-2.914575	38934.703010
HLA A*2403	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.296639	1.381752	-2.914888	19798.828493
HLA A*6801	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.588142	1.673173	-2.914970	38738.468511
HLA B*7301	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.287834	1.372792	-2.915042	19401.424757
HLA A*0203	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.356086	1.440990	-2.915096	22703.152330
HLA A*0216	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-3.777300	0.862117	-2.915183	5988.250105
HLA B*0702	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.443421	1.528166	-2.915255	27760.112361
HLA A*2301	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.519927	1.604651	-2.915277	33107.584773
HLA B*4001	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.325604	1.410054	-2.915550	21164.301742
HLA B*1503	1:69-77	9	SVYADGAPK	0.472549	0.433678	-3.822161	0.906227	-2.915934	6639.891724
HLA B*4601	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.289908	1.373907	-2.916001	19494.325760
HLA A*0219	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.288905	1.372792	-2.916113	19449.345398
HLA B*3901	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.245815	1.329702	-2.916114	17612.274029
HLA A*0219	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.457974	1.541660	-2.916314	28706.082570
HLA B*2705	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.298153	1.381752	-2.916401	19867.927289
HLA A*0301	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.326567	1.410054	-2.916513	21211.297418
HLA B*1503	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.047542	1.130410	-2.917132	11156.870565
HLA B*0801	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.445308	1.528166	-2.917142	27880.968521
HLA B*4002	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.630661	1.713482	-2.917179	42722.934702
HLA B*1801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-3.731809	0.813920	-2.917889	5392.736523
HLA B*1509	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.505852	1.587869	-2.917983	32051.749149
HLA A*3002	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.083226	1.165167	-2.918060	12112.293137
HLA A*2501	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.199305	1.281231	-2.918074	15823.590269
HLA A*0206	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.413700	1.495512	-2.918189	25923.893841
HLA B*4801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.292706	1.374504	-2.918203	19620.336689
HLA A*3301	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.146606	1.228391	-2.918215	14015.418823
HLA B*7301	1:48-56	9	ASIEEIRAR	0.914030	0.758309	-4.590602	1.672339	-2.918263	38958.511751
HLA A*0219	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.831357	0.912830	-2.918527	6781.985887

HLA A*6801	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.545697	1.627062	-2.918635	35131.496611
HLA B*4601	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.300204	1.381432	-2.918772	19961.982124
HLA A*3301	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.591946	1.673173	-2.918774	39079.253894
HLA B*5301	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.597442	1.678625	-2.918817	39576.894111
HLA B*7301	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.597486	1.678625	-2.918862	39580.962346
HLA A*3301	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.414476	1.495512	-2.918964	25970.216157
HLA A*6801	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.532070	1.612498	-2.919571	34046.277784
HLA A*1101	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.441325	1.521566	-2.919759	27626.475277
HLA B*1502	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.441793	1.521566	-2.920227	27656.233070
HLA B*4801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.301785	1.381432	-2.920353	20034.793281
HLA B*4402	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.333216	1.412655	-2.920561	21538.540744
HLA B*3501	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.061287	1.140721	-2.920565	11515.608244
HLA A*0212	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.416264	1.495512	-2.920752	26077.353994
HLA A*0219	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.423890	1.503120	-2.920770	26539.329764
HLA A*0250	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.596779	1.675762	-2.921017	39516.562080
HLA A*3101	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.042928	1.121826	-2.921102	11038.956098
HLA A*2301	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.158147	1.236980	-2.921166	14392.848389
HLA B*4001	1:490-498	9	YEVLERIST	1.211490	-0.403834	-3.728882	0.807656	-2.921226	5356.507827
HLA B*1502	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.597026	1.675762	-2.921264	39539.015379
HLA A*2603	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.597371	1.675762	-2.921609	39570.471434
HLA A*0301	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.362665	1.440990	-2.921675	23049.670483
HLA A*2601	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.345960	1.424271	-2.921689	22179.915270
HLA A*0206	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.530763	1.608922	-2.921841	33944.023902
HLA B*4501	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.208219	1.286148	-2.922071	16151.727356
HLA B*5701	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.332464	1.410054	-2.922410	21501.286243
HLA B*1502	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.590104	1.667650	-2.922454	38913.855983
HLA B*0702	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-3.024628	0.101982	-2.922646	1058.347561
HLA B*4801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.349089	1.426359	-2.922731	22340.320369
HLA A*2602	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.601401	1.678625	-2.922776	39939.313084
HLA A*3001	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.206504	1.283502	-2.923002	16088.066434
HLA A*6801	1:306-314	9	RKIIGRQFI	1.295789	0.432607	-4.651555	1.728396	-2.923159	44828.586733
HLA A*3101	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.296221	1.372792	-2.923430	19779.772185
HLA B*5701	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.351801	1.428368	-2.923433	22480.227526
HLA A*0216	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.590159	0.666703	-2.923456	3891.873820
HLA B*4001	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.350069	1.426359	-2.923710	22390.775319
HLA B*4402	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.401614	1.477798	-2.923817	25212.417115
HLA A*0212	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.350257	1.426359	-2.923898	22400.467945
HLA A*2601	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.383291	1.459325	-2.923965	24170.790267
HLA B*4002	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.635376	1.711364	-2.924013	43189.332678
HLA A*2301	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.075910	1.151838	-2.924072	11909.953795
HLA B*5301	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.591866	1.667650	-2.924216	39072.066464
HLA B*5301	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.825807	0.901531	-2.924276	6695.875934
HLA B*2705	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.419896	1.495512	-2.924384	26296.371483
HLA B*0702	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.050352	1.125828	-2.924524	11229.292094
HLA A*2402	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.529241	1.604651	-2.924590	33825.237785
HLA B*0702	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.071958	1.147258	-2.924700	11802.071540
HLA B*4801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.402820	1.477798	-2.925022	25282.485643
HLA A*3001	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.153246	1.228069	-2.925177	14231.337721
HLA A*2601	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.366372	1.440990	-2.925383	23247.283318
HLA A*0206	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.453625	1.528166	-2.925459	28420.062782
HLA B*3501	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-3.389564	0.463883	-2.925682	2452.248180
HLA A*0250	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.056179	1.130410	-2.925769	11380.965362
HLA B*7301	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.593596	1.667650	-2.925946	39227.948999
HLA A*2301	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.534882	1.608922	-2.925960	34267.464520
HLA A*6901	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.209478	1.283502	-2.925976	16198.630499
HLA A*0101	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.065422	1.139224	-2.926198	11625.776660
HLA B*5401	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.227541	1.301147	-2.926394	16886.558143
HLA A*2602	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.562197	1.635727	-2.926470	36491.951116
HLA A*2902	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.308253	1.381752	-2.926501	20335.413041
HLA B*5801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.350786	1.424271	-2.926515	22427.750957
HLA B*3901	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.221912	1.295300	-2.926612	16669.085478
HLA A*0219	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.454809	1.528166	-2.926643	28497.658211
HLA A*0201	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.219684	1.293038	-2.926646	16583.815667
HLA A*2301	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.514629	1.587869	-2.926761	32706.149010
HLA A*2602	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.602596	1.675762	-2.926834	40049.442876

HLA A*0216	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.190090	1.263086	-2.927004	15491.388615
HLA A*0216	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.468824	1.541660	-2.927164	29432.276274
HLA A*0301	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.322096	1.394918	-2.927178	20994.046925
HLA B*0802	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.430302	1.503120	-2.927181	26934.052069
HLA B*1501	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.162465	1.235042	-2.927423	14536.675776
HLA B*4501	1:198-206	9	DFAGLGAQW	1.397213	0.316269	-4.641109	1.713482	-2.927628	43763.216802
HLA B*7301	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.623530	1.695841	-2.927689	42027.193580
HLA B*1517	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.305375	1.377330	-2.928044	20201.093503
HLA B*5401	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.533000	1.604651	-2.928349	34119.293857
HLA B*0801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.198201	1.269596	-2.928605	15783.407558
HLA B*4002	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.649643	1.720897	-2.928745	44631.611362
HLA A*2501	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.306580	1.377330	-2.929250	20257.234923
HLA B*1502	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.283146	1.353717	-2.929429	19193.156354
HLA A*2403	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.432592	1.503120	-2.929472	27076.494886
HLA B*0702	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.233370	1.303793	-2.929578	17114.736298
HLA A*0101	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.389254	1.459325	-2.929928	24504.951252
HLA A*0201	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-3.712130	0.781791	-2.930339	5153.827942
HLA B*1501	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-3.967369	1.036964	-2.930405	9276.167209
HLA A*0250	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.218284	1.287816	-2.930468	16530.430682
HLA A*0216	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.433605	1.503120	-2.930485	27139.701786
HLA B*4001	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.279361	1.348830	-2.930532	19026.608450
HLA A*0250	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.179701	1.249052	-2.930649	15125.193036
HLA B*0801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.279500	1.348830	-2.930670	19032.682398
HLA B*2705	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.343641	1.412655	-2.930986	22061.799892
HLA A*0201	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.833236	0.902116	-2.931121	6811.401328
HLA B*2705	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.434533	1.503120	-2.931413	27197.758793
HLA A*2301	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.357799	1.426359	-2.931440	22792.866021
HLA A*0202	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.486875	0.555251	-2.931625	3068.141540
HLA B*1517	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.019053	1.087303	-2.931750	10448.466138
HLA A*6901	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.387306	1.455494	-2.931812	24395.297564
HLA A*0202	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.557771	1.625692	-2.932079	36121.905713
HLA B*4501	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.626345	1.694140	-2.932205	42300.458370
HLA B*2705	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.356779	1.424271	-2.932508	22739.413611
HLA B*7301	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.608383	1.675762	-2.932621	40586.655068
HLA B*7301	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.607650	1.675016	-2.932634	40518.207227
HLA B*7301	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.568393	1.635727	-2.932666	37016.271882
HLA A*0206	1:2-10	9	VQPADIDVP	0.784967	0.117421	-3.835154	0.902388	-2.932765	6841.536519
HLA A*2501	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.222288	1.289353	-2.932935	16683.520189
HLA B*5301	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.571306	1.638021	-2.933285	37265.421498
HLA B*1502	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.608353	1.675016	-2.933337	40583.800767
HLA B*4501	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.654290	1.720897	-2.933392	45111.767994
HLA A*0250	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.848569	0.915104	-2.933465	7056.172817
HLA B*0802	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.282399	1.348830	-2.933569	19160.165894
HLA B*1801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.287383	1.353717	-2.933665	19381.282984
HLA B*4501	1:363-371	9	LPDDLKFTL	1.521641	0.196855	-4.652241	1.718496	-2.933745	44899.457860
HLA A*0250	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.527216	1.593295	-2.933921	33667.866948
HLA B*4402	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.389458	1.455494	-2.933964	24516.487475
HLA B*5401	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.561069	1.627062	-2.934007	36397.313687
HLA B*4001	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.273570	1.339557	-2.934013	18774.565736
HLA A*3101	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.223486	1.289353	-2.934133	16729.614304
HLA B*4403	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.628312	1.694140	-2.934172	42492.432420
HLA B*1517	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.362545	1.428368	-2.934177	23043.311856
HLA A*6901	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.223744	1.289436	-2.934308	16739.572857
HLA B*5401	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.835868	0.901531	-2.934337	6852.797410
HLA A*2902	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-3.985455	1.050933	-2.934522	9670.633042
HLA B*5301	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.598565	1.663852	-2.934713	39679.369510
HLA A*3201	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.557439	1.622722	-2.934718	36094.362633
HLA A*0201	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.125287	1.190433	-2.934854	13344.025199
HLA B*1502	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.613601	1.678625	-2.934977	41077.259989
HLA B*1502	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.560759	1.625692	-2.935067	36371.331448
HLA A*2403	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.359411	1.424271	-2.935140	22877.611696
HLA A*0219	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.082517	1.147258	-2.935259	12092.520392
HLA B*0802	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.330223	1.394918	-2.935305	21390.603233
HLA B*5301	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.558187	1.622722	-2.935465	36156.510823
HLA A*0216	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.463740	1.528166	-2.935573	29089.721668

HLA A*3002	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.540243	1.604651	-2.935593	34693.131045
HLA A*2501	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.477289	1.541660	-2.935629	30011.592845
HLA B*3501	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.222067	1.286148	-2.935918	16675.038282
HLA B*1502	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-3.737312	0.801202	-2.936110	5461.496957
HLA A*1101	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.414212	1.477798	-2.936415	25954.485372
HLA A*0301	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.362864	1.426359	-2.936506	23060.272095
HLA B*5101	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.464926	1.528166	-2.936760	29169.303273
HLA A*0201	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.024104	1.087303	-2.936801	10570.704496
HLA A*8001	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.346937	1.410054	-2.936883	22229.887688
HLA B*4403	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.648355	1.711364	-2.936991	44499.491567
HLA A*0301	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.349851	1.412655	-2.937196	22379.512912
HLA B*5401	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.363748	1.426359	-2.937389	23107.227156
HLA A*3201	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.613162	1.675762	-2.937400	41035.725222
HLA A*2902	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.415462	1.477798	-2.937665	26029.291562
HLA A*3101	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.241544	1.303793	-2.937751	17439.903210
HLA A*0301	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.366610	1.428368	-2.938242	23259.989077
HLA B*3901	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.441528	1.503120	-2.938407	27639.331498
HLA B*4601	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.218613	1.280105	-2.938508	16542.955316
HLA B*4001	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.379647	1.440990	-2.938657	23968.827989
HLA B*0803	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.441887	1.503120	-2.938767	27662.218403
HLA A*3101	1:54-62	9	RARQPVALV	0.737262	0.289291	-3.965465	1.026553	-2.938912	9235.607880
HLA A*6802	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-3.951787	1.012736	-2.939051	8949.252958
HLA B*0801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.174166	1.235042	-2.939123	14933.635243
HLA A*2601	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.257060	1.317518	-2.939542	18074.241018
HLA B*4601	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.367923	1.428368	-2.939555	23330.436730
HLA A*3101	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.368132	1.428368	-2.939764	23341.672576
HLA A*0101	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.381033	1.440990	-2.940043	24045.454748
HLA A*2601	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.395952	1.455494	-2.940458	24885.835420
HLA B*5101	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.443677	1.503120	-2.940557	27776.486713
HLA A*1101	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.400130	1.459325	-2.940804	25126.361799
HLA A*2602	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.436537	1.495512	-2.941026	27323.556567
HLA B*5401	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.563858	1.622722	-2.941136	36631.792487
HLA A*0201	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.396669	1.455494	-2.941174	24926.931347
HLA B*4501	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.173188	1.231855	-2.941333	14900.064680
HLA A*3001	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.271331	1.329702	-2.941629	18678.020217
HLA B*4002	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.620441	1.678625	-2.941816	41729.272908
HLA B*4801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.314761	1.372792	-2.941970	20642.441924
HLA A*0203	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.132443	1.190433	-2.942010	13565.736738
HLA B*0801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.157564	1.215498	-2.942066	14373.551136
HLA A*0101	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.368470	1.426359	-2.942111	23359.863385
HLA A*0216	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-3.569450	0.627189	-2.942262	3710.653403
HLA A*0211	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.551244	1.608922	-2.942322	35583.100344
HLA B*1509	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-3.986070	1.043307	-2.942764	9684.349828
HLA A*2603	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.337727	1.394918	-2.942809	21763.427215
HLA A*2603	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.621465	1.678625	-2.942840	41827.816403
HLA B*1509	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.223040	1.280105	-2.942935	16712.427121
HLA A*2902	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.355590	1.412655	-2.942936	22677.251771
HLA B*7301	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.581449	1.638021	-2.943428	38145.978927
HLA A*2603	1:265-273	9	AGERAQVQR	1.125671	0.585693	-4.654833	1.711364	-2.943469	45168.178707
HLA A*6802	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.849053	0.905240	-2.943813	7064.040862
HLA B*1501	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.292692	1.348830	-2.943863	19619.699837
HLA A*6901	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.159415	1.215498	-2.943917	14434.956270
HLA B*5401	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.556713	1.612498	-2.944215	36034.075688
HLA A*2601	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.354780	1.410054	-2.944726	22634.966155
HLA B*7301	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.574389	1.629570	-2.944819	37530.863970
HLA B*5701	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.422760	1.477798	-2.944962	26470.360044
HLA A*0201	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.386108	1.440990	-2.945118	24328.082645
HLA A*2402	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.355215	1.410054	-2.945160	22657.631237
HLA A*0202	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.155445	1.210159	-2.945286	14303.583082
HLA B*2705	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.473577	1.528166	-2.945411	29756.158243
HLA B*0802	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.423225	1.477798	-2.945427	26498.729174
HLA A*0250	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.322780	1.377330	-2.945449	21027.123415
HLA A*6801	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.568172	1.622722	-2.945450	36997.452799
HLA A*2602	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.371818	1.426359	-2.945460	23540.642648
HLA A*0219	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.386512	1.440990	-2.945522	24350.730484

HLA A*2603	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.001474	1.055834	-2.945639	10033.990668
HLA A*2402	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.033023	1.087303	-2.945720	10790.028142
HLA A*6901	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.370185	1.424271	-2.945914	23452.299007
HLA B*1501	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.227330	1.281231	-2.946099	16878.338247
HLA A*3201	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.555205	1.608922	-2.946283	35909.141064
HLA B*1501	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.268530	1.322138	-2.946393	18557.960886
HLA A*0212	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.111589	1.165167	-2.946423	12929.727019
HLA A*0212	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.209535	1.263068	-2.946467	16200.733822
HLA A*2601	1:481-489	9	MTADWTRVP	0.898983	0.129318	-3.974812	1.028301	-2.946510	9436.517225
HLA A*8001	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.424355	1.477798	-2.946558	26567.772811
HLA A*2902	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.402082	1.455494	-2.946588	25239.574611
HLA A*1101	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.821263	0.874608	-2.946656	6626.184041
HLA A*6802	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.232959	1.286148	-2.946811	17098.540921
HLA A*0211	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.551566	1.604651	-2.946915	35609.482706
HLA B*4002	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.632440	1.685162	-2.947278	42898.256093
HLA A*0211	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.442904	1.495512	-2.947393	27727.092606
HLA B*4002	1:25-33	9	QYAQLIARR	0.855428	0.838712	-4.641748	1.694140	-2.947609	43827.661335
HLA B*4002	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-3.556937	0.609194	-2.947744	3605.263680
HLA B*7301	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.573446	1.625692	-2.947755	37449.534056
HLA B*5701	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.329880	1.381752	-2.948128	21373.714668
HLA A*2601	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.329605	1.381432	-2.948173	21360.190306
HLA B*4501	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.627033	1.678625	-2.948409	42367.561890
HLA B*4002	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.644302	1.695841	-2.948461	44086.151353
HLA B*0801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.372735	1.424271	-2.948464	23590.362464
HLA A*2902	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.244074	1.295300	-2.948775	17541.812541
HLA B*1501	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-3.961556	1.012736	-2.948820	9152.841518
HLA B*4402	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.323534	1.374504	-2.949030	21063.670304
HLA A*2902	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.444659	1.495512	-2.949148	27839.369691
HLA A*0206	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.160059	1.210159	-2.949900	14456.369211
HLA B*3501	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-3.585403	0.635184	-2.950220	3849.491755
HLA A*8001	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.409603	1.459325	-2.950277	25680.456083
HLA A*2603	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.579938	1.629570	-2.950368	38013.516423
HLA A*0216	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.185650	1.235042	-2.950607	15333.800977
HLA A*0206	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.555680	1.604651	-2.951029	35948.403937
HLA A*3101	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.377565	1.426359	-2.951206	23854.216414
HLA B*7301	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.588669	1.637421	-2.951248	38785.440830
HLA B*5401	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.568268	1.617007	-2.951262	37005.659946
HLA B*4001	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.252718	1.301147	-2.951572	17894.444496
HLA A*2402	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.539830	1.587869	-2.951961	34660.114031
HLA A*3001	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.959282	1.007289	-2.951992	9105.035451
HLA B*1502	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.288386	1.336347	-2.952038	19426.105938
HLA B*7301	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.615925	1.663852	-2.952073	41297.627955
HLA A*0250	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.577805	1.625692	-2.952113	37827.245086
HLA B*5101	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.288642	1.336347	-2.952295	19437.564462
HLA A*2601	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.334062	1.381752	-2.952310	21580.529221
HLA B*5101	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.494095	1.541660	-2.952435	31195.712710
HLA B*1501	1:69-77	9	SVYADGAPK	0.472549	0.433678	-3.858742	0.906227	-2.952515	7223.413540
HLA B*1509	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.411868	1.459325	-2.952542	25814.732912
HLA B*4801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.241936	1.289353	-2.952583	17455.666436
HLA A*3201	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.117815	1.165167	-2.952649	13116.425327
HLA A*0216	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.245985	1.293038	-2.952946	17619.135558
HLA A*0206	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.216188	1.263086	-2.953102	16450.853246
HLA B*4601	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.289476	1.336347	-2.953129	19474.930381
HLA A*2402	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.301992	1.348830	-2.953162	20044.333521
HLA B*5401	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.562122	1.608922	-2.953200	36485.634306
HLA B*4801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.330749	1.377330	-2.953419	21416.540403
HLA B*1501	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.394517	1.440990	-2.953527	24803.712529
HLA B*0801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.264957	1.311116	-2.953841	18405.884327
HLA A*2601	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.348777	1.394918	-2.953859	22324.251949
HLA B*4403	1:298-306	9	GVSAPEGKR	1.073317	0.647580	-4.674958	1.720897	-2.954061	47310.579492
HLA B*5301	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.570261	1.616065	-2.954196	37175.816599
HLA B*4801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.395276	1.440990	-2.954286	24847.092282
HLA A*3001	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.265405	1.311116	-2.954289	18424.912751
HLA A*3301	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.566981	1.612498	-2.954482	36896.114714
HLA B*1502	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.570622	1.616065	-2.954558	37206.801529

HLA B*5301	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.559350	1.604651	-2.954699	36253.463924
HLA B*4601	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.267992	1.313175	-2.954817	18534.984320
HLA A*0250	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.571010	1.616065	-2.954945	37240.028327
HLA A*3002	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.367876	1.412655	-2.955221	23327.912565
HLA B*0801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.410787	1.455494	-2.955292	25750.571551
HLA A*0250	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.239317	1.284024	-2.955293	17350.690323
HLA B*4001	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.244810	1.289353	-2.955457	17571.541172
HLA A*3002	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.543347	1.587869	-2.955478	34941.952278
HLA A*2403	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.218585	1.263068	-2.955517	16541.881404
HLA A*0201	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.243341	1.287816	-2.955525	17512.228945
HLA B*1501	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.239075	1.283502	-2.955573	17341.024889
HLA B*1509	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.483832	1.528166	-2.955666	30467.187245
HLA B*4501	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.651574	1.695841	-2.955733	44830.526917
HLA B*0801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.243579	1.287816	-2.955762	17521.800221
HLA A*2602	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.237205	1.281231	-2.955974	17266.510278
HLA B*0702	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.225591	1.269596	-2.955996	16810.903963
HLA A*3201	1:481-489	9	MTADWTRVP	0.898983	0.129318	-3.984473	1.028301	-2.956172	9648.789221
HLA B*1801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.330766	1.374504	-2.956262	21417.351446
HLA B*0801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.384762	1.428368	-2.956394	24252.785603
HLA B*2705	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.434202	1.477798	-2.956404	27177.020406
HLA B*4403	1:368-376	9	KFTLVEPLR	0.910090	0.768535	-4.635118	1.678625	-2.956493	43163.638879
HLA A*2301	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.459760	1.503120	-2.956639	28824.351046
HLA B*4501	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.632470	1.675762	-2.956708	42901.273171
HLA A*3001	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.160524	1.203805	-2.956720	14471.862564
HLA B*4002	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.632527	1.675762	-2.956764	42906.843720
HLA B*4402	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.398227	1.440990	-2.957237	25016.498712
HLA B*1501	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.412763	1.455494	-2.957268	25867.996280
HLA A*0211	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.296830	1.339557	-2.957273	19807.506261
HLA B*3501	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.270454	1.313175	-2.957279	18640.368054
HLA A*2402	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.435186	1.477798	-2.957389	27238.693614
HLA A*0203	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.238847	1.281231	-2.957616	17331.927413
HLA B*3501	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.250691	1.293038	-2.957652	17811.094809
HLA A*6901	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.109592	1.151838	-2.957754	12870.407380
HLA B*0802	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.386131	1.428368	-2.957764	24329.398803
HLA A*1101	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.370444	1.412655	-2.957789	23466.259337
HLA B*5301	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.574840	1.617007	-2.957833	37569.867483
HLA B*0802	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.384205	1.426359	-2.957846	24221.709972
HLA B*1509	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.197101	1.239243	-2.957858	15743.497227
HLA B*4403	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.583801	1.625692	-2.958109	38353.111145
HLA B*3801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.479932	1.521566	-2.958366	30194.804117
HLA A*0203	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.242425	1.284024	-2.958401	17475.319601
HLA A*6901	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.242474	1.284024	-2.958451	17477.305044
HLA B*4402	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.368569	1.410054	-2.958515	23365.171707
HLA B*5701	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.414095	1.455494	-2.958601	25947.465777
HLA A*0301	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.084631	1.126026	-2.958606	12151.541234
HLA A*3101	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.873727	0.915104	-2.958623	7477.001956
HLA A*6901	1:210-218	9	NIANALIEQ	0.827718	0.099249	-3.885776	0.926967	-2.958809	7687.332276
HLA B*4601	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.383084	1.424271	-2.958813	24159.286012
HLA B*4002	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.567737	1.608922	-2.958815	36960.443180
HLA B*5301	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.585927	1.627062	-2.958865	38541.346467
HLA A*0216	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.248275	1.289353	-2.958922	17712.315719
HLA A*3001	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.222067	1.263086	-2.958980	16675.038282
HLA B*5301	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.462163	1.503120	-2.959043	28984.316371
HLA A*0216	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.454572	1.495512	-2.959060	28482.091378
HLA A*2603	1:241-249	9	AAALVQRAI	1.328858	0.344315	-4.632273	1.673173	-2.959100	42881.781945
HLA B*4601	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.414621	1.455494	-2.959127	25978.928369
HLA A*3002	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.106397	1.147258	-2.959139	12776.061509
HLA B*4801	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.371858	1.412655	-2.959203	23542.807736
HLA A*2403	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.298782	1.339557	-2.959225	19896.753701
HLA A*0101	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.387774	1.428368	-2.959406	24421.574901
HLA B*1517	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.222650	1.263086	-2.959563	16697.425403
HLA A*2403	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.372286	1.412655	-2.959631	23565.999396
HLA B*4001	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.372319	1.412655	-2.959664	23567.784316
HLA A*2902	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.308803	1.348830	-2.959973	20361.172227
HLA A*6801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.086149	1.126026	-2.960123	12194.082593

HLA A*3002	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.784846	0.824605	-2.960241	6093.214636
HLA B*4001	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.415841	1.455494	-2.960346	26051.972747
HLA A*0101	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.384966	1.424271	-2.960695	24264.203114
HLA B*4002	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.635844	1.675016	-2.960828	43235.853966
HLA A*2301	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.456353	1.495512	-2.960841	28599.127577
HLA B*4002	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.600357	1.639403	-2.960954	39843.494346
HLA A*0301	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.230581	1.269596	-2.960986	17005.185481
HLA B*5101	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.222006	1.260962	-2.961044	16672.692984
HLA A*3201	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.250571	1.289436	-2.961135	17806.181328
HLA A*2902	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.389660	1.428368	-2.961293	24527.896436
HLA B*7301	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.600712	1.639403	-2.961309	39876.055525
HLA A*0201	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-3.968980	1.007289	-2.961691	9310.656731
HLA B*5301	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.439653	1.477798	-2.961855	27520.267164
HLA B*4501	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.647065	1.685162	-2.961904	44367.522852
HLA B*4002	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.579083	1.617007	-2.962076	37938.733875
HLA B*0801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.279655	1.317518	-2.962137	19039.479282
HLA A*2501	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.336052	1.373907	-2.962145	21679.641908
HLA B*5801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.357139	1.394918	-2.962221	22758.243112
HLA A*0206	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.403325	1.440990	-2.962335	25311.909472
HLA B*4403	1:105-113	9	GIVAHTGTR	1.053544	0.642297	-4.658305	1.695841	-2.962464	45530.782886
HLA B*0801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.302062	1.339557	-2.962505	20047.586914
HLA A*2403	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.339886	1.377330	-2.962556	21871.897604
HLA A*0203	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.635870	0.673013	-2.962857	4323.847135
HLA A*2602	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.191331	1.228391	-2.962940	15535.701809
HLA A*2403	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-3.860998	0.897730	-2.963268	7261.025877
HLA A*3002	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.252911	1.289353	-2.963558	17902.384428
HLA B*4801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.419247	1.455494	-2.963753	26257.136896
HLA A*6901	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.358805	1.394918	-2.963886	22845.702511
HLA B*5801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.341463	1.377330	-2.964132	21951.437651
HLA B*1503	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.253935	1.289436	-2.964499	17944.660830
HLA A*2301	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.493188	1.528166	-2.965022	31130.637255
HLA B*5801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.130254	1.165167	-2.965087	13497.510212
HLA A*0101	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.339654	1.374504	-2.965150	21860.186611
HLA A*0301	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.339168	1.373907	-2.965260	21835.720247
HLA A*2601	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.342626	1.377330	-2.965295	22010.300077
HLA A*0206	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.468612	1.503120	-2.965492	29417.949480
HLA A*2602	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.339480	1.373907	-2.965573	21851.437035
HLA A*0201	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.009650	1.044058	-2.965592	10224.684137
HLA B*0702	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.468814	1.503120	-2.965694	29431.639379
HLA A*2403	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.421233	1.455494	-2.965738	26377.442395
HLA A*6901	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.340267	1.374504	-2.965763	21891.074582
HLA A*2602	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.595367	1.629570	-2.965797	39388.288811
HLA A*0203	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-3.978646	1.012736	-2.965910	9520.200534
HLA A*8001	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.314747	1.348830	-2.965917	20641.771895
HLA B*4501	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.633612	1.667650	-2.965962	43014.217874
HLA A*0301	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.340486	1.374504	-2.965982	21902.091184
HLA B*4402	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.392494	1.426359	-2.966135	24688.447611
HLA B*5401	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-3.874804	0.908582	-2.966222	7495.550912
HLA B*7301	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.598891	1.632644	-2.966247	39709.218610
HLA B*5701	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.407498	1.440990	-2.966508	25556.277424
HLA B*2705	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.393243	1.426359	-2.966884	24731.090599
HLA A*0219	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.289116	1.322138	-2.966979	19458.817396
HLA B*5101	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.910732	0.943730	-2.967002	8142.014716
HLA B*0802	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.426681	1.459325	-2.967356	26710.445953
HLA A*6802	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.251407	1.284024	-2.967383	17840.507663
HLA A*3001	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.182971	1.215498	-2.967473	15239.524245
HLA A*0250	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.230586	1.263086	-2.967500	17005.369474
HLA B*4601	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.230941	1.263068	-2.967873	17019.266721
HLA A*2602	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-3.950485	0.982586	-2.967899	8922.471497
HLA B*4601	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.257283	1.289353	-2.967930	18083.532471
HLA A*6802	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.396540	1.428368	-2.968172	24919.515593
HLA A*3001	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-3.782187	0.813884	-2.968303	6056.013848
HLA A*2601	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.342349	1.373907	-2.968441	21996.253913
HLA B*5401	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.556448	1.587869	-2.968579	36012.054159
HLA A*2402	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.577650	1.608922	-2.968728	37813.741178

HLA B*5801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.341604	1.372792	-2.968812	21958.564098
HLA A*0212	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.409967	1.440990	-2.968977	25701.999019
HLA A*3101	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.343674	1.374504	-2.969170	22063.470881
HLA A*2601	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.381930	1.412655	-2.969276	24095.197929
HLA B*7301	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.596344	1.627062	-2.969283	39477.032524
HLA B*1509	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.204446	1.235042	-2.969403	16012.004449
HLA A*8001	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.410427	1.440990	-2.969438	25729.266286
HLA A*0101	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.129117	1.159455	-2.969662	13462.214744
HLA B*3901	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.379908	1.410054	-2.969854	23983.225537
HLA A*3101	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.410947	1.440990	-2.969957	25760.046220
HLA A*0250	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.121796	1.151838	-2.969957	13237.181348
HLA A*0250	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.411092	1.440990	-2.970103	25768.687927
HLA B*4601	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.411111	1.440990	-2.970121	25769.803197
HLA B*1503	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.283353	1.313175	-2.970178	19202.295820
HLA A*1101	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.351634	1.381432	-2.970202	22471.594480
HLA A*2301	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.351662	1.381432	-2.970230	22473.053354
HLA B*0803	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.498667	1.528166	-2.970501	31525.864889
HLA A*2301	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.380685	1.410054	-2.970631	24026.210133
HLA A*6801	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.606835	1.635727	-2.971108	40442.216519
HLA B*4002	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.638962	1.667650	-2.971312	43547.357621
HLA A*0201	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.395764	1.424271	-2.971493	24875.067382
HLA A*3002	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.397869	1.426359	-2.971511	24995.936022
HLA A*2602	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.588610	1.617007	-2.971603	38780.195561
HLA B*0803	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.431145	1.459325	-2.971820	26986.412874
HLA B*0802	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.384651	1.412655	-2.971996	24246.619757
HLA B*0802	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.396335	1.424271	-2.972064	24907.789725
HLA B*5801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.259889	1.287816	-2.972072	18192.351945
HLA A*0202	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.581026	1.608922	-2.972104	38108.851214
HLA B*5701	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.396481	1.424271	-2.972210	24916.145526
HLA B*1501	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.000741	1.028301	-2.972439	10017.068726
HLA A*0212	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.103531	1.131046	-2.972485	12692.016333
HLA A*0202	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.577417	1.604651	-2.972766	37793.494354
HLA A*2501	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.132251	1.159455	-2.972796	13559.720164
HLA A*0101	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.346709	1.373907	-2.972802	22218.225409
HLA B*4403	1:501-509	9	TNEVAEVNR	1.165759	0.510003	-4.648606	1.675762	-2.972844	44525.257916
HLA A*0203	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.397186	1.424271	-2.972915	24956.616434
HLA A*0301	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.354472	1.381432	-2.973040	22618.930540
HLA A*2602	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.577983	1.604651	-2.973333	37842.801015
HLA B*1501	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.888759	0.915104	-2.973655	7740.330402
HLA B*5101	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.327422	1.353717	-2.973705	21253.107851
HLA A*3301	1:236-244	9	VDSAVAAAL	1.340868	0.294859	-4.609499	1.635727	-2.973772	40691.084606
HLA A*0101	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.327575	1.353717	-2.973858	21260.582667
HLA A*2402	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.133421	1.159455	-2.973966	13596.300997
HLA A*2403	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.348610	1.374504	-2.974106	22315.678803
HLA B*2705	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.384306	1.410054	-2.974252	24227.345208
HLA B*1502	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.578918	1.604651	-2.974268	37924.369491
HLA B*1503	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.398602	1.424271	-2.974331	25038.161924
HLA B*1509	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.477533	1.503120	-2.974413	30028.482973
HLA B*1503	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.328163	1.353717	-2.974445	21289.356470
HLA B*3501	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-2.993972	0.019419	-2.974553	986.216429
HLA A*0250	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.579449	1.604651	-2.974799	37970.765507
HLA A*0203	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.237985	1.263086	-2.974898	17297.550234
HLA B*2705	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.096736	1.121826	-2.974910	12494.989965
HLA A*0301	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.356735	1.381752	-2.974983	22737.076395
HLA A*2601	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.403428	1.428368	-2.975061	25317.935313
HLA B*5801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.349040	1.373907	-2.975133	22337.782482
HLA A*3002	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.496719	1.521566	-2.975153	31384.794323
HLA A*2501	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.434526	1.459325	-2.975201	27197.317386
HLA A*3001	1:397-405	9	VARQPFPGP	0.713125	0.118777	-3.807251	0.831902	-2.975349	6415.805147
HLA B*3901	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.352797	1.377330	-2.975466	22531.851699
HLA A*0216	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.062913	1.087303	-2.975610	11558.799369
HLA B*4601	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.329370	1.353717	-2.975653	21348.637805
HLA A*2602	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.135183	1.159455	-2.975728	13651.578925
HLA B*5801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.350379	1.374504	-2.975875	22406.770402
HLA A*2603	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.076606	1.100487	-2.976118	11929.040806

HLA A*0212	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.643060	0.666703	-2.976357	4396.020973
HLA B*0702	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.417664	1.440990	-2.976674	26161.570745
HLA B*5101	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.417809	1.440990	-2.976820	26170.347151
HLA A*0206	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.358325	1.381432	-2.976894	22820.503505
HLA A*2301	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.011426	1.034513	-2.976913	10266.587461
HLA A*0206	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.766483	0.789472	-2.977011	5840.942109
HLA B*4801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.272503	1.295300	-2.977204	18728.510300
HLA B*1501	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.290489	1.313175	-2.977313	19520.392320
HLA A*8001	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.390008	1.412655	-2.977353	24547.542894
HLA A*0216	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-3.884253	0.906788	-2.977466	7660.430682
HLA B*7301	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.590269	1.612498	-2.977771	38928.595149
HLA B*4002	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.605002	1.627062	-2.977940	40271.921502
HLA B*5801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.334866	1.356576	-2.978289	21620.494089
HLA B*0702	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.406729	1.428368	-2.978362	25511.107472
HLA A*2601	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.034216	1.055834	-2.978382	10819.722337
HLA B*7301	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.594651	1.616065	-2.978586	39323.351085
HLA A*8001	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.405031	1.426359	-2.978672	25411.519495
HLA B*4501	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.587609	1.608922	-2.978687	38690.925134
HLA A*2603	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.254497	1.275786	-2.978711	17967.877628
HLA B*4403	1:30-38	9	IARRVREAR	0.966536	0.718626	-4.663913	1.685162	-2.978752	46122.553003
HLA B*4002	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.642643	1.663852	-2.978792	43918.090660
HLA B*0702	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.241918	1.263068	-2.978850	17454.910986
HLA A*0206	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.210756	1.231855	-2.978901	16246.372957
HLA A*2902	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.259135	1.280105	-2.979030	18160.786988
HLA B*2705	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.290167	1.311116	-2.979051	19505.930048
HLA B*3501	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.308782	1.329702	-2.979080	20360.180886
HLA B*3501	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.356422	1.377330	-2.979092	22720.722605
HLA B*0803	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.407580	1.428368	-2.979212	25561.116864
HLA B*1502	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.520891	1.541660	-2.979231	33181.100703
HLA A*8001	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.434860	1.455494	-2.979365	27218.218508
HLA B*0801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.093141	1.113445	-2.979697	12391.994147
HLA B*4001	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.297227	1.317518	-2.979709	19825.623976
HLA B*4501	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.643675	1.663852	-2.979823	44022.517504
HLA A*0206	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.521659	1.541660	-2.979999	33239.851140
HLA B*4501	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.655105	1.675016	-2.980089	45196.532764
HLA A*0101	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.293273	1.313175	-2.980097	19645.934040
HLA A*2602	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.568071	1.587869	-2.980202	36988.847258
HLA A*6802	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.404547	1.424271	-2.980276	25383.215727
HLA B*1509	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.458465	1.477798	-2.980667	28738.557942
HLA A*2602	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.213454	1.232655	-2.980799	16347.585882
HLA A*3001	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.264889	1.284024	-2.980865	18402.996913
HLA B*0702	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.436641	1.455494	-2.981146	27330.061307
HLA A*3002	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.590147	1.608922	-2.981225	38917.645521
HLA A*6802	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.270654	1.289353	-2.981301	18648.941623
HLA B*1517	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.264858	1.283502	-2.981356	18401.702702
HLA A*6802	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.422419	1.440990	-2.981429	26449.603937
HLA A*0202	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.216865	1.235408	-2.981457	16476.504444
HLA A*0203	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.210113	1.228391	-2.981722	16222.308642
HLA B*5101	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.410127	1.428368	-2.981759	25711.455816
HLA A*2902	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.069111	1.087303	-2.981808	11724.941027
HLA A*3002	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.523583	1.541660	-2.981923	33387.453672
HLA A*3001	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.806711	0.824605	-2.982106	6407.827088
HLA A*6901	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.359556	1.377330	-2.982226	22885.286434
HLA B*4403	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.621820	1.639403	-2.982417	41861.999225
HLA A*6802	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.951636	0.969193	-2.982443	8946.154969
HLA B*0801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.423507	1.440990	-2.982517	26515.937381
HLA A*2403	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.262657	1.280105	-2.982552	18308.659276
HLA A*3201	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.460643	1.477798	-2.982845	28883.042859
HLA A*2501	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.364347	1.381432	-2.982915	23139.126076
HLA A*1101	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.478553	1.495512	-2.983041	30099.069437
HLA B*2705	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.322660	1.339557	-2.983103	21021.322741
HLA A*0211	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-3.889915	0.906788	-2.983128	7760.960015
HLA A*3201	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.046288	1.062990	-2.983298	11124.686207
HLA B*2705	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-3.675844	0.692424	-2.983420	4740.721790
HLA A*6901	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.175387	1.191820	-2.983568	14975.704831

HLA B*4002	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.577387	1.593295	-2.984092	37790.836485
HLA A*3101	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.295256	1.311116	-2.984140	19735.841422
HLA B*5801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.337913	1.353717	-2.984196	21772.730483
HLA B*7301	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.606971	1.622722	-2.984249	40454.908209
HLA A*0212	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.439787	1.455494	-2.984292	27528.754724
HLA A*0101	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.149538	1.165167	-2.984372	14110.364662
HLA B*0702	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.361922	1.377330	-2.984592	23010.300158
HLA A*0219	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.005745	1.020890	-2.984855	10133.163649
HLA A*0203	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.440607	1.455494	-2.985112	27580.779523
HLA A*2603	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.594065	1.608922	-2.985144	39270.415740
HLA B*1509	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-3.771581	0.786323	-2.985259	5909.915676
HLA B*3901	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.158053	1.172675	-2.985377	14389.734177
HLA B*4403	1:109-117	9	HTGTREYGR	1.076414	0.591236	-4.653150	1.667650	-2.985500	44993.559053
HLA A*6802	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.022516	1.036964	-2.985552	10532.117133
HLA B*5101	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.395922	1.410054	-2.985868	24884.085297
HLA A*3002	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.410207	1.424271	-2.985936	25716.185519
HLA B*4801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.410465	1.424271	-2.986194	25731.493462
HLA A*2403	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.223223	1.236980	-2.986242	16719.480775
HLA B*5701	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.290082	1.303793	-2.986289	19502.131521
HLA A*0101	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.367749	1.381432	-2.986317	23321.098683
HLA A*6901	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.275699	1.289353	-2.986345	18866.812515
HLA A*0250	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.003640	1.017185	-2.986455	10084.164416
HLA B*4001	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.410801	1.424271	-2.986530	25751.407411
HLA B*1503	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-3.949395	0.962750	-2.986645	8900.102498
HLA B*5401	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.482223	1.495512	-2.986711	30354.491674
HLA A*0301	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.359923	1.372792	-2.987131	22904.608457
HLA A*2902	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.202637	1.215498	-2.987138	15945.443339
HLA A*0219	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.275344	1.287816	-2.987527	18851.406637
HLA A*0219	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.892810	0.905240	-2.987570	7812.859447
HLA A*0301	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.305102	1.317518	-2.987584	20188.420342
HLA B*4001	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.382800	1.394918	-2.987882	24143.476601
HLA B*5801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.220568	1.232655	-2.987913	16617.583443
HLA A*3001	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.109931	1.121826	-2.988104	12880.437643
HLA A*0250	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.360900	1.372792	-2.988109	22956.213644
HLA B*0803	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.369692	1.381432	-2.988260	23425.670525
HLA B*4403	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.621183	1.632644	-2.988539	41800.671154
HLA B*3901	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.102196	1.113445	-2.988752	12653.075948
HLA A*6802	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.444338	1.455494	-2.988843	27818.744052
HLA A*0250	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.597799	1.608922	-2.988877	39609.451700
HLA A*0216	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.033398	1.044058	-2.989341	10799.371842
HLA B*5401	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.302588	1.313175	-2.989413	20071.895609
HLA B*5401	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.517970	1.528166	-2.989804	32958.723176
HLA B*0801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.364338	1.374504	-2.989834	23138.625361
HLA A*3101	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.329422	1.339557	-2.989865	21351.178819
HLA A*0101	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.384905	1.394918	-2.989987	24260.790421
HLA B*0803	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.384910	1.394918	-2.989992	24261.052919
HLA B*2705	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.445510	1.455494	-2.990015	27893.943172
HLA A*0301	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.270243	1.280105	-2.990138	18631.294454
HLA B*4403	1:487-495	9	RVPYEVLER	0.866973	0.808043	-4.665213	1.675016	-2.990196	46260.743008
HLA A*2403	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.339264	1.348830	-2.990434	21840.564066
HLA A*2902	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.414748	1.424271	-2.990477	25986.518807
HLA A*6802	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.371995	1.381432	-2.990563	23550.196006
HLA A*8001	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.266418	1.275786	-2.990632	18467.923547
HLA B*4001	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.372363	1.381432	-2.990932	23570.206923
HLA B*3501	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.419325	1.428368	-2.990957	26261.824905
HLA B*2705	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.432019	1.440990	-2.991029	27040.777141
HLA B*4801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.271213	1.280105	-2.991109	18672.968600
HLA A*0101	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.363959	1.372792	-2.991168	23118.480574
HLA A*0211	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.519340	1.528166	-2.991174	33062.837948
HLA A*3301	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.584494	1.593295	-2.991199	38414.368407
HLA A*6901	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.292462	1.301147	-2.991315	19609.300834
HLA B*0702	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.415686	1.424271	-2.991415	26042.672480
HLA B*0803	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.415744	1.424271	-2.991473	26046.194918
HLA B*4002	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.621066	1.629570	-2.991496	41789.365833
HLA A*1101	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.373306	1.381752	-2.991554	23621.394820

HLA B*1801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.494725	1.503120	-2.991604	31240.974627
HLA A*0211	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.047444	1.055834	-2.991609	11154.335841
HLA B*4403	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.629047	1.637421	-2.991626	42564.445609
HLA A*3001	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-3.755074	0.763388	-2.991686	5689.496082
HLA B*5401	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.181919	1.190075	-2.991844	15202.633994
HLA B*7301	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.585499	1.593295	-2.992204	38503.417339
HLA B*3501	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.433391	1.440990	-2.992402	27126.344202
HLA B*4801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.402594	1.410054	-2.992540	25269.358610
HLA B*0802	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.374104	1.381432	-2.992673	23664.883107
HLA B*4801	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.231953	1.239243	-2.992710	17058.996202
HLA A*0216	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.280609	1.287816	-2.992792	19081.343838
HLA B*2705	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.225488	1.232655	-2.992833	16806.902853
HLA A*8001	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.374656	1.381752	-2.992905	23694.987972
HLA A*3001	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-3.765571	0.772641	-2.992930	5828.694613
HLA A*0212	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.417372	1.424271	-2.993101	26144.026761
HLA A*2403	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.374588	1.381432	-2.993157	23691.270833
HLA B*3901	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.448705	1.455494	-2.993211	28099.928276
HLA B*5401	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.367784	1.374504	-2.993280	23322.991228
HLA B*1503	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.297185	1.303793	-2.993392	19823.693490
HLA A*0219	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.124610	1.131046	-2.993564	13323.250754
HLA B*4002	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.626366	1.632644	-2.993722	42302.517987
HLA A*6802	1:210-218	9	NIANALIEQ	0.827718	0.099249	-3.920731	0.926967	-2.993765	8331.655249
HLA A*6901	1:208-216	9	PANIANALI	0.995189	0.008861	-3.998001	1.004050	-2.993951	9954.080622
HLA A*6802	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.283602	1.289436	-2.994166	19213.310501
HLA A*2602	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.274608	1.280105	-2.994504	18819.512649
HLA B*4801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.334234	1.339557	-2.994676	21589.053528
HLA A*0101	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.372025	1.377330	-2.994695	23551.852316
HLA A*0219	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.287848	1.293038	-2.994809	19402.054524
HLA B*3801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.331344	1.336347	-2.994996	21445.873333
HLA B*5801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.050846	1.055834	-2.995011	11242.056681
HLA A*0301	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.343897	1.348830	-2.995067	22074.813084
HLA B*4501	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.632505	1.637421	-2.995084	42904.754680
HLA A*6901	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.335098	1.339557	-2.995541	21632.076674
HLA B*0702	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.256557	1.260962	-2.995595	18053.328283
HLA B*5801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.299426	1.303793	-2.995633	19926.268721
HLA B*4801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.313328	1.317518	-2.995810	20574.433474
HLA A*0201	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.373193	1.377330	-2.995862	23615.261739
HLA A*2902	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-3.901193	0.905240	-2.995953	7965.131936
HLA B*3801	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.537706	1.541660	-2.996046	34491.021179
HLA B*5701	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.377600	1.381432	-2.996169	23856.152222
HLA B*4403	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.608834	1.612498	-2.996336	40628.834276
HLA A*3002	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.524699	1.528166	-2.996533	33473.359652
HLA B*4403	1:456-464	9	SVGVQGDGR	0.950204	0.713648	-4.660551	1.663852	-2.996700	45766.871430
HLA B*4403	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.605717	1.608922	-2.996795	40338.207450
HLA B*0801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.280905	1.284024	-2.996881	19094.354995
HLA B*5301	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.605806	1.608922	-2.996884	40346.500861
HLA A*2301	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.538613	1.541660	-2.996953	34563.121177
HLA A*0211	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.538810	1.541660	-2.997150	34578.831289
HLA A*0219	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.378608	1.381432	-2.997177	23911.582891
HLA A*0201	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.162409	1.165167	-2.997242	14534.788495
HLA B*3501	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.127660	1.130410	-2.997250	13417.136350
HLA B*1801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.475123	1.477798	-2.997325	29862.270202
HLA A*6801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-3.805108	0.807776	-2.997332	6384.228686
HLA B*3801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.456733	1.459325	-2.997408	28624.202897
HLA A*0202	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.500711	1.503120	-2.997591	31674.594368
HLA A*0203	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.337403	1.339557	-2.997846	21747.185472
HLA B*0802	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.327667	1.329702	-2.997965	21265.068819
HLA A*3201	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.602824	1.604651	-2.998174	40070.464707
HLA A*0203	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.026496	1.028301	-2.998194	10629.080789
HLA A*0250	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.085562	1.087303	-2.998259	12177.601582
HLA B*0802	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.453832	1.455494	-2.998337	28433.595950
HLA A*2501	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.426794	1.428368	-2.998426	26717.382880
HLA B*1509	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.188530	1.190075	-2.998455	15435.840798
HLA B*1801	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.411118	1.412655	-2.998463	25770.221436
HLA A*2501	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.268091	1.269596	-2.998495	18539.196231

HLA A*0211	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.291576	1.293038	-2.998538	19569.347869
HLA A*3101	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.278718	1.280105	-2.998613	18998.426018
HLA A*3001	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.051189	1.052564	-2.998625	11250.939657
HLA B*1509	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.119446	1.120820	-2.998626	13165.763022
HLA A*3101	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.352397	1.353717	-2.998680	22511.139106
HLA B*4403	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.309851	1.311116	-2.998735	20410.359194
HLA B*0802	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.408865	1.410054	-2.998811	25636.869589
HLA A*0301	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.335437	1.336347	-2.999089	21648.935147
HLA B*4002	1:491-499	9	EVLERISTR	1.036599	0.600822	-4.636697	1.637421	-2.999276	43320.843517
HLA B*4002	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.622811	1.622722	-3.000090	41957.678223
HLA A*0219	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.455686	1.455494	-3.000191	28555.221371
HLA A*1101	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.426796	1.426359	-3.000437	26717.527418
HLA A*0203	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.204422	1.203805	-3.000617	16011.138241
HLA A*1101	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.293700	1.293038	-3.000662	19665.286949
HLA B*4403	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.623385	1.622722	-3.000663	42013.099472
HLA A*0101	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.141531	1.140721	-3.000810	13852.596771
HLA A*0101	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.357630	1.356576	-3.001053	22783.989655
HLA B*1501	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.396100	1.394918	-3.001182	24894.318531
HLA A*0202	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.205014	1.203805	-3.001209	16032.980984
HLA B*4402	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.302440	1.301147	-3.001294	20065.055811
HLA A*6901	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.374095	1.372792	-3.001303	23664.371015
HLA B*4001	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.378672	1.377330	-3.001341	23915.075840
HLA B*4501	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.628488	1.627062	-3.001426	42509.676869
HLA B*3501	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.291059	1.289436	-3.001623	19546.070763
HLA B*7301	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.606558	1.604651	-3.001907	40416.407785
HLA B*5401	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.331640	1.329702	-3.001938	21460.496811
HLA A*0250	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.717600	0.715584	-3.002016	5219.146852
HLA B*1502	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.374842	1.372792	-3.002051	23705.116930
HLA A*1101	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.376564	1.374504	-3.002060	23799.304981
HLA B*0702	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.374920	1.372792	-3.002128	23709.349295
HLA A*0216	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.379670	1.377330	-3.002340	23970.124711
HLA A*0201	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.397519	1.394918	-3.002601	24975.795579
HLA B*3501	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.141870	1.139224	-3.002645	13863.392481
HLA A*2501	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.505814	1.503120	-3.002694	32048.974926
HLA A*3002	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.065704	1.062990	-3.002714	11633.326410
HLA A*3002	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.286372	1.283502	-3.002870	19336.249629
HLA A*2402	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.384550	1.381432	-3.003118	24240.980037
HLA B*0801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.380486	1.377330	-3.003155	24015.164447
HLA A*8001	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.427546	1.424271	-3.003275	26763.675123
HLA B*1801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.385185	1.381752	-3.003433	24276.413984
HLA A*0101	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.296590	1.293038	-3.003552	19796.579322
HLA B*0803	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.459146	1.455494	-3.003652	28783.680328
HLA A*6802	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.376480	1.372792	-3.003688	23794.670375
HLA B*5401	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.507139	1.503120	-3.004019	32146.911371
HLA A*0206	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.896837	0.892605	-3.004232	7885.641493
HLA B*4001	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.340669	1.336347	-3.004322	21911.335189
HLA B*1503	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.060244	1.055834	-3.004409	11487.981053
HLA B*1501	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.361196	1.356576	-3.004620	22971.866990
HLA B*1517	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-3.937629	0.932998	-3.004631	8662.211578
HLA A*2301	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.482869	1.477798	-3.005071	30399.684252
HLA A*0301	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.358967	1.353717	-3.005249	22854.232001
HLA A*2603	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.483254	1.477798	-3.005457	30426.667483
HLA B*4601	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.382880	1.377330	-3.005549	24147.917869
HLA B*4001	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.359406	1.353717	-3.005689	22877.364167
HLA A*0201	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.268784	1.263068	-3.005716	18568.806877
HLA A*0201	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.215930	1.210159	-3.005771	16441.066456
HLA B*1517	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.058439	1.052564	-3.005876	11440.349866
HLA A*0216	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.387398	1.381432	-3.005966	24400.445165
HLA B*4402	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.430255	1.424271	-3.005984	26931.138022
HLA B*1503	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-3.988646	0.982586	-3.006059	9741.941216
HLA A*6901	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.362672	1.356576	-3.006095	23050.044575
HLA A*2501	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.286288	1.280105	-3.006183	19332.484145
HLA B*1503	1:429-437	9	IVREELTAA	1.079993	-0.117018	-3.969253	0.962975	-3.006278	9316.501441
HLA B*1517	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.098225	1.091915	-3.006311	12537.919732
HLA B*1801	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.245571	1.239243	-3.006328	17602.367650

HLA B*5401	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.548110	1.541660	-3.006449	35327.228902
HLA A*3002	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.501977	1.495512	-3.006466	31767.090065
HLA A*0212	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.294433	1.287816	-3.006617	19698.507728
HLA A*6901	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.722209	0.715584	-3.006626	5274.838975
HLA A*0219	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-3.918706	0.911989	-3.006717	8292.892489
HLA B*0801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.293439	1.286148	-3.007291	19653.481534
HLA B*1502	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.616296	1.608922	-3.007374	41332.942709
HLA B*4601	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.402533	1.394918	-3.007615	25265.804544
HLA A*2403	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.270877	1.263086	-3.007791	18658.528513
HLA A*2902	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.381726	1.373907	-3.007819	24083.859943
HLA B*0803	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.325404	1.317518	-3.007886	21154.571775
HLA B*3501	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.463469	1.455494	-3.007975	29071.629497
HLA B*3501	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.223547	1.215498	-3.008049	16731.967609
HLA B*4501	1:370-378	9	TLVEPLRLL	1.235357	0.404046	-4.647465	1.639403	-3.008061	44408.345596
HLA A*3001	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.148786	1.140721	-3.008065	14085.958431
HLA B*4501	1:254-262	9	TCVFVDHGL	1.162394	0.470250	-4.640747	1.632644	-3.008103	43726.771847
HLA B*3801	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.511415	1.503120	-3.008295	32464.993151
HLA A*2602	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.617445	1.608922	-3.008523	41442.431113
HLA B*0802	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.345384	1.336347	-3.009037	22150.536977
HLA A*0206	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.212857	1.203805	-3.009052	16325.137897
HLA A*6802	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.148133	1.138932	-3.009201	14064.789787
HLA B*5701	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.322538	1.313175	-3.009362	21015.409975
HLA B*4403	1:119-127	9	ELKVLGGKL	1.287477	0.339585	-4.636601	1.627062	-3.009539	43311.235783
HLA A*3101	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.476425	0.466612	-3.009813	2995.193478
HLA A*0201	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.030729	1.020890	-3.009840	10733.206377
HLA A*3301	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.627064	1.617007	-3.010057	42370.541644
HLA B*7301	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.627452	1.617007	-3.010445	42408.379819
HLA B*0803	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.488442	1.477798	-3.010644	30792.294464
HLA B*2705	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.405740	1.394918	-3.010822	25453.070426
HLA B*5101	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.083767	1.072837	-3.010929	12127.373535
HLA B*3501	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.421002	1.410054	-3.010948	26363.461595
HLA A*2601	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.385497	1.374504	-3.010993	24293.887519
HLA B*3901	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.423674	1.412655	-3.011019	26526.124166
HLA A*0101	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.333165	1.322138	-3.011027	21535.977432
HLA B*4403	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.604450	1.593295	-3.011155	40220.755375
HLA B*1503	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.452180	1.440990	-3.011190	28325.664031
HLA B*4001	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.324688	1.313175	-3.011512	21119.695170
HLA B*3501	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.435891	1.424271	-3.011620	27282.937001
HLA B*3901	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-3.933151	0.921448	-3.011703	8573.352272
HLA B*4002	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.649788	1.638021	-3.011767	44646.583901
HLA A*0216	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.790015	0.778023	-3.011992	6166.167865
HLA A*0212	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.298371	1.286148	-3.012223	19877.925750
HLA B*2705	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.386380	1.373907	-3.012473	24343.354455
HLA B*1509	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.282235	1.269596	-3.012639	19152.911461
HLA B*1502	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.490467	1.477798	-3.012670	30936.224259
HLA B*0702	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.425450	1.412655	-3.012795	26634.834885
HLA B*5301	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.600700	1.587869	-3.012832	39874.976915
HLA A*0211	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.139280	1.126421	-3.012859	13780.989001
HLA A*2603	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.600797	1.587869	-3.012928	39883.822383
HLA A*0203	1:1-9	9	VVQPADIDV	0.757996	0.154834	-3.925773	0.912830	-3.012944	8428.946281
HLA A*0212	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.248033	1.235042	-3.012991	17702.448837
HLA B*0802	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.394834	1.381752	-3.013082	24821.834166
HLA A*2603	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.617821	1.604651	-3.013170	41478.318476
HLA A*3101	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.274251	1.260962	-3.013289	18804.043666
HLA B*4601	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.330820	1.317518	-3.013302	21420.016518
HLA B*3901	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.352933	1.339557	-3.013376	22538.922708
HLA A*2501	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.454572	1.440990	-3.013582	28482.091378
HLA A*6802	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.408508	1.394918	-3.013590	25615.796976
HLA A*0202	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.144144	1.130410	-3.013734	13936.182342
HLA A*6802	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.388370	1.374504	-3.013866	24455.155943
HLA A*2403	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.386857	1.372792	-3.014066	24370.103194
HLA B*7301	1:380-388	9	KDEVRAVGR	1.160311	0.448611	-4.623185	1.608922	-3.014263	41993.784585
HLA B*1517	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.387057	1.372792	-3.014266	24381.312134
HLA A*3001	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.249889	1.235408	-3.014481	17778.267685
HLA B*5701	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.391902	1.377330	-3.014571	24654.812978

HLA B*1503	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.206405	1.191820	-3.014586	16084.411394
HLA B*4601	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.387489	1.372792	-3.014698	24405.593853
HLA A*2902	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.327888	1.313175	-3.014712	21275.885485
HLA A*3002	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.242834	1.228069	-3.014765	17491.777226
HLA B*1503	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.058261	1.043307	-3.014954	11435.647115
HLA A*2602	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.153889	1.138932	-3.014957	14252.448613
HLA B*0702	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.389136	1.373907	-3.015229	24498.323695
HLA B*5301	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.276483	1.260962	-3.015521	18900.933833
HLA B*0802	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.456933	1.440990	-3.015943	28637.368494
HLA A*0206	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.244617	1.228391	-3.016226	17563.747973
HLA B*4002	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.642065	1.625692	-3.016374	43859.681903
HLA A*0216	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.471902	1.455494	-3.016407	29641.602351
HLA A*6901	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.181604	1.165167	-3.016437	15191.617216
HLA A*3001	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.292323	1.275786	-3.016537	19603.042869
HLA B*5301	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.444951	1.428368	-3.016583	27858.051336
HLA A*0301	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.356157	1.339557	-3.016600	22706.837275
HLA A*1101	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.094222	1.077535	-3.016687	12422.870634
HLA A*2902	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.394094	1.377330	-3.016763	24779.570925
HLA A*3002	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.370481	1.353717	-3.016764	23468.290623
HLA A*6802	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.394190	1.377330	-3.016860	24785.067778
HLA B*4402	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.398652	1.381752	-3.016900	25041.006613
HLA B*3801	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.512435	1.495512	-3.016923	32541.306998
HLA B*1501	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.130897	1.113845	-3.017052	13517.532537
HLA A*2403	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.305145	1.287816	-3.017328	20190.386346
HLA B*4002	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.633490	1.616065	-3.017425	43002.119064
HLA B*3501	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.334943	1.317518	-3.017425	21624.354261
HLA A*0201	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.176919	1.159455	-3.017464	15028.621122
HLA B*4501	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.655490	1.638021	-3.017469	45236.649908
HLA B*4501	1:479-487	9	DAMTADWTR	1.140857	0.484835	-4.643388	1.625692	-3.017697	43993.471944
HLA A*3002	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.390664	1.372792	-3.017872	24584.621926
HLA B*1509	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.428157	1.410054	-3.018103	26801.346625
HLA A*0201	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.987349	0.969193	-3.018155	9712.892653
HLA B*1517	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.392745	1.374504	-3.018241	24702.742857
HLA A*0211	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.222227	1.203805	-3.018422	16681.173698
HLA B*4002	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.630945	1.612498	-3.018447	42750.910145
HLA A*3301	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.299858	1.281231	-3.018627	19946.113594
HLA B*4801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.413703	1.394918	-3.018785	25924.034087
HLA B*4402	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.329927	1.311116	-3.018811	21376.027382
HLA A*2403	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.251581	1.232655	-3.018926	17847.651215
HLA B*5101	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.282134	1.263086	-3.019047	19148.456529
HLA A*0212	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.303220	1.284024	-3.019196	20101.126704
HLA A*2402	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.560971	1.541660	-3.019310	36389.044598
HLA A*0212	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.358976	1.339557	-3.019419	22854.726562
HLA B*1517	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.254962	1.235408	-3.019554	17987.134376
HLA B*4601	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.394258	1.374504	-3.019754	24788.956533
HLA A*0219	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.305965	1.286148	-3.019816	20228.542840
HLA B*4002	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.624534	1.604651	-3.019883	42124.389569
HLA B*4501	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.636328	1.616065	-3.020263	43284.064468
HLA B*0802	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.303787	1.283502	-3.020284	20127.351309
HLA B*5701	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.415216	1.394918	-3.020298	26014.510124
HLA A*0202	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.833650	0.813260	-3.020390	6817.889828
HLA B*0801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.253052	1.232655	-3.020397	17908.196366
HLA A*0216	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.093334	1.072837	-3.020496	12397.492590
HLA B*1517	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.301808	1.281231	-3.020577	20035.877171
HLA A*1101	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.342830	1.322138	-3.020693	22020.661891
HLA B*0803	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.447103	1.426359	-3.020744	27996.443367
HLA A*2601	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.369579	1.348830	-3.020749	23419.588261
HLA B*4403	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.637782	1.617007	-3.020776	43429.253703
HLA B*4801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.357336	1.336347	-3.020989	22768.587506
HLA A*0211	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.524384	1.503120	-3.021264	33449.102765
HLA B*5101	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.922869	0.901531	-3.021338	8372.773109
HLA B*4501	1:21-29	9	DFGAQYAQL	1.321005	0.301717	-4.644121	1.622722	-3.021400	44067.790586
HLA B*4403	1:411-419	9	IVGEVTAKR	0.937293	0.700728	-4.659480	1.638021	-3.021459	45654.107849
HLA A*8001	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.339015	1.317518	-3.021497	21828.043223
HLA B*4403	1:46-54	9	HTASIEEIR	1.076887	0.539178	-4.637620	1.616065	-3.021555	43413.045355

HLA A*6901	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.282634	1.260962	-3.021672	19170.534135
HLA A*6901	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.194578	1.172675	-3.021903	15652.289256
HLA B*5401	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-3.511334	0.489404	-3.021930	3245.887994
HLA A*2501	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.477432	1.455494	-3.021938	30021.498402
HLA B*3501	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.291630	1.269596	-3.022035	19571.782984
HLA A*3001	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.009344	0.987241	-3.022104	10217.495792
HLA A*2501	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.285449	1.263086	-3.022363	19295.182762
HLA B*5801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.292183	1.269596	-3.022587	19596.680884
HLA B*3901	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.340138	1.317518	-3.022620	21884.561995
HLA A*2402	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.550887	1.528166	-3.022721	35553.852276
HLA A*0301	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.315980	1.293038	-3.022942	20700.481821
HLA B*4001	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.396899	1.373907	-3.022992	24940.150340
HLA B*4601	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.379588	1.356576	-3.023012	23965.586490
HLA A*0101	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.303117	1.280105	-3.023012	20096.342499
HLA A*2601	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.395889	1.372792	-3.023097	24882.200686
HLA B*4501	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.652676	1.629570	-3.023106	44944.417056
HLA B*2705	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.261066	1.237896	-3.023170	18241.726549
HLA A*3002	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.379795	1.356576	-3.023218	23976.998509
HLA A*0212	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.400571	1.377330	-3.023241	25151.929795
HLA A*2403	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.227071	1.203805	-3.023266	16868.297142
HLA A*2902	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.362970	1.339557	-3.023413	23065.886686
HLA B*4001	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.258648	1.235042	-3.023606	18140.461067
HLA A*0203	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.144858	1.120820	-3.024038	13959.120733
HLA B*3801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.479538	1.455494	-3.024043	30167.373693
HLA B*3501	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.325583	1.301147	-3.024436	21163.271299
HLA A*0203	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-3.800334	0.775707	-3.024627	6314.431870
HLA A*2501	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.397505	1.372792	-3.024714	24974.984894
HLA A*2602	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.320043	1.295300	-3.024743	20895.016273
HLA A*0219	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.364338	1.339557	-3.024780	23138.625361
HLA A*6802	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.317916	1.293038	-3.024878	20792.965347
HLA B*4501	1:207-215	9	TPANIANAL	1.335334	0.257961	-4.618181	1.593295	-3.024886	41512.664833
HLA A*0219	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.449309	1.424271	-3.025038	28139.023945
HLA A*0101	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.320360	1.295300	-3.025060	20910.282209
HLA B*0702	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.165811	1.140721	-3.025089	14649.094167
HLA B*3901	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.338338	1.313175	-3.025163	21794.060563
HLA B*1801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.435240	1.410054	-3.025186	27242.083066
HLA B*0702	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.313011	1.287816	-3.025194	20559.412730
HLA B*5701	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.399758	1.374504	-3.025254	25104.893904
HLA A*0250	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.364817	1.339557	-3.025260	23164.175646
HLA B*4601	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.294887	1.269596	-3.025291	19719.085851
HLA A*8001	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.406779	1.381432	-3.025347	25514.005895
HLA A*0250	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.240872	1.215498	-3.025374	17412.940562
HLA A*0219	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.240900	1.215498	-3.025402	17414.071024
HLA A*2403	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.098319	1.072837	-3.025482	12540.633176
HLA A*0301	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.313307	1.287816	-3.025490	20573.431750
HLA A*2601	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.336621	1.311116	-3.025505	21708.043335
HLA B*0803	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.466594	1.440990	-3.025604	29281.558637
HLA B*1501	1:29-37	9	LIARRVREA	1.156929	-0.187736	-3.994811	0.969193	-3.025617	9881.219649
HLA A*8001	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.309369	1.283502	-3.025867	20387.736096
HLA A*2403	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.318943	1.293038	-3.025905	20842.180597
HLA B*4403	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.554206	1.528166	-3.026040	35826.673504
HLA A*0211	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.146916	1.120820	-3.026096	14025.430883
HLA A*1101	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.454513	1.428368	-3.026146	28478.239515
HLA A*2902	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-3.459527	0.433361	-3.026166	2880.894704
HLA A*2902	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.314138	1.287816	-3.026322	20612.869696
HLA A*0202	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.554493	1.528166	-3.026327	35850.327146
HLA A*3101	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.362698	1.336347	-3.026350	23051.416296
HLA A*8001	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.400273	1.373907	-3.026366	25134.654948
HLA A*0202	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-2.729293	-0.297084	-3.026377	536.158690
HLA B*5801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.339574	1.313175	-3.026398	21856.166100
HLA A*0301	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.309928	1.283502	-3.026426	20414.003306
HLA A*2602	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.450789	1.424271	-3.026518	28235.091833
HLA B*4501	1:359-367	9	NVGGLPDDL	1.200302	0.412196	-4.639039	1.612498	-3.026541	43555.132665
HLA A*3201	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.467703	1.440990	-3.026713	29356.423693
HLA A*3101	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.289899	1.263068	-3.026831	19493.903916

HLA B*1801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.453329	1.426359	-3.026970	28400.696960
HLA A*3301	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.404615	1.377330	-3.027284	25387.198331
HLA A*2501	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.338409	1.311116	-3.027293	21797.597954
HLA A*3001	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.061959	1.034513	-3.027446	11533.439310
HLA A*3002	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.971217	0.943730	-3.027487	9358.732303
HLA A*2301	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.262600	1.235042	-3.027558	18306.282282
HLA A*0301	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.331367	1.303793	-3.027575	21447.033562
HLA A*1101	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.483081	1.455494	-3.027586	30414.489159
HLA B*5701	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.381338	1.353717	-3.027621	24062.371518
HLA B*1503	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.035043	1.007289	-3.027754	10840.345759
HLA A*0216	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.452032	1.424271	-3.027761	28316.011638
HLA B*4501	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.505582	1.477798	-3.027784	32031.814763
HLA B*5801	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.357494	1.329702	-3.027792	22776.841763
HLA B*5701	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.364229	1.336347	-3.027882	23132.867917
HLA A*0202	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.468873	1.440990	-3.027883	29435.620196
HLA A*0206	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.149160	0.120764	-3.028397	1409.809447
HLA B*2705	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.382126	1.353717	-3.028408	24106.019603
HLA B*0802	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.350602	1.322138	-3.028465	22418.289086
HLA B*3901	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.314820	1.286148	-3.028671	20645.233946
HLA B*4402	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.423662	1.394918	-3.028744	26525.406658
HLA B*1502	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.238938	1.210159	-3.028779	17335.584587
HLA B*1509	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.385563	1.356576	-3.028986	24297.567761
HLA A*2602	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.264118	1.235042	-3.029076	18370.370788
HLA A*0202	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.143063	1.113845	-3.029218	13901.544586
HLA A*3101	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.330383	1.301147	-3.029236	21398.473695
HLA A*3101	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.342588	1.313175	-3.029413	22008.394987
HLA B*3901	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.305318	1.275786	-3.029532	20198.470817
HLA B*0803	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.442199	1.412655	-3.029545	27682.128954
HLA A*6801	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.582673	1.553110	-3.029563	38253.647025
HLA A*2902	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.402467	1.372792	-3.029676	25261.977649
HLA B*4002	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.170124	1.140437	-3.029688	14795.322128
HLA A*2602	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-3.756897	0.727191	-3.029706	5713.431213
HLA A*3002	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.264797	1.235042	-3.029755	18399.114554
HLA B*7301	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.617765	1.587869	-3.029896	41472.933391
HLA B*5801	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.313798	1.283502	-3.030296	20596.706602
HLA A*1101	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.403092	1.372792	-3.030301	25298.356574
HLA A*0202	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.056856	1.026553	-3.030303	11398.711274
HLA B*1502	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.456719	1.426359	-3.030361	28623.273789
HLA B*4403	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.635158	1.604651	-3.030507	43167.608740
HLA A*2603	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.325907	1.295300	-3.030607	21179.076949
HLA B*1501	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.047965	1.017228	-3.030737	11167.740194
HLA A*0219	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.314775	1.284024	-3.030751	20643.111975
HLA A*3201	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.533893	1.503120	-3.030773	34189.507010
HLA A*0201	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.370559	1.339557	-3.031002	23472.480705
HLA A*2402	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.342194	1.311116	-3.031078	21988.401494
HLA A*3101	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.266200	1.235042	-3.031157	18458.634308
HLA A*0301	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.353603	1.322138	-3.031465	22573.700437
HLA B*1503	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.204159	1.172675	-3.031484	16001.439909
HLA A*3101	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.315170	1.283502	-3.031668	20661.882231
HLA B*2705	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.380502	1.348830	-3.031672	24016.073899
HLA A*2501	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.455998	1.424271	-3.031727	28575.774682
HLA A*2602	1:69-77	9	SVYADGAPK	0.472549	0.433678	-3.938009	0.906227	-3.031782	8669.806485
HLA B*5701	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.404643	1.372792	-3.031851	25388.846487
HLA B*1517	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.487850	1.455494	-3.032356	30750.344175
HLA A*3101	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.327697	1.295300	-3.032398	21266.564413
HLA B*4601	1:155-163	9	VASSAGAPV	0.740279	0.203451	-3.976160	0.943730	-3.032431	9465.865763
HLA A*0301	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.343627	1.311116	-3.032511	22061.083792
HLA B*0803	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.362265	1.329702	-3.032564	23028.481881
HLA B*4001	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.320421	1.287816	-3.032605	20913.223596
HLA B*3901	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.222725	1.190075	-3.032649	16700.316253
HLA B*4403	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-3.925393	0.892605	-3.032787	8421.562371
HLA B*4001	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.326262	1.293038	-3.033223	21196.385063
HLA B*3801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.461747	1.428368	-3.033380	28956.575711
HLA B*0801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.296487	1.263086	-3.033400	19791.867602
HLA A*3001	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.198652	1.165167	-3.033485	15799.810280

HLA A*0206	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.215869	1.182210	-3.033659	16438.754066
HLA B*4601	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.198882	1.165167	-3.033715	15808.189073
HLA A*2601	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.296837	1.263068	-3.033769	19807.827733
HLA A*0202	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.575620	1.541660	-3.033960	37637.406726
HLA B*4402	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.407916	1.373907	-3.034008	25580.898957
HLA B*4501	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.651160	1.617007	-3.034154	44787.862272
HLA B*4001	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.356598	1.322138	-3.034461	22729.943220
HLA A*3001	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.295476	1.260962	-3.034514	19745.880233
HLA B*5101	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.490181	1.455494	-3.034686	30915.812887
HLA B*4402	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.416308	1.381432	-3.034876	26080.034568
HLA A*1101	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.475891	1.440990	-3.034901	29915.144320
HLA B*4601	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.321081	1.286148	-3.034933	20945.039613
HLA B*5801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.346091	1.311116	-3.034975	22186.635777
HLA B*5801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.207895	1.172675	-3.035219	16139.673546
HLA B*1517	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.459644	1.424271	-3.035373	28816.711168
HLA B*1509	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.324843	1.289353	-3.035490	21127.237361
HLA A*2902	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.346681	1.311116	-3.035565	22216.783078
HLA B*1509	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.284756	1.249052	-3.035704	19264.413805
HLA A*0219	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.298789	1.263068	-3.035721	19897.076622
HLA B*4601	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.339576	1.303793	-3.035784	21856.284340
HLA B*5401	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.108643	1.072837	-3.035806	12842.308597
HLA B*2705	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.319408	1.283502	-3.035906	20864.517827
HLA A*0203	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.430847	1.394918	-3.035929	26967.878067
HLA A*0101	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.375596	1.339557	-3.036039	23746.318393
HLA B*4001	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.392879	1.356576	-3.036303	24710.361460
HLA A*1101	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.385716	1.348830	-3.036886	24306.113328
HLA A*2402	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.492594	1.455494	-3.037099	31088.057837
HLA A*0301	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.366915	1.329702	-3.037213	23276.353246
HLA A*2902	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.313044	1.275786	-3.037258	20560.969927
HLA A*0101	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.354808	1.317518	-3.037290	22636.435635
HLA B*3901	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.131325	1.094025	-3.037300	13530.848451
HLA B*0801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.317536	1.280105	-3.037431	20774.750332
HLA B*4501	1:416-424	9	TAKRLDTLR	0.927892	0.676759	-4.642249	1.604651	-3.037598	43878.193337
HLA A*2601	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.350821	1.313175	-3.037645	22429.571006
HLA A*0250	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.533207	1.495512	-3.037695	34135.540904
HLA A*2501	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.386578	1.348830	-3.037748	24354.419336
HLA B*3501	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.129323	1.091476	-3.037847	13468.625230
HLA B*4403	1:215-223	9	LIEQVRTQI	1.336305	0.293265	-4.667583	1.629570	-3.038014	46513.951338
HLA B*3501	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.341952	1.303793	-3.038159	21976.152561
HLA A*2902	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.412793	1.374504	-3.038289	25869.815603
HLA B*1509	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.479439	1.440990	-3.038449	30160.519982
HLA B*1509	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.411365	1.372792	-3.038573	25784.864068
HLA A*2501	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.451604	1.412655	-3.038950	28288.145419
HLA B*1801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.498404	1.459325	-3.039078	31506.768914
HLA B*1801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.416665	1.377330	-3.039335	26101.489082
HLA A*2902	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.323034	1.283502	-3.039531	21039.412481
HLA B*4402	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.388422	1.348830	-3.039592	24458.066710
HLA A*0201	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.323663	1.284024	-3.039639	21069.938603
HLA B*0803	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.352997	1.313175	-3.039821	22542.215141
HLA A*2301	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.388728	1.348830	-3.039898	24475.273765
HLA A*0301	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.341073	1.301147	-3.039926	21931.733196
HLA A*2902	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.326170	1.286148	-3.040022	21191.913401
HLA A*2902	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.329459	1.289436	-3.040023	21353.027019
HLA B*4001	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.369802	1.329702	-3.040101	23431.627605
HLA B*4601	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.255961	1.215498	-3.040462	18028.538027
HLA B*4002	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.275508	1.235042	-3.040466	18858.546870
HLA B*0802	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.417868	1.377330	-3.040538	26173.886857
HLA B*5101	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.324627	1.284024	-3.040603	21116.724744
HLA A*0211	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.940660	0.899837	-3.040822	8722.874477
HLA A*0201	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.397400	1.356576	-3.040823	24968.905599
HLA B*0802	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.358713	1.317518	-3.041195	22840.882904
HLA B*4403	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-3.132526	0.091322	-3.041204	1356.831953
HLA A*0212	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.436133	1.394918	-3.041215	27298.143797
HLA A*0203	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.397919	1.356576	-3.041342	24998.775913
HLA B*1509	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.352595	1.311116	-3.041479	22521.371183

HLA B*1509	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.377962	1.336347	-3.041615	23876.035611
HLA A*0211	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.133125	1.091476	-3.041649	13587.036290
HLA A*0101	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.325324	1.283502	-3.041822	21150.681041
HLA A*0219	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.419177	1.377330	-3.041846	26252.875795
HLA A*3002	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-3.944029	0.902116	-3.041913	8790.807792
HLA B*4601	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.381533	1.339557	-3.041976	24073.178449
HLA B*0702	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.335187	1.293038	-3.042149	21636.524162
HLA B*4402	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.396441	1.353717	-3.042724	24913.854140
HLA A*2601	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.382483	1.339557	-3.042926	24125.850211
HLA A*0211	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.234780	1.191820	-3.042960	17170.379853
HLA B*5801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.332403	1.289436	-3.042967	21498.262146
HLA A*3301	1:221-229	9	TQIGDGHAI	1.211106	0.342004	-4.596093	1.553110	-3.042983	39454.187535
HLA A*8001	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.417619	1.374504	-3.043115	26158.881790
HLA A*3002	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.379656	1.336347	-3.043309	23969.346669
HLA A*3001	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.143885	1.100487	-3.043398	13927.891557
HLA B*5801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.329751	1.286148	-3.043602	21367.355996
HLA B*4002	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.329835	1.286148	-3.043687	21371.517822
HLA B*1509	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.456477	1.412655	-3.043822	28607.328812
HLA A*6901	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.072903	1.028966	-3.043937	11827.766325
HLA A*8001	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.333414	1.289436	-3.043977	21548.330742
HLA B*1501	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.259769	1.215498	-3.044271	18187.333289
HLA B*4501	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.426049	1.381752	-3.044297	26671.603574
HLA B*4001	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.330601	1.286148	-3.044453	21409.242397
HLA A*3301	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.566255	1.521566	-3.044688	36834.488635
HLA A*2301	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.457429	1.412655	-3.044774	28670.076331
HLA B*1801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.500431	1.455494	-3.044937	31654.209561
HLA A*0211	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.154077	1.109115	-3.044963	14258.618281
HLA A*2403	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.356136	1.311116	-3.045019	22705.731729
HLA A*0219	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.334638	1.289436	-3.045201	21609.151511
HLA A*0101	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.314834	1.269596	-3.045238	20645.904087
HLA A*2603	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.471728	1.426359	-3.045369	29629.738250
HLA A*0216	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.197266	1.151838	-3.045427	15749.460296
HLA B*2705	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.334861	1.289353	-3.045508	21620.260161
HLA B*4402	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.280658	1.235042	-3.045616	19083.511749
HLA A*3101	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.331936	1.286148	-3.045787	21475.130260
HLA B*4402	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.382135	1.336347	-3.045788	24106.541253
HLA A*2602	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.335244	1.289436	-3.045808	21639.333573
HLA A*2403	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.359150	1.313175	-3.045974	22863.877867
HLA A*0101	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.382337	1.336347	-3.045990	24117.759441
HLA B*1501	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.945946	0.899837	-3.046109	8829.700327
HLA A*8001	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.423516	1.377330	-3.046186	26516.511181
HLA A*8001	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.368503	1.322138	-3.046366	23361.632691
HLA A*6802	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.006910	0.960386	-3.046525	10160.390531
HLA B*5801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.327805	1.281231	-3.046574	21271.857360
HLA A*8001	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.400301	1.353717	-3.046584	25136.286710
HLA B*5801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.336466	1.289353	-3.047113	21700.293804
HLA B*3801	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.473490	1.426359	-3.047131	29750.202671
HLA B*3501	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.327427	1.280105	-3.047322	21253.337806
HLA B*5301	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.575540	1.528166	-3.047374	37630.484479
HLA B*4002	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.635384	1.587869	-3.047515	43190.033633
HLA A*0219	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.442484	1.394918	-3.047566	27700.255513
HLA A*3201	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.030198	0.982586	-3.047612	10720.091603
HLA A*0250	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.422306	1.374504	-3.047802	26442.736536
HLA B*3901	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.282904	1.235042	-3.047862	19182.464550
HLA A*1101	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.442785	1.394918	-3.047866	27719.443636
HLA B*1801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.337586	1.289353	-3.048233	21756.364097
HLA B*5701	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.422266	1.373907	-3.048359	26440.304759
HLA B*4601	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.336195	1.287816	-3.048379	21686.797441
HLA A*2902	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.221094	1.172675	-3.048419	16637.733089
HLA A*3101	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.365954	1.317518	-3.048436	23224.907883
HLA A*8001	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.421322	1.372792	-3.048530	26382.865516
HLA A*0216	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.264144	1.215498	-3.048646	18371.464018
HLA A*2403	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.187661	1.138932	-3.048729	15404.974411
HLA A*3001	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.285921	1.236980	-3.048941	19316.175519
HLA B*3801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.430447	1.381432	-3.049016	26943.087619

HLA A*0301	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.338430	1.289353	-3.049077	21798.659283
HLA B*1517	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.344578	1.295300	-3.049279	22109.472730
HLA B*5801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.350513	1.301147	-3.049367	22413.680902
HLA A*0202	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.077682	1.028301	-3.049380	11958.634386
HLA B*4801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.337203	1.287816	-3.049387	21737.187532
HLA B*1517	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.490399	1.440990	-3.049409	30931.371155
HLA A*2501	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.431263	1.381752	-3.049511	26993.713536
HLA B*2705	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.344877	1.295300	-3.049577	22124.668393
HLA A*2301	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.473852	1.424271	-3.049581	29774.998575
HLA B*1502	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.360787	1.311116	-3.049671	22950.253270
HLA A*6901	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.196956	1.147258	-3.049698	15738.217537
HLA B*4801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.406342	1.356576	-3.049765	25488.345609
HLA A*0250	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.577995	1.528166	-3.049829	37843.824656
HLA A*3301	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.505349	1.455494	-3.049855	32014.663788
HLA B*3501	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.406504	1.356576	-3.049927	25497.861735
HLA B*1509	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-3.776027	0.726094	-3.049932	5970.717315
HLA A*3101	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.319782	1.269596	-3.050186	20882.472630
HLA A*6801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-3.825901	0.775312	-3.050590	6697.325049
HLA B*0702	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.445599	1.394918	-3.050681	27899.678081
HLA B*2705	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.338517	1.287816	-3.050700	21803.023068
HLA A*2902	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.172591	1.121826	-3.050765	14879.604385
HLA A*1101	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.340286	1.289353	-3.050933	21892.022029
HLA A*6801	1:77-85	9	KLDPALLDL	1.284905	0.332102	-4.667947	1.617007	-3.050941	46552.971171
HLA A*0202	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.095002	1.044058	-3.050944	12445.203193
HLA B*1517	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.724051	0.673013	-3.051038	5297.258941
HLA B*0802	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.407810	1.356576	-3.051234	25574.672173
HLA A*0203	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.124620	1.072837	-3.051782	13323.539066
HLA A*0202	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.283863	1.231855	-3.052008	19224.851514
HLA B*4402	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.283995	1.231855	-3.052139	19230.676638
HLA B*5701	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.328228	1.275786	-3.052442	21292.581559
HLA A*3002	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.426956	1.374504	-3.052452	26727.357869
HLA B*1501	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.139783	1.087303	-3.052480	13796.952715
HLA A*1101	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.392101	1.339557	-3.052544	24666.152869
HLA A*0301	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.365738	1.313175	-3.052562	23213.351495
HLA A*0216	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.059863	1.007289	-3.052574	11477.917373
HLA A*6901	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.161788	1.108898	-3.052890	14514.044571
HLA B*3901	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.268450	1.215498	-3.052952	18554.547718
HLA A*0201	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.178973	1.125828	-3.053144	15099.848353
HLA A*0206	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-3.709221	0.656026	-3.053195	5119.425807
HLA B*5101	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.477531	1.424271	-3.053260	30028.320523
HLA B*1503	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.260685	1.207422	-3.053263	18225.746466
HLA B*2705	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.409875	1.356576	-3.053299	25696.576837
HLA A*2501	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.427898	1.374504	-3.053394	26785.402215
HLA B*7301	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.595123	1.541660	-3.053463	39366.134071
HLA B*0802	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.302626	1.249052	-3.053574	20073.633072
HLA B*7301	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.582121	1.528166	-3.053955	38205.045148
HLA B*1517	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.427893	1.373907	-3.053986	26785.112404
HLA B*0801	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.071192	1.017185	-3.054008	11781.275468
HLA A*0219	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.343399	1.289353	-3.054046	22049.510071
HLA A*2902	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.410641	1.356576	-3.054065	25741.935920
HLA A*0301	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.349461	1.295300	-3.054161	22359.424200
HLA A*6901	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.383866	1.329702	-3.054165	24202.848025
HLA B*4002	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.532013	1.477798	-3.054216	34041.857593
HLA A*6801	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.509747	1.455494	-3.054253	32340.533600
HLA B*1801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.435689	1.381432	-3.054257	27270.246554
HLA B*1517	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.408202	1.353717	-3.054485	25597.788089
HLA B*5301	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.596298	1.541660	-3.054637	39472.761427
HLA A*0101	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.338705	1.284024	-3.054681	21812.461265
HLA B*5401	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.338897	1.284024	-3.054873	21822.139657
HLA A*0250	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.596664	1.541660	-3.055004	39506.088237
HLA A*3002	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.146601	1.091476	-3.055125	14015.267180
HLA A*1101	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.335721	1.280105	-3.055616	21663.111105
HLA B*1509	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.432982	1.377330	-3.055652	27100.821627
HLA A*2602	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.404622	1.348830	-3.055792	25387.610360
HLA A*2403	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.385537	1.329702	-3.055835	24296.121885

HLA A*6901	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-3.486514	0.430602	-3.055911	3065.586465
HLA B*1509	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.369116	1.313175	-3.055941	23394.642173
HLA B*3901	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.480360	1.424271	-3.056089	30224.548557
HLA A*3201	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.367474	1.311116	-3.056358	23306.342100
HLA A*2601	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.413052	1.356576	-3.056475	25885.214997
HLA A*0301	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.345927	1.289436	-3.056491	22178.235461
HLA B*5101	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.378679	1.322138	-3.056541	23915.463976
HLA B*0801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.093606	1.036964	-3.056643	12405.275043
HLA A*8001	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.352329	1.295300	-3.057030	22507.607682
HLA A*3002	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.178996	1.121826	-3.057170	15100.665260
HLA A*2902	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.198083	1.140721	-3.057362	15779.138811
HLA B*5401	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.183540	1.125828	-3.057712	15259.488792
HLA A*0206	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.063040	1.005151	-3.057889	11562.176581
HLA B*5401	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.517313	1.459325	-3.057987	32908.836118
HLA A*2603	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.293172	1.235042	-3.058129	19641.364431
HLA B*1509	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.406983	1.348830	-3.058153	25526.017152
HLA A*2403	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.362047	1.303793	-3.058254	23016.898712
HLA B*3901	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.380537	1.322138	-3.058400	24018.022843
HLA A*2403	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.453533	1.394918	-3.058615	28414.067189
HLA B*4402	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.436004	1.377330	-3.058673	27290.022609
HLA B*1801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-3.960250	0.901531	-3.058719	9125.352064
HLA A*2603	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.600381	1.541660	-3.058721	39845.649893
HLA A*6802	1:208-216	9	PANIANALI	0.995189	0.008861	-4.062894	1.004050	-3.058844	11558.299126
HLA A*0203	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-3.958849	0.899837	-3.059012	9095.976630
HLA B*1503	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.290890	1.231855	-3.059035	19538.458816
HLA B*4801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.412824	1.353717	-3.059107	25871.635054
HLA A*6901	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.363182	1.303793	-3.059389	23077.119971
HLA B*7301	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-3.575592	0.516095	-3.059497	3763.500208
HLA A*3101	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.389289	1.329702	-3.059587	24506.939868
HLA B*0803	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.441382	1.381752	-3.059630	27630.062458
HLA B*3901	1:51-59	9	EEIRARQPV	0.859860	0.021658	-3.941177	0.881518	-3.059659	8733.262410
HLA A*2403	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.416529	1.356576	-3.059953	26093.300409
HLA A*6901	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-3.993236	0.933159	-3.060077	9845.468757
HLA A*3001	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.219684	1.159455	-3.060230	16583.815667
HLA A*6801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-3.772742	0.712255	-3.060487	5925.730962
HLA B*3801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.538397	1.477798	-3.060599	34545.923053
HLA A*3101	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.353718	1.293038	-3.060680	22579.685170
HLA A*0101	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.348624	1.287816	-3.060808	22316.403167
HLA B*1502	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.589038	1.528166	-3.060872	38818.397339
HLA A*3001	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.251071	1.190075	-3.060996	17826.711331
HLA A*2403	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.434923	1.373907	-3.061016	27222.194482
HLA A*0216	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.324145	1.263068	-3.061077	21093.318702
HLA B*1517	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.465594	0.404390	-3.061204	2921.418368
HLA B*4402	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.374405	1.313175	-3.061230	23681.275904
HLA A*0101	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.347379	1.286148	-3.061231	22252.508300
HLA A*0211	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.191641	1.130410	-3.061231	15546.799899
HLA A*8001	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.417856	1.356576	-3.061280	26173.178877
HLA A*6802	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.401100	1.339557	-3.061543	25182.563995
HLA A*0202	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.095157	1.033365	-3.061792	12449.647580
HLA A*2402	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.474514	1.412655	-3.061859	29820.457644
HLA B*0702	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.324960	1.263086	-3.061874	21132.952934
HLA B*1801	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.398316	1.336347	-3.061969	25021.642027
HLA B*1501	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.337838	1.275786	-3.062052	21768.961591
HLA B*1801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.503171	1.440990	-3.062181	31854.513209
HLA A*3001	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.269780	1.207422	-3.062358	18611.448763
HLA A*2902	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.886988	0.824605	-3.062383	7708.821465
HLA B*3501	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.244808	1.182210	-3.062598	17571.446112
HLA B*3901	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.188582	1.125828	-3.062754	15437.678044
HLA B*4402	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.325879	1.263068	-3.062811	21177.702076
HLA A*0101	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.374076	1.311116	-3.062960	23663.346864
HLA A*3301	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.358358	1.295300	-3.063058	22822.231959
HLA B*2705	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.140869	1.077535	-3.063333	13831.479518
HLA A*0203	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.245552	1.182210	-3.063342	17601.605851
HLA B*1801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.487740	1.424271	-3.063469	30742.526440
HLA A*2902	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.417236	1.353717	-3.063519	26135.824744

HLA A*1101	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.400024	1.336347	-3.063677	25120.245656
HLA A*2403	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.364951	1.301147	-3.063804	23171.319738
HLA B*5801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.204558	1.140721	-3.063837	16016.162901
HLA A*3101	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.141404	1.077535	-3.063869	13848.550547
HLA A*0216	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.189832	1.125828	-3.064004	15482.172621
HLA B*0802	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.377187	1.313175	-3.064011	23833.448624
HLA B*3901	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.292436	1.228069	-3.064367	19608.133943
HLA B*5301	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.120203	1.055834	-3.064368	13188.717562
HLA A*2602	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.592599	1.528166	-3.064433	39138.071324
HLA B*5801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.359775	1.295300	-3.064475	22896.803370
HLA B*0801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.224078	1.159455	-3.064623	16752.437208
HLA A*3201	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.606393	1.541660	-3.064733	40401.105302
HLA A*2403	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.418517	1.353717	-3.064800	26212.997048
HLA A*6802	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.085858	1.020917	-3.064941	12185.905225
HLA B*0702	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.413827	1.348830	-3.064997	25931.468199
HLA A*2601	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.394792	1.329702	-3.065090	24819.417183
HLA B*0801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.358151	1.293038	-3.065113	22811.369560
HLA B*0802	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.345250	1.280105	-3.065146	22143.707609
HLA B*1502	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.328381	1.263068	-3.065313	21300.070259
HLA B*4801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.414149	1.348830	-3.065319	25950.694555
HLA A*2403	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.354679	1.289353	-3.065326	22629.701303
HLA A*3301	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.419245	1.353717	-3.065528	26256.994848
HLA A*0211	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.093860	1.028301	-3.065559	12412.525166
HLA A*0250	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.568926	1.503120	-3.065806	37061.757447
HLA A*8001	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.304057	1.237896	-3.066161	20139.877180
HLA A*8001	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.461139	1.394918	-3.066221	28916.031290
HLA B*4801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.440170	1.373907	-3.066262	27553.040614
HLA A*8001	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.402611	1.336347	-3.066263	25270.315559
HLA B*1509	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.367481	1.301147	-3.066335	23306.720358
HLA B*1509	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.350917	1.284024	-3.066893	22434.546559
HLA A*2501	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.406537	1.339557	-3.066980	25499.792977
HLA A*2601	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.356417	1.289436	-3.066981	22720.476774
HLA A*0206	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.471430	0.404390	-3.067040	2960.941836
HLA B*1509	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.491313	1.424271	-3.067042	30996.533123
HLA B*1502	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.350579	1.283502	-3.067077	22417.076314
HLA B*1509	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.448841	1.381752	-3.067090	28108.746674
HLA A*0250	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.495481	1.428368	-3.067114	31295.443342
HLA B*4601	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.389484	1.322138	-3.067347	24517.946465
HLA B*3501	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.389606	1.322138	-3.067469	24524.844683
HLA A*0201	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.397437	1.329702	-3.067735	24971.066957
HLA B*0802	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.440569	1.372792	-3.067777	27578.392282
HLA A*0216	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.407721	1.339557	-3.068164	25569.415180
HLA A*2601	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.390316	1.322138	-3.068178	24564.945793
HLA B*4001	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.363778	1.295300	-3.068479	23108.852311
HLA B*3501	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.089504	1.020917	-3.068587	12288.650617
HLA B*0802	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.443229	1.374504	-3.068725	27747.800403
HLA A*0211	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.169377	1.100487	-3.068890	14769.890955
HLA B*4501	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.656792	1.587869	-3.068923	45372.431075
HLA A*0216	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.095547	1.026553	-3.068994	12460.832903
HLA A*0216	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.372864	1.303793	-3.069071	23597.382677
HLA B*1517	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.464083	1.394918	-3.069165	29112.707081
HLA B*3901	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.510302	1.440990	-3.069312	32381.850223
HLA A*2402	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.493649	1.424271	-3.069378	31163.663768
HLA B*0802	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.423298	1.353717	-3.069581	26503.173557
HLA A*3001	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.279810	1.210159	-3.069651	19046.278592
HLA B*4002	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.591241	1.521566	-3.069675	39015.881004
HLA A*3101	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.357494	1.287816	-3.069677	22776.841763
HLA B*4402	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.362731	1.293038	-3.069692	23053.162240
HLA B*1502	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.052312	0.982586	-3.069725	11280.071416
HLA A*0101	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.370987	1.301147	-3.069840	23495.603087
HLA A*0216	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.273819	1.203805	-3.070014	18785.335065
HLA A*0219	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.229508	1.159455	-3.070053	16963.195160
HLA B*5801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.354200	1.284024	-3.070176	22604.740548
HLA B*0803	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.480360	1.410054	-3.070306	30224.548557
HLA B*1517	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.161817	1.091476	-3.070341	14514.986834

HLA B*5101	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.444283	1.373907	-3.070376	27815.282852
HLA B*1801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.333592	1.263068	-3.070524	21557.192194
HLA B*0702	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.371931	1.301147	-3.070784	23546.756350
HLA B*0801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.427407	1.356576	-3.070831	26755.133964
HLA A*3201	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.599131	1.528166	-3.070965	39731.136548
HLA A*2301	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.526555	1.455494	-3.071061	33616.724652
HLA B*1801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.443877	1.372792	-3.071085	27789.262406
HLA A*0206	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.261205	1.190075	-3.071129	18247.549935
HLA A*6802	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.427882	1.356576	-3.071305	26784.387892
HLA A*0203	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.401102	1.329702	-3.071401	25182.700230
HLA A*0101	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.401114	1.329702	-3.071412	25183.381418
HLA B*1503	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.001229	0.929716	-3.071514	10028.346847
HLA B*5701	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.389141	1.317518	-3.071623	24498.588762
HLA A*3001	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.151239	1.079304	-3.071935	14165.739945
HLA B*2705	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.341533	1.269596	-3.071938	21955.000585
HLA B*4402	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.389794	1.317518	-3.072276	24535.461115
HLA B*0702	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.321525	1.249052	-3.072474	20966.466220
HLA B*5401	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.211894	1.139224	-3.072669	16288.967979
HLA A*0101	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.362049	1.289353	-3.072696	23017.023231
HLA A*2602	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.614534	1.541660	-3.072874	41165.577495
HLA B*1503	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.116185	1.043287	-3.072898	13067.272521
HLA A*0250	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.366177	1.293038	-3.073139	23236.847148
HLA B*0803	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.336226	1.263068	-3.073158	21688.322696
HLA B*0702	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.354472	1.281231	-3.073241	22618.930540
HLA B*3801	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.450648	1.377330	-3.073318	28225.928397
HLA B*0801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.374480	1.301147	-3.073334	23685.375878
HLA A*2902	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.277160	1.203805	-3.073355	18930.405349
HLA A*2603	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.422318	1.348830	-3.073488	26443.451807
HLA B*5701	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.403233	1.329702	-3.073532	25306.569585
HLA B*3501	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.468554	1.394918	-3.073636	29413.971053
HLA A*3001	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.213280	1.139224	-3.074055	16341.042733
HLA A*8001	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.413952	1.339557	-3.074395	25938.904442
HLA B*4002	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.569993	1.495512	-3.074481	37152.896324
HLA B*1517	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.363926	1.289436	-3.074490	23116.729683
HLA A*0219	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.130540	1.055834	-3.074706	13506.421596
HLA A*8001	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.387973	1.313175	-3.074798	24432.807515
HLA B*7301	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.570477	1.495512	-3.074965	37194.323972
HLA A*2501	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.469947	1.394918	-3.075029	29508.484484
HLA B*0803	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.452525	1.377330	-3.075195	28348.199080
HLA B*0803	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.397381	1.322138	-3.075243	24967.824990
HLA A*2501	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.303765	1.228391	-3.075374	20126.371352
HLA A*2501	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-3.856614	0.781170	-3.075444	7188.095616
HLA B*0802	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.449358	1.373907	-3.075451	28142.220935
HLA A*0212	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.368536	1.293038	-3.075498	23363.402132
HLA A*2603	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.603825	1.528166	-3.075659	40162.918105
HLA A*2902	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.470652	1.394918	-3.075734	29556.414657
HLA A*6901	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.357186	1.281231	-3.075955	22760.705636
HLA A*0203	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.325014	1.249052	-3.075963	21135.582617
HLA B*4801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.398417	1.322138	-3.076279	25027.463369
HLA A*0101	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.365837	1.289436	-3.076400	23218.626524
HLA B*4402	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.415989	1.339557	-3.076432	26060.853372
HLA B*4601	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.360094	1.283502	-3.076592	22913.655775
HLA B*3801	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.489335	1.412655	-3.076680	30855.661077
HLA A*3001	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.127754	1.050933	-3.076820	13420.040073
HLA A*6801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.357054	1.280105	-3.076949	22753.811239
HLA B*1503	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.082329	1.005151	-3.077178	12087.287989
HLA A*6901	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.340279	1.263068	-3.077211	21891.666732
HLA B*1801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.365134	1.287816	-3.077318	23181.099435
HLA A*3001	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.259630	1.182210	-3.077421	18181.529119
HLA B*1503	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.472365	1.394918	-3.077446	29673.209674
HLA B*4601	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.407380	1.329702	-3.077678	25549.365528
HLA B*4801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.390884	1.313175	-3.077709	24597.127113
HLA A*2602	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.208191	1.130410	-3.077781	16150.678841
HLA B*3801	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.431516	1.353717	-3.077799	27009.489708
HLA B*5101	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.459346	1.381432	-3.077914	28796.919275

HLA A*2301	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.455253	1.377330	-3.077923	28526.811086
HLA B*4402	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.364100	1.286148	-3.077952	23125.985897
HLA A*2402	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.315057	1.236980	-3.078077	20656.517560
HLA B*1503	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.407890	1.329702	-3.078188	25579.376714
HLA A*0206	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-3.764491	0.686294	-3.078197	5814.207654
HLA B*4402	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.157508	1.079304	-3.078204	14371.685033
HLA A*0201	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.282099	1.203805	-3.078294	19146.902727
HLA A*1101	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.366177	1.287816	-3.078361	23236.847148
HLA B*1517	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.408071	1.329702	-3.078369	25590.034316
HLA B*5801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.313791	1.235408	-3.078383	20596.372327
HLA A*1101	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.379541	1.301147	-3.078394	23962.993607
HLA B*1517	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.313438	1.235042	-3.078396	20579.665493
HLA B*0702	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.434972	1.356576	-3.078396	27225.287308
HLA B*4403	1:391-399	9	GLPEEIVAR	0.998590	0.589279	-4.666427	1.587869	-3.078558	46390.311378
HLA B*3801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.488806	1.410054	-3.078752	30818.125642
HLA A*0203	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.192618	1.113845	-3.078773	15581.827588
HLA A*0201	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.342079	1.263086	-3.078992	21982.573481
HLA B*3501	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.354857	1.275786	-3.079071	22639.007454
HLA A*6901	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.261310	1.182210	-3.079100	18251.992751
HLA B*5301	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.342224	1.263086	-3.079138	21989.947961
HLA A*6801	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.600769	1.521566	-3.079202	39881.233263
HLA A*0202	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.316403	1.236980	-3.079423	20720.649354
HLA A*2601	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.360809	1.281231	-3.079578	22951.370722
HLA B*1509	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.409513	1.329702	-3.079812	25675.177345
HLA B*4001	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.363901	1.284024	-3.079877	23115.354075
HLA A*0301	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.366126	1.286148	-3.079977	23234.081719
HLA B*1502	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.539379	1.459325	-3.080053	34624.131306
HLA B*1801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.475019	1.394918	-3.080101	29855.162778
HLA A*8001	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.360423	1.280105	-3.080319	22931.016796
HLA A*0203	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-3.995506	0.915104	-3.080402	9897.055390
HLA B*1501	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.410246	1.329702	-3.080545	25718.550697
HLA A*0201	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.315699	1.235042	-3.080656	20687.047704
HLA A*8001	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.384538	1.303793	-3.080746	24240.324341
HLA A*2403	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.361997	1.281231	-3.080767	23014.283964
HLA B*0802	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.320040	1.239243	-3.080797	20894.903233
HLA A*0203	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.189776	1.108898	-3.080877	15480.162588
HLA A*2301	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.320292	1.239243	-3.081049	20907.001919
HLA A*0219	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.011078	0.929716	-3.081363	10258.370668
HLA B*0801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.202270	1.120820	-3.081450	15931.991976
HLA B*4601	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.195311	1.113845	-3.081466	15678.730835
HLA B*0702	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.361683	1.280105	-3.081578	22997.606377
HLA B*4801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.365606	1.284024	-3.081582	23206.319987
HLA A*6802	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.383037	1.301147	-3.081890	24156.672172
HLA B*2705	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.418369	1.336347	-3.082021	26204.064578
HLA B*2705	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.411856	1.329702	-3.082154	25814.034647
HLA B*4001	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.386007	1.303793	-3.082214	24322.423977
HLA B*3901	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.456202	1.373907	-3.082295	28589.227332
HLA A*0201	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.386218	1.303793	-3.082426	24334.269206
HLA A*3101	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.310847	1.228069	-3.082778	20457.230068
HLA B*7301	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.560700	1.477798	-3.082903	36366.412659
HLA B*4601	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.315675	1.232655	-3.083020	20685.928588
HLA A*0301	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.315687	1.232655	-3.083032	20686.488139
HLA A*2603	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.604669	1.521566	-3.083102	40240.996320
HLA B*0802	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.422875	1.339557	-3.083318	26477.377858
HLA B*4001	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.353314	1.269596	-3.083718	22558.684524
HLA A*2601	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.371586	1.287816	-3.083769	23528.038149
HLA A*0101	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.387595	1.303793	-3.083802	24411.535996
HLA A*8001	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.413557	1.329702	-3.083855	25915.340284
HLA B*0803	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.457953	1.373907	-3.084045	28704.684934
HLA B*3501	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.198111	1.113845	-3.084267	15780.163205
HLA B*4002	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.496950	1.412655	-3.084295	31401.437984
HLA B*4001	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.364474	1.280105	-3.084369	23145.886789
HLA A*0203	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.011600	0.926967	-3.084633	10270.698325
HLA B*4801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.320052	1.235408	-3.084644	20895.468436
HLA B*4402	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.441236	1.356576	-3.084660	27620.796526

HLA B*4601	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.395818	1.311116	-3.084702	24878.162715
HLA A*0212	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.347797	1.263086	-3.084711	22273.946902
HLA A*0301	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.368964	1.284024	-3.084940	23386.417062
HLA B*3801	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.509275	1.424271	-3.085004	32305.386014
HLA A*0301	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.346089	1.260962	-3.085127	22186.515751
HLA B*4403	1:118-126	9	TELKVLGGK	0.614308	0.199612	-3.899125	0.813920	-3.085205	7927.302431
HLA B*1502	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-3.909853	0.824605	-3.085248	8125.557644
HLA B*7301	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.378305	1.293038	-3.085267	23894.901400
HLA A*0212	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.441847	1.356576	-3.085271	27659.674478
HLA A*0206	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.185772	1.100487	-3.085285	15338.115200
HLA A*3301	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.497974	1.412655	-3.085319	31475.592342
HLA A*2602	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.588497	1.503120	-3.085377	38770.126634
HLA B*5401	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.177375	1.091915	-3.085460	15044.402217
HLA B*4402	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.389320	1.303793	-3.085527	24508.663467
HLA A*0219	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.415244	1.329702	-3.085542	26016.199007
HLA B*4801	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.102746	1.017185	-3.085561	12669.103797
HLA B*0803	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.367063	1.281231	-3.085832	23284.287715
HLA A*2902	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.348955	1.263068	-3.085887	22333.432488
HLA A*0301	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.314087	1.228069	-3.086018	20610.416549
HLA B*1502	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.366255	1.280105	-3.086150	23240.995907
HLA A*0212	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.130230	1.044058	-3.086173	13496.780031
HLA A*2902	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.379325	1.293038	-3.086287	23951.069958
HLA B*2705	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.379424	1.293038	-3.086385	23956.512627
HLA B*1503	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.296729	1.210159	-3.086569	19802.899071
HLA A*0211	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.542132	1.455494	-3.086638	34844.359232
HLA A*0206	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.207566	1.120820	-3.086745	16127.454236
HLA B*5401	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.397867	1.311116	-3.086751	24995.800797
HLA B*4601	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.379790	1.293038	-3.086752	23976.739085
HLA A*0211	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.390781	1.303793	-3.086988	24591.272830
HLA A*0211	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.511446	1.424271	-3.087175	32467.276447
HLA A*0206	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.277653	1.190433	-3.087220	18951.923963
HLA A*0203	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.277296	1.190075	-3.087221	18936.346142
HLA B*3801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.528221	1.440990	-3.087231	33745.912944
HLA A*0216	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.208064	1.120820	-3.087244	16145.961368
HLA B*0803	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.460199	1.372792	-3.087407	28853.525934
HLA A*2601	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.380777	1.293038	-3.087739	24031.279854
HLA A*0216	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.143707	1.055834	-3.087872	13922.166260
HLA A*6901	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.363825	1.275786	-3.088039	23111.352773
HLA A*3002	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.469594	1.381432	-3.088163	29484.548553
HLA A*2402	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.351333	1.263068	-3.088265	22456.039056
HLA A*0203	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-3.881439	0.793168	-3.088271	7610.943606
HLA B*7301	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.591399	1.503120	-3.088279	39030.025364
HLA B*1501	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.298451	1.210159	-3.088292	19881.582357
HLA B*2705	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.115109	1.026553	-3.088556	13034.935436
HLA A*2403	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.327845	1.239243	-3.088602	21273.813783
HLA A*6802	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.304111	1.215498	-3.088613	20142.383289
HLA B*1503	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.364415	1.275786	-3.088629	23142.756584
HLA A*0301	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.364450	1.275786	-3.088664	23144.634656
HLA B*4402	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.372746	1.284024	-3.088722	23591.000579
HLA A*2301	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.445371	1.356576	-3.088795	27885.041308
HLA B*4801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.392731	1.303793	-3.088938	24701.941035
HLA B*3901	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.437989	1.348830	-3.089159	27415.060605
HLA A*0212	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.281246	1.191820	-3.089426	19109.339131
HLA B*0802	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.384849	1.295300	-3.089549	24257.640669
HLA A*2601	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.373141	1.283502	-3.089639	23612.451275
HLA B*4402	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.419344	1.329702	-3.089642	26262.961518
HLA A*2601	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.393671	1.303793	-3.089878	24755.452818
HLA A*8001	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.401058	1.311116	-3.089942	25180.111887
HLA B*5801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.350908	1.260962	-3.089946	22434.061091
HLA A*2601	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.318349	1.228391	-3.089958	20813.673377
HLA A*0219	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.255204	1.165167	-3.090037	17997.159934
HLA A*6802	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.134107	1.044058	-3.090049	13617.795879
HLA B*4001	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.373595	1.283502	-3.090092	23637.118114
HLA B*0803	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.464954	1.374504	-3.090450	29171.196966
HLA A*3002	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.467790	1.377330	-3.090460	29362.300436

HLA A*0216	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.485449	1.394918	-3.090531	30580.797527
HLA B*4002	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.632219	1.541660	-3.090559	42876.446606
HLA B*0803	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.444328	1.353717	-3.090611	27818.142073
HLA A*0202	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-3.863324	0.772641	-3.090683	7300.018734
HLA A*0201	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.053830	0.962975	-3.090855	11319.561844
HLA B*4601	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.375068	1.284024	-3.091044	23717.431364
HLA A*2403	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.386409	1.295300	-3.091109	24344.934844
HLA B*1501	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.183032	1.091915	-3.091118	15241.667943
HLA A*2902	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.301343	1.210159	-3.091184	20014.427070
HLA A*0206	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.515579	1.424271	-3.091308	32777.709585
HLA B*4801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.372551	1.281231	-3.091320	23580.410107
HLA A*2601	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.354493	1.263086	-3.091407	22620.031860
HLA B*4501	1:7-15	9	IDVPETPAR	1.034494	0.493672	-4.619588	1.528166	-3.091422	41647.405801
HLA B*4601	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.319505	1.228069	-3.091436	20869.146205
HLA B*5701	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.386766	1.295300	-3.091466	24364.961994
HLA B*4402	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.413902	1.322138	-3.091765	25935.957751
HLA B*4801	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.421839	1.329702	-3.092137	26414.284452
HLA A*3002	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.431812	1.339557	-3.092255	27027.906896
HLA A*2403	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.376311	1.284024	-3.092287	23785.403870
HLA B*4601	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.393546	1.301147	-3.092400	24748.355850
HLA A*2603	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.410007	1.317518	-3.092489	25704.362892
HLA B*2705	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.372699	1.280105	-3.092595	23588.448223
HLA B*3801	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.422398	1.329702	-3.092696	26448.316164
HLA A*2601	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.325508	1.232655	-3.092852	21159.607905
HLA B*3801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.465744	1.372792	-3.092952	29224.270337
HLA B*5401	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.503194	1.410054	-3.093140	31856.236549
HLA A*2601	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.394301	1.301147	-3.093154	24791.370550
HLA A*0250	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.474756	1.381432	-3.093325	29837.078788
HLA B*4403	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.615006	1.521566	-3.093440	41210.364784
HLA A*0201	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.098691	1.005151	-3.093540	12551.357021
HLA B*0803	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.342887	1.249052	-3.093835	22023.521181
HLA A*0203	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.397642	1.303793	-3.093849	24982.822614
HLA A*0206	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.423554	1.329702	-3.093852	26518.806502
HLA A*6801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.649206	0.555251	-3.093955	4458.676965
HLA A*2603	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.549484	1.455494	-3.093990	35439.209095
HLA A*2402	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.475762	1.381752	-3.094010	29906.244575
HLA B*3501	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.241304	1.147258	-3.094046	17430.282374
HLA A*6802	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.375667	1.281231	-3.094436	23750.172655
HLA B*5401	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.448167	1.353717	-3.094450	28065.137824
HLA A*1101	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.220291	1.125828	-3.094463	16606.978712
HLA A*6901	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.138599	1.044058	-3.094541	13759.385401
HLA B*1502	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.504675	1.410054	-3.094621	31964.995167
HLA A*3301	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.123816	1.028966	-3.094850	13298.910884
HLA A*8001	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.378972	1.284024	-3.094949	23931.641947
HLA B*4001	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.298850	1.203805	-3.095046	19899.875484
HLA A*0216	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.451637	1.356576	-3.095061	28290.288000
HLA A*2601	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.381324	1.286148	-3.095176	24061.590482
HLA A*2403	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.381392	1.286148	-3.095244	24065.365724
HLA B*3501	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.469383	1.373907	-3.095476	29470.196314
HLA B*5101	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.470043	1.374504	-3.095539	29515.030353
HLA B*4402	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.332692	1.236980	-3.095712	21512.572202
HLA B*5801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.359143	1.263086	-3.096057	22863.506797
HLA B*3801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.371917	1.275786	-3.096131	23545.992051
HLA B*1517	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.324201	1.228069	-3.096132	21096.057580
HLA B*0801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.187684	1.091476	-3.096208	15405.807826
HLA A*2403	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.379807	1.283502	-3.096304	23977.647083
HLA B*5301	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.477754	1.381432	-3.096323	30043.757228
HLA A*0202	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.377676	1.281231	-3.096445	23860.282472
HLA B*3801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.445327	1.348830	-3.096497	27882.175210
HLA B*3901	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.376604	1.280105	-3.096500	23801.493859
HLA A*2603	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.473854	1.377330	-3.096524	29775.159655
HLA A*2603	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.131048	1.034513	-3.096534	13522.213562
HLA A*3201	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.469416	1.372792	-3.096624	29472.428426
HLA B*5401	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.001878	0.905240	-3.096637	10043.331651
HLA A*0219	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.453230	1.356576	-3.096654	28394.244619

HLA B*1501	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.328536	1.231855	-3.096681	21307.676864
HLA B*4402	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.384510	1.287816	-3.096694	24238.750743
HLA A*0212	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.426444	1.329702	-3.096742	26695.855383
HLA B*5701	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.366511	1.269596	-3.096915	23254.704651
HLA A*0201	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-3.910187	0.813260	-3.096926	8131.802131
HLA A*2501	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.357945	1.260962	-3.096982	22800.512330
HLA B*1503	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.024649	0.927581	-3.097068	10583.980056
HLA A*3101	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.381228	1.284024	-3.097204	24056.254082
HLA A*8001	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.386651	1.289353	-3.097298	24358.504075
HLA B*1509	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.492626	1.394918	-3.097708	31090.412488
HLA B*5701	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.408827	1.311116	-3.097711	25634.650604
HLA B*4002	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.390835	1.293038	-3.097797	24594.332850
HLA B*5301	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.553387	1.455494	-3.097892	35759.094723
HLA B*0801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.189827	1.091915	-3.097913	15482.005109
HLA B*1503	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.238379	1.140437	-3.097943	17313.278456
HLA B*3501	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.333479	1.235408	-3.098071	21551.595064
HLA A*2902	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.359070	1.260962	-3.098108	22859.672758
HLA B*4402	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.305600	1.207422	-3.098178	20211.587653
HLA B*3501	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.361490	1.263086	-3.098404	22987.406651
HLA B*1501	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.337654	1.239243	-3.098411	21759.777651
HLA B*1503	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.565297	0.466612	-3.098684	3675.331367
HLA A*2902	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.336694	1.237896	-3.098798	21711.684222
HLA B*0801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.380182	1.281231	-3.098952	23998.410694
HLA B*1801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.472971	1.373907	-3.099063	29714.655015
HLA B*5301	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.540077	1.440990	-3.099087	34679.807898
HLA B*5801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.362272	1.263068	-3.099204	23028.855628
HLA A*0101	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.380589	1.281231	-3.099358	24020.881580
HLA A*2602	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.291215	1.191820	-3.099395	19553.050986
HLA B*5701	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.388878	1.289436	-3.099442	24483.749378
HLA B*3901	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.494417	1.394918	-3.099499	31218.842133
HLA B*1503	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.213003	1.113445	-3.099558	16330.614481
HLA B*1509	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.387381	1.287816	-3.099565	24399.521157
HLA B*4601	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.187130	1.087303	-3.099827	15386.151260
HLA B*4001	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.381080	1.281231	-3.099849	24048.056554
HLA B*5301	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.387797	1.287816	-3.099981	24422.896117
HLA A*0216	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.331992	1.231855	-3.100137	21477.918715
HLA B*0702	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.315666	1.215498	-3.100167	20685.480959
HLA B*4801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.369908	1.269596	-3.100313	23437.332612
HLA A*3002	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.474228	1.373907	-3.100320	29800.782443
HLA B*5801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.200809	1.100487	-3.100322	15878.471700
HLA B*5401	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.473276	1.372792	-3.100485	29735.560254
HLA A*0212	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.404373	1.303793	-3.100580	25373.056053
HLA A*8001	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.336017	1.235408	-3.100609	21677.882713
HLA B*4402	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.380810	1.280105	-3.100705	24033.100015
HLA B*0702	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.387024	1.286148	-3.100876	24379.465601
HLA A*0211	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.214727	1.113845	-3.100882	16395.589962
HLA A*3001	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.252723	1.151838	-3.100885	17894.638111
HLA B*1502	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.604032	1.503120	-3.100912	40182.043027
HLA B*5101	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.384433	1.283502	-3.100931	24234.423873
HLA B*5401	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.556619	1.455494	-3.101125	36026.278917
HLA A*0201	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.192618	1.091476	-3.101142	15581.827588
HLA A*0301	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.311439	1.210159	-3.101280	20485.138267
HLA B*5101	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.387499	1.286148	-3.101350	24406.121985
HLA B*5801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.336409	1.235042	-3.101367	21697.476478
HLA B*5301	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.440985	1.339557	-3.101428	27604.812630
HLA B*0802	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.377431	1.275786	-3.101645	23846.861774
HLA B*5401	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.215131	1.113445	-3.101687	16410.853173
HLA A*0201	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.232160	1.130410	-3.101750	17067.119416
HLA A*0206	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.008212	0.906227	-3.101985	10190.887698
HLA A*2602	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-3.976654	0.874608	-3.102046	9476.625823
HLA B*3801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.382339	1.280105	-3.102235	24117.889916
HLA A*0301	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.365632	1.263086	-3.102546	23207.701008
HLA B*4001	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.318079	1.215498	-3.102580	20800.728442
HLA A*0201	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.384038	1.281231	-3.102807	24212.408148
HLA B*4601	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.338239	1.235408	-3.102831	21789.109181

HLA A*3002	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.416017	1.313175	-3.102841	26062.545263
HLA A*2301	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.414029	1.311116	-3.102913	25943.535633
HLA A*1101	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.420490	1.317518	-3.102972	26332.388020
HLA A*0301	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.366055	1.263068	-3.102987	23230.311211
HLA A*2402	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.456705	1.353717	-3.102988	28622.344712
HLA B*5701	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.384423	1.281231	-3.103192	24233.899457
HLA B*3801	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.498131	1.394918	-3.103213	31487.003134
HLA B*4001	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.364220	1.260962	-3.103258	23132.367337
HLA A*8001	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.389705	1.286148	-3.103557	24530.417737
HLA A*2301	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.421082	1.317518	-3.103564	26368.311237
HLA B*4501	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.197698	1.094025	-3.103673	15765.145423
HLA B*4001	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.335596	1.231855	-3.103741	21656.900659
HLA B*2705	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.407815	1.303793	-3.104022	25574.948886
HLA B*4601	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.367277	1.263086	-3.104190	23295.753389
HLA B*0702	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.415364	1.311116	-3.104248	26023.377979
HLA A*2402	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.417452	1.313175	-3.104277	26148.836037
HLA B*5701	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.387795	1.283502	-3.104293	24422.763992
HLA B*5101	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.477101	1.372792	-3.104310	29998.606904
HLA B*7301	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.181919	1.077535	-3.104383	15202.633994
HLA A*0203	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-3.508387	0.403979	-3.104408	3223.942410
HLA B*4601	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.365451	1.260962	-3.104489	23198.035588
HLA A*1101	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.458387	1.353717	-3.104670	28733.427810
HLA A*0250	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.528945	1.424271	-3.104674	33802.188803
HLA A*6802	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.434458	1.329702	-3.104756	27193.050821
HLA B*3501	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.085628	0.980728	-3.104900	12179.446347
HLA A*2601	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.385116	1.280105	-3.105012	24272.605634
HLA B*5401	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.546016	1.440990	-3.105026	35157.353943
HLA A*2902	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.406335	1.301147	-3.105188	25487.931945
HLA A*0211	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.148537	1.043307	-3.105231	14077.883178
HLA B*4601	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.394881	1.289436	-3.105445	24824.519979
HLA A*3001	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.219487	1.113845	-3.105642	16576.281185
HLA A*3002	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.020801	0.915104	-3.105697	10490.605518
HLA B*4501	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.647453	1.541660	-3.105793	44407.144391
HLA B*1509	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.321478	1.215498	-3.105980	20964.197817
HLA A*0211	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.135235	1.028966	-3.106269	13653.203799
HLA A*2501	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.428645	1.322138	-3.106508	26831.522001
HLA A*2402	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.376118	1.269596	-3.106522	23774.854745
HLA A*6901	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.006441	0.899837	-3.106603	10149.403159
HLA A*3001	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.134967	1.028301	-3.106665	13644.786091
HLA A*3002	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.547734	1.440990	-3.106744	35296.663510
HLA B*1501	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.335173	1.228391	-3.106782	21635.821866
HLA A*0301	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.245808	1.138932	-3.106876	17611.988190
HLA A*6901	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.013104	0.906227	-3.106876	10306.320494
HLA B*5301	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.194263	1.087303	-3.106960	15640.946629
HLA B*5101	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.501888	1.394918	-3.106970	31760.560192
HLA A*3002	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.535566	1.428368	-3.107198	34321.453512
HLA B*5801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.344214	1.236980	-3.107234	22090.940982
HLA B*5401	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-3.571330	0.463883	-3.107447	3726.747584
HLA A*0206	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.562949	1.455494	-3.107454	36555.179401
HLA A*1101	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.396991	1.289436	-3.107554	24945.412910
HLA A*8001	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.342631	1.235042	-3.107588	22010.538225
HLA B*5701	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.400630	1.293038	-3.107592	25155.331754
HLA B*0801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.368576	1.260962	-3.107614	23365.550919
HLA B*3501	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.388932	1.281231	-3.107701	24486.796018
HLA B*5801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.134276	1.026553	-3.107723	13623.101207
HLA B*0702	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.397294	1.289436	-3.107858	24962.827783
HLA A*6801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.489781	1.381752	-3.108029	30887.393267
HLA B*5401	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.532340	1.424271	-3.108069	34067.465832
HLA A*6901	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.336496	1.228391	-3.108105	21701.820008
HLA B*1502	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.536536	1.428368	-3.108168	34398.223125
HLA A*3001	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-3.883816	0.775634	-3.108182	7652.726331
HLA A*2501	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.397649	1.289436	-3.108212	24983.228080
HLA A*2402	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.464888	1.356576	-3.108312	29166.778539
HLA A*0101	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.234155	1.125828	-3.108327	17145.688922
HLA A*3001	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.300159	1.191820	-3.108340	19959.930379

HLA B*2705	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-3.386496	0.278063	-3.108433	2434.983336
HLA B*1502	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.521152	1.412655	-3.108497	33201.031861
HLA A*0301	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.346573	1.237896	-3.108677	22211.255011
HLA B*5101	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.403983	1.295300	-3.108683	25350.280221
HLA B*1501	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.371774	1.263086	-3.108687	23538.223079
HLA B*5801	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.347943	1.239243	-3.108700	22281.419129
HLA A*2601	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.392881	1.284024	-3.108857	24710.495141
HLA B*1801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.404288	1.295300	-3.108989	25368.114979
HLA A*3101	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.324573	1.215498	-3.109074	21114.097407
HLA A*0101	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.384888	1.275786	-3.109102	24259.871701
HLA B*0801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.248499	1.138932	-3.109566	17721.421117
HLA B*2705	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.372718	1.263086	-3.109632	23589.469133
HLA A*8001	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.379240	1.269596	-3.109645	23946.405798
HLA A*0250	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.338075	1.228391	-3.109684	21780.859376
HLA B*3901	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.346714	1.236980	-3.109734	22218.465807
HLA A*3101	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.358814	1.249052	-3.109762	22846.196888
HLA B*0801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.385598	1.275786	-3.109812	24299.539548
HLA A*2602	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.144407	1.034513	-3.109894	13944.628939
HLA B*1503	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-3.928433	0.818458	-3.109975	8480.723481
HLA A*0201	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.717773	0.607629	-3.110145	5221.236661
HLA B*4801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.396342	1.286148	-3.110194	24908.193973
HLA B*4601	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.386094	1.275786	-3.110308	24327.292984
HLA A*3002	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.398140	1.287816	-3.110323	25011.491763
HLA B*0803	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.467088	1.356576	-3.110511	29314.843638
HLA B*7301	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.538890	1.428368	-3.110523	34585.192174
HLA A*2602	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.338608	1.228069	-3.110539	21807.623679
HLA A*6901	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.115833	1.005094	-3.110739	13056.672948
HLA A*0101	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.346272	1.235408	-3.110864	22195.879800
HLA A*2402	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.128102	1.017185	-3.110917	13430.789313
HLA A*3201	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.424179	1.313175	-3.111003	26556.995345
HLA A*3001	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.301447	1.190433	-3.111014	20019.191774
HLA A*3001	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.202552	1.091476	-3.111076	15942.338171
HLA B*7301	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.398974	1.287816	-3.111157	25059.572754
HLA A*3101	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.032821	0.921448	-3.111373	10785.009244
HLA B*5701	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.412549	1.301147	-3.111402	25855.264602
HLA B*1801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.424975	1.313175	-3.111800	26605.744299
HLA A*2601	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.381444	1.269596	-3.111849	24068.230095
HLA A*0206	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.092638	0.980728	-3.111911	12377.656035
HLA A*2402	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.489321	1.377330	-3.111990	30854.659539
HLA B*4002	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.522049	1.410054	-3.111995	33269.715317
HLA B*3501	1:208-216	9	PANIANALI	0.995189	0.008861	-4.116335	1.004050	-3.112285	13071.797624
HLA B*5101	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.400165	1.287816	-3.112348	25128.400844
HLA B*4501	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.571797	1.459325	-3.112472	37307.580104
HLA A*2402	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.168358	1.055834	-3.112523	14735.253526
HLA A*2602	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.525200	1.412655	-3.112545	33511.953450
HLA B*1503	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.251915	1.139224	-3.112690	17861.367124
HLA B*1502	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.537192	1.424271	-3.112921	34450.181597
HLA B*3801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.469505	1.356576	-3.112929	29478.487866
HLA B*0802	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.402317	1.289353	-3.112964	25253.232635
HLA A*3201	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.416790	1.303793	-3.112997	26108.974082
HLA B*2705	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.348063	1.235042	-3.113020	22287.567518
HLA A*0206	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-3.975164	0.862117	-3.113048	9444.177909
HLA B*0702	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.348117	1.235042	-3.113074	22290.340876
HLA B*5101	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.430633	1.317518	-3.113115	26954.605050
HLA B*1801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.397357	1.284024	-3.113333	24966.474295
HLA B*4403	1:260-268	9	HGLLRAGER	1.105522	0.436138	-4.655145	1.541660	-3.113485	45200.689595
HLA B*5301	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.254255	1.140721	-3.113533	17957.868381
HLA A*2301	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.487641	1.373907	-3.113734	30735.542059
HLA B*1501	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.351667	1.237896	-3.113771	22473.296509
HLA B*5101	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.383453	1.269596	-3.113857	24179.814481
HLA B*3901	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.417654	1.303793	-3.113862	26161.004626
HLA B*1509	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.431427	1.317518	-3.113909	27003.937782
HLA B*4001	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.403543	1.289436	-3.114107	25324.647597
HLA B*3901	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.017727	0.903619	-3.114108	10416.634600
HLA B*4403	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.488639	1.374504	-3.114135	30806.290608

HLA A*0203	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.020439	0.906227	-3.114211	10481.869194
HLA A*0219	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.377318	1.263086	-3.114232	23840.670152
HLA B*4801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.377492	1.263086	-3.114406	23850.216241
HLA B*4801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.407458	1.293038	-3.114419	25553.927170
HLA B*5701	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.398445	1.284024	-3.114421	25029.088172
HLA B*0801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.077423	0.962975	-3.114449	11951.520065
HLA B*2705	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.329981	1.215498	-3.114483	21378.687312
HLA A*0203	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.351563	1.236980	-3.114583	22467.947711
HLA A*3101	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.377753	1.263086	-3.114667	23864.542542
HLA A*3001	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.027652	0.912830	-3.114822	10657.409531
HLA A*1101	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.400971	1.286148	-3.114822	25175.072192
HLA A*0101	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.376069	1.260962	-3.115106	23772.153892
HLA B*4601	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.396479	1.281231	-3.115248	24916.010733
HLA B*0803	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.416400	1.301147	-3.115253	26085.537662
HLA A*2902	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.350518	1.235042	-3.115475	22413.923414
HLA B*0803	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.354890	1.239243	-3.115647	22640.722162
HLA B*5301	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.464498	1.348830	-3.115669	29140.597316
HLA B*1501	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.399763	1.284024	-3.115739	25105.165535
HLA B*4403	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.416931	1.301147	-3.115784	26117.450257
HLA B*1801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.455434	1.339557	-3.115877	28538.696732
HLA A*0216	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.049239	0.933159	-3.116079	11200.533849
HLA A*2601	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.391993	1.275786	-3.116207	24660.015339
HLA A*0202	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.905742	0.789472	-3.116270	8048.993504
HLA B*0803	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.465107	1.348830	-3.116277	29181.456611
HLA B*5701	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.379435	1.263086	-3.116349	23957.160646
HLA B*0702	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.344543	1.228069	-3.116474	22107.678656
HLA B*5801	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.365623	1.249052	-3.116571	23207.198809
HLA B*3901	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.349345	1.232655	-3.116690	22353.497848
HLA A*1101	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.386303	1.269596	-3.116707	24339.008913
HLA B*4501	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.044366	0.927581	-3.116785	11075.565019
HLA A*2301	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.498550	1.381752	-3.116798	31517.338471
HLA B*3901	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.018944	0.902116	-3.116829	10445.866309
HLA A*0101	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.379924	1.263068	-3.116856	23984.133781
HLA B*1503	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.217344	1.100487	-3.116857	16494.698238
HLA A*2403	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.392668	1.275786	-3.116882	24698.333160
HLA A*0212	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.276361	1.159455	-3.116906	18895.617479
HLA A*2501	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.473582	1.356576	-3.117005	29756.480200
HLA B*5701	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.406440	1.289353	-3.117087	25494.137611
HLA A*0206	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.145826	1.028301	-3.117525	13990.268558
HLA A*0216	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.086722	0.969193	-3.117529	12210.189568
HLA B*4001	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.366661	1.249052	-3.117610	23262.757589
HLA A*2902	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.439782	1.322138	-3.117644	27528.456870
HLA A*0216	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.398969	1.281231	-3.117738	25059.301617
HLA A*0203	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.017934	0.900138	-3.117797	10421.594830
HLA B*1509	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.209455	1.091476	-3.117979	16197.754194
HLA B*5101	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.419153	1.301147	-3.118007	26251.455582
HLA B*2705	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.233718	1.115576	-3.118142	17128.444932
HLA A*2603	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.546613	1.428368	-3.118245	35205.697286
HLA A*0301	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.367519	1.249052	-3.118467	23308.737833
HLA A*0201	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.310351	1.191820	-3.118532	20433.891737
HLA A*0216	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.354016	1.235408	-3.118608	22595.204007
HLA A*0101	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.351272	1.232655	-3.118617	22452.880676
HLA A*0201	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.394510	1.275786	-3.118724	24803.309976
HLA A*3201	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.411875	1.293038	-3.118836	25815.151880
HLA A*3001	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.175016	1.055834	-3.119182	14962.909630
HLA A*0212	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.400482	1.281231	-3.119251	25146.759699
HLA A*2603	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.101980	0.982586	-3.119393	12646.779955
HLA A*1101	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.432736	1.313175	-3.119560	27085.431692
HLA A*3301	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.579050	1.459325	-3.119725	37935.860563
HLA A*6802	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.382950	1.263068	-3.119882	24151.837314
HLA A*3101	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.395729	1.275786	-3.119943	24873.048893
HLA B*4501	1:488-496	9	VPYEVLERI	1.256779	0.264787	-4.641598	1.521566	-3.120032	43812.489383
HLA B*2705	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.348103	1.228069	-3.120034	22289.617358
HLA B*5801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.351958	1.231855	-3.120103	22488.377244
HLA A*2601	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.381106	1.260962	-3.120144	24049.487667

HLA A*0211	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.348636	1.228391	-3.120245	22317.006822
HLA A*2902	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.193192	1.072837	-3.120354	15602.409384
HLA A*2602	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.715983	0.595350	-3.120633	5199.757275
HLA B*5801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.358565	1.237896	-3.120669	22833.099532
HLA B*4002	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.404718	1.284024	-3.120694	25393.242095
HLA A*0250	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.421905	1.301147	-3.120758	26418.285909
HLA B*1501	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.032872	0.911989	-3.120883	10786.292926
HLA B*5701	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.407039	1.286148	-3.120891	25529.331597
HLA A*2603	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.076361	0.955413	-3.120949	11922.331075
HLA B*4801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.353631	1.232655	-3.120976	22575.165939
HLA B*5401	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.064745	0.943730	-3.121016	11607.677244
HLA B*4402	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.324925	1.203805	-3.121120	21131.238100
HLA B*5401	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.549557	1.428368	-3.121189	35445.152981
HLA B*3501	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.384282	1.263068	-3.121214	24226.034571
HLA B*5401	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.251656	1.130410	-3.121246	17850.741204
HLA B*4002	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.200616	1.079304	-3.121312	15871.429398
HLA A*3301	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.280950	1.159455	-3.121495	19096.317764
HLA A*0203	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.028328	0.906788	-3.121541	10674.027229
HLA A*3101	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.411238	1.289436	-3.121802	25777.332533
HLA B*3801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.384935	1.263086	-3.121849	24262.496707
HLA B*5101	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.478454	1.356576	-3.121878	30092.231243
HLA A*2602	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.581475	1.459325	-3.122149	38148.249016
HLA B*4001	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.385335	1.263068	-3.122267	24284.820732
HLA B*1509	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.415406	1.293038	-3.122368	26025.912207
HLA B*5801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.350856	1.228391	-3.122465	22431.391202
HLA B*1509	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.357876	1.235408	-3.122468	22796.935512
HLA B*1503	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.236403	1.113845	-3.122558	17234.686863
HLA B*4403	1:36-44	9	EARVFSEVI	1.251732	0.243780	-4.618091	1.495512	-3.122580	41504.131712
HLA B*1501	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.330087	1.207422	-3.122665	21383.892480
HLA A*0219	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.357724	1.235042	-3.122681	22788.920543
HLA A*0216	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.151808	1.028966	-3.122842	14184.297780
HLA B*5801	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.333024	1.210159	-3.122864	21528.988131
HLA A*6802	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.022878	0.899837	-3.123040	10540.895337
HLA A*0101	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.358579	1.235042	-3.123537	22833.840691
HLA A*0216	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.453317	1.329702	-3.123615	28399.928748
HLA B*3801	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.505506	1.381752	-3.123755	32026.270009
HLA A*0212	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.384823	1.260962	-3.123860	24256.197169
HLA A*2602	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.497546	1.372792	-3.124755	31444.616731
HLA A*2902	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.405987	1.281231	-3.124756	25467.532854
HLA B*3901	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.142090	1.017185	-3.124906	13870.444219
HLA A*0216	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.085458	0.960386	-3.125073	12174.703230
HLA B*4801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.400896	1.275786	-3.125109	25170.714350
HLA B*4801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.340655	1.215498	-3.125157	21910.623973
HLA A*0250	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.251750	1.126421	-3.125329	17854.604444
HLA B*4402	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.414769	1.289353	-3.125416	25987.784095
HLA A*0212	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.234662	1.109115	-3.125548	17165.735988
HLA B*4801	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.409173	1.283502	-3.125671	25655.044763
HLA B*3901	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.374814	1.249052	-3.125762	23703.578075
HLA B*7301	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.581268	1.455494	-3.125773	38130.092092
HLA B*3901	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.387113	1.260962	-3.126151	24384.477944
HLA B*1801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.407406	1.281231	-3.126175	25550.885985
HLA A*6801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-3.940227	0.813920	-3.126307	8714.195877
HLA A*3101	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.358182	1.231855	-3.126327	22812.973907
HLA A*3001	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.266886	1.140437	-3.126449	18487.816228
HLA A*2403	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.396058	1.269596	-3.126462	24891.894490
HLA A*0301	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-3.881011	0.754547	-3.126464	7603.453560
HLA A*0202	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.581996	1.455494	-3.126502	38194.092410
HLA A*2403	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.415965	1.289436	-3.126529	26059.443547
HLA B*4501	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.629712	1.503120	-3.126592	42629.661626
HLA B*1503	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.389688	1.263086	-3.126602	24529.488806
HLA A*6901	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.362091	1.235408	-3.126683	23019.264692
HLA A*0219	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.430483	1.303793	-3.126690	26945.274094
HLA A*8001	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.299440	1.172675	-3.126765	19926.915525
HLA B*1501	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.059887	0.932998	-3.126889	11478.538333
HLA B*4001	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.389980	1.263086	-3.126893	24545.949352

HLA B*4403	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.630147	1.503120	-3.127026	42672.348006
HLA A*2603	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.355445	1.228391	-3.127054	22669.646799
HLA A*0101	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.390170	1.263086	-3.127084	24556.707769
HLA B*2705	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.413345	1.286148	-3.127197	25902.725434
HLA B*3901	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.483788	1.356576	-3.127211	30464.055748
HLA A*2601	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.362324	1.235042	-3.127282	23031.596630
HLA A*1101	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.360130	1.232655	-3.127475	22915.515256
HLA B*0801	1:84-92 9		DLGVPVLGI	1.157263	0.052896	-4.337706	1.210159	-3.127547	21762.367601
HLA B*0803	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.407676	1.280105	-3.127571	25566.787088
HLA B*1503	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-3.903345	0.775707	-3.127638	8004.700776
HLA A*2603	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.501663	1.373907	-3.127755	31744.069648
HLA A*0101	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.343500	1.215498	-3.128002	22054.639940
HLA A*2902	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.457969	1.329702	-3.128267	28705.771978
HLA A*0301	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.363731	1.235408	-3.128323	23106.352120
HLA A*0301	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.172408	1.044058	-3.128351	14873.326943
HLA A*3001	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.259593	1.131046	-3.128547	18179.955426
HLA B*0801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.360426	1.231855	-3.128570	22931.140851
HLA A*0203	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.364150	1.235408	-3.128742	23128.613336
HLA A*8001	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.416795	1.287816	-3.128978	26109.256577
HLA B*0702	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.412753	1.283502	-3.129251	25867.436514
HLA B*0802	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.440576	1.311116	-3.129460	27578.839874
HLA A*6801	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.607288	1.477798	-3.129491	40484.464637
HLA A*0203	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.172845	1.043307	-3.129538	14888.300602
HLA A*2501	1:26-34 9		YAQLIARRV	1.199062	0.114113	-4.442766	1.313175	-3.129590	27718.243989
HLA A*0206	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.044775	0.915104	-3.129671	11085.995587
HLA A*0101	1:31-39 9		ARRVREARV	0.936445	0.312607	-4.378740	1.249052	-3.129688	23918.828093
HLA B*5101	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.392795	1.263068	-3.129726	24705.549437
HLA B*3901	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.411045	1.281231	-3.129814	25765.899963
HLA A*0219	1:16-24 9		PVLVVDFGA	0.941651	-0.314462	-3.757010	0.627189	-3.129821	5714.915039
HLA A*0203	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.337257	1.207422	-3.129835	21739.892403
HLA A*0301	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.364908	1.235042	-3.129866	23169.063471
HLA A*0211	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.312181	1.182210	-3.129972	20520.188073
HLA A*0201	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.390978	1.260962	-3.130016	24602.450398
HLA B*0801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.238981	1.108898	-3.130083	17337.272774
HLA B*1517	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.431272	1.301147	-3.130125	26994.297674
HLA A*1101	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.459863	1.329702	-3.130161	28831.213070
HLA A*0206	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.486851	1.356576	-3.130275	30679.724111
HLA B*2705	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.908434	0.778023	-3.130411	8099.050122
HLA B*2705	1:37-45 9		ARVFSEVIP	0.871286	0.157261	-4.159007	1.028547	-3.130460	14421.374740
HLA A*2403	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.358572	1.228069	-3.130503	22833.470108
HLA A*2603	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.589836	1.459325	-3.130511	38889.864142
HLA B*5801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.358605	1.228069	-3.130536	22835.199545
HLA B*1502	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.391507	1.260962	-3.130545	24632.415351
HLA B*1517	1:84-92 9		DLGVPVLGI	1.157263	0.052896	-4.340739	1.210159	-3.130580	21914.891615
HLA A*3002	1:54-62 9		RARQPVALV	0.737262	0.289291	-4.157169	1.026553	-3.130616	14360.493505
HLA A*6901	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.369990	1.239243	-3.130747	23441.770801
HLA A*2601	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.193807	1.062990	-3.130817	15624.539778
HLA B*1509	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.406605	1.275786	-3.130819	25503.793871
HLA B*1509	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.452970	1.322138	-3.130832	28377.199059
HLA A*8001	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.432040	1.301147	-3.130894	27042.093762
HLA A*1101	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.261468	1.130410	-3.131058	18258.609614
HLA A*2402	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.505187	1.373907	-3.131280	32002.715509
HLA A*2602	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.572488	1.440990	-3.131498	37366.965300
HLA A*0301	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.363445	1.231855	-3.131589	23091.106810
HLA A*3101	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.367133	1.235408	-3.131725	23288.066984
HLA A*2902	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.359798	1.228069	-3.131729	22898.042095
HLA B*7301	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.591082	1.459325	-3.131756	39001.530776
HLA A*8001	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.371043	1.239243	-3.131800	23498.653891
HLA A*2403	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.232346	1.100487	-3.131859	17074.415142
HLA A*0301	1:45-53 9		PHTASIEEI	1.223034	0.013946	-4.368910	1.236980	-3.131929	23383.507331
HLA A*3002	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.240992	1.108898	-3.132094	17417.745531
HLA A*0219	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.232640	1.100487	-3.132152	17085.965383
HLA A*0212	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.407963	1.275786	-3.132177	25583.666903
HLA B*1517	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.279472	1.147258	-3.132214	19031.446862
HLA A*0219	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.408043	1.275786	-3.132257	25588.373099

HLA A*8001	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.413637	1.281231	-3.132406	25920.107492
HLA B*4001	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.365139	1.232655	-3.132484	23181.350250
HLA B*0802	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.420565	1.287816	-3.132749	26336.946984
HLA A*0202	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.557106	1.424271	-3.132835	36066.645437
HLA A*0203	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.922508	0.789472	-3.133036	8365.800464
HLA A*0101	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.364923	1.231855	-3.133067	23169.815536
HLA B*3901	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.224647	1.091476	-3.133171	16774.383748
HLA A*2403	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.368743	1.235408	-3.133335	23374.527401
HLA A*3002	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.588998	1.455494	-3.133503	38814.827448
HLA A*0219	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.264045	1.130410	-3.133635	18367.290214
HLA A*6901	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.264712	1.131046	-3.133666	18395.531565
HLA A*3001	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.154561	1.020890	-3.133672	14274.517473
HLA A*2902	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.040649	0.906788	-3.133861	10981.179881
HLA A*2501	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.417410	1.283502	-3.133908	26146.289840
HLA A*2602	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.445155	1.311116	-3.134039	27871.166102
HLA B*1503	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.849688	0.715584	-3.134104	7074.366634
HLA A*2402	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.506979	1.372792	-3.134188	32135.087583
HLA B*1517	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.383303	1.249052	-3.134251	24171.444083
HLA B*1509	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.415507	1.281231	-3.134276	26031.967195
HLA B*5701	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.369786	1.235408	-3.134378	23430.740284
HLA A*2403	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.369441	1.235042	-3.134398	23412.114309
HLA B*1501	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.326243	1.191820	-3.134424	21195.467722
HLA B*5801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.350050	1.215498	-3.134552	22389.806287
HLA B*5301	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.447730	1.313175	-3.134555	28036.911781
HLA A*0250	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.590057	1.455494	-3.134563	38909.645818
HLA B*5101	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.512019	1.377330	-3.134689	32510.161971
HLA A*6802	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.009302	0.874608	-3.134695	10216.500881
HLA A*2301	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.421129	1.286148	-3.134981	26371.164384
HLA A*2602	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.529918	1.394918	-3.134999	33877.980209
HLA A*3001	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.255906	1.120820	-3.135086	18026.294921
HLA B*0702	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.373031	1.237896	-3.135135	23606.448223
HLA A*2902	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.438936	1.303793	-3.135143	27474.895720
HLA B*3501	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.418721	1.283502	-3.135219	26225.337370
HLA A*3301	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.613035	1.477798	-3.135238	41023.739042
HLA A*0206	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.439180	1.303793	-3.135388	27490.358228
HLA A*2402	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.457619	1.322138	-3.135482	28682.642340
HLA B*0702	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.419588	1.284024	-3.135564	26277.741965
HLA B*5401	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.148613	1.012736	-3.135876	14080.320502
HLA B*1502	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.449246	1.313175	-3.136070	28134.914062
HLA B*4501	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.489849	1.353717	-3.136132	30892.239471
HLA B*4801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.162926	1.026553	-3.136373	14552.097744
HLA A*2402	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.375643	1.239243	-3.136400	23748.887831
HLA A*6901	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.157310	1.020890	-3.136421	14365.155582
HLA A*0206	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.017995	0.881518	-3.136477	10423.060805
HLA A*2403	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.364970	1.228391	-3.136579	23172.322594
HLA A*3201	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.518400	1.381752	-3.136649	32991.368789
HLA B*5701	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.399904	1.263068	-3.136836	25113.315827
HLA A*0203	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.268147	1.131046	-3.137101	18541.603467
HLA A*0211	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.246050	1.108898	-3.137152	17621.804652
HLA B*4001	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.374227	1.236980	-3.137246	23671.541312
HLA A*3101	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.150018	1.012736	-3.137281	14125.945702
HLA A*0219	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.341155	1.203805	-3.137350	21935.886277
HLA A*6802	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.441159	1.303793	-3.137366	27615.865926
HLA A*2601	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.347550	1.210159	-3.137391	22261.298039
HLA B*0702	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.267950	1.130410	-3.137540	18533.179508
HLA A*6901	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.369565	1.231855	-3.137710	23418.828089
HLA A*8001	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.430786	1.293038	-3.137747	26964.085110
HLA A*0101	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.377088	1.239243	-3.137845	23828.033914
HLA B*5801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.229576	1.091476	-3.138100	16965.856670
HLA B*1509	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.512052	1.373907	-3.138145	32512.624333
HLA A*0250	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.442016	1.303793	-3.138224	27670.450352
HLA B*1801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.408123	1.269596	-3.138527	25593.080161
HLA B*5701	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.366774	1.228069	-3.138705	23268.799122
HLA A*0201	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.370580	1.231855	-3.138725	23473.623585
HLA B*1501	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.387797	1.249052	-3.138745	24422.896117

HLA B*4402	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.279213	1.140437	-3.138777	19020.124849
HLA B*1801	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.487653	1.348830	-3.138823	30736.373450
HLA B*0702	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.414668	1.275786	-3.138882	25981.739384
HLA B*5101	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.375881	1.236980	-3.138900	23761.867741
HLA A*0101	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.367035	1.228069	-3.138966	23282.776179
HLA B*4402	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.377034	1.237896	-3.139139	23825.069237
HLA A*3101	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.377128	1.237896	-3.139233	23830.225434
HLA B*4801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.428674	1.289436	-3.139237	26833.263924
HLA A*3201	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.402390	1.263086	-3.139303	25257.468123
HLA B*5101	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.478931	1.339557	-3.139374	30125.296910
HLA B*0801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.261216	1.121826	-3.139390	18248.043528
HLA B*4801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.253259	1.113845	-3.139414	17916.723955
HLA B*1509	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.402777	1.263086	-3.139691	25280.023805
HLA B*1503	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.400698	1.260962	-3.139736	25159.278603
HLA B*0801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.322007	1.182210	-3.139797	20989.731501
HLA A*0211	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.291647	1.151838	-3.139809	19572.524166
HLA B*5401	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-3.350864	0.210953	-3.139910	2243.177829
HLA A*2301	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.512731	1.372792	-3.139939	32563.496213
HLA B*2705	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.157136	1.017185	-3.139952	14359.405905
HLA B*4402	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.403066	1.263086	-3.139980	25296.851145
HLA B*5701	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.312722	1.172675	-3.140046	20545.736711
HLA B*3801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.377058	1.236980	-3.140077	23826.358182
HLA A*3301	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.046316	0.906227	-3.140089	11125.408430
HLA B*4402	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.429604	1.289436	-3.140168	26890.810877
HLA A*2902	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.070027	0.929716	-3.140311	11749.705088
HLA B*1509	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.426517	1.286148	-3.140368	26700.332829
HLA A*0216	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.389423	1.249052	-3.140371	24514.498084
HLA A*2902	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.424588	1.284024	-3.140564	26582.005764
HLA B*0802	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.421806	1.281231	-3.140575	26412.283951
HLA A*0101	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.322794	1.182210	-3.140584	21027.805953
HLA B*4501	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-3.402007	0.261282	-3.140725	2523.523152
HLA B*4601	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.389815	1.249052	-3.140764	24536.655751
HLA A*0203	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.241309	1.100487	-3.140822	17430.470967
HLA A*0219	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.422142	1.281231	-3.140911	26432.724773
HLA B*4001	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-3.891147	0.750232	-3.140915	7782.991857
HLA A*2902	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.170124	1.028966	-3.141159	14795.322128
HLA A*1101	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-3.833777	0.692424	-3.141353	6819.881856
HLA B*0802	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.410994	1.269596	-3.141398	25762.833551
HLA B*3801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.516020	1.374504	-3.141516	32811.063413
HLA A*2403	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.402517	1.260962	-3.141554	25264.847766
HLA A*0301	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.314376	1.172675	-3.141700	20624.135621
HLA B*0702	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.307010	1.165167	-3.141843	20277.299713
HLA A*6901	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.378824	1.236980	-3.141844	23923.486882
HLA B*4002	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.645268	1.503120	-3.142148	44184.284400
HLA A*6802	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.379184	1.236980	-3.142204	23943.296862
HLA B*1801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.443597	1.301147	-3.142451	27771.378081
HLA B*2705	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.432017	1.289436	-3.142581	27040.630854
HLA A*0201	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.377997	1.235408	-3.142589	23877.973191
HLA B*4601	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.380549	1.237896	-3.142653	24018.672526
HLA A*0216	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.815709	0.673013	-3.142696	6541.981499
HLA B*0803	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.412399	1.269596	-3.142803	25846.314208
HLA A*0206	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.315482	1.172675	-3.142807	20676.754120
HLA A*2403	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.160050	1.017185	-3.142865	14456.056385
HLA A*2902	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.294830	1.151838	-3.142992	19716.525743
HLA B*1517	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.454252	1.311116	-3.143136	28461.143531
HLA B*5801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.076216	0.932998	-3.143218	11918.332839
HLA A*2902	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.375904	1.232655	-3.143249	23763.153267
HLA A*3001	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.148406	1.005151	-3.143255	14073.618876
HLA B*4601	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.378451	1.235042	-3.143409	23902.917408
HLA B*5301	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.553598	1.410054	-3.143544	35776.509708
HLA A*3001	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.180551	1.036964	-3.143588	15154.842933
HLA B*0802	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.282829	1.139224	-3.143605	19179.144037
HLA B*5701	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.376625	1.232655	-3.143970	23802.652758
HLA A*0201	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.326245	1.182210	-3.144036	21195.582388
HLA B*1502	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.379372	1.235042	-3.144330	23953.661551

HLA A*2301	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.407530	1.263068	-3.144462	25558.213090
HLA A*0202	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.187793	1.043307	-3.144486	15409.642113
HLA A*0101	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.372878	1.228391	-3.144487	23598.148645
HLA A*2902	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.127134	0.982586	-3.144547	13400.887108
HLA A*2902	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.383803	1.239243	-3.144560	24199.313046
HLA B*4801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.405555	1.260962	-3.144592	25442.194585
HLA B*0803	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.448407	1.303793	-3.144614	28080.628685
HLA B*0803	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.420417	1.275786	-3.144631	26327.972276
HLA B*5801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.352163	1.207422	-3.144741	22498.964122
HLA A*3201	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.600280	1.455494	-3.144785	39836.381867
HLA A*2602	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.270800	1.125828	-3.144972	18655.197772
HLA B*5701	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.394108	1.249052	-3.145056	24780.375266
HLA B*0801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.310471	1.165167	-3.145304	20439.530314
HLA B*4402	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.426636	1.281231	-3.145406	26707.700583
HLA B*1517	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.304947	1.159455	-3.145492	20181.213299
HLA A*2301	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.467668	1.322138	-3.145530	29354.041564
HLA A*2501	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.297441	1.151838	-3.145602	19835.386532
HLA B*1502	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.519622	1.373907	-3.145715	33084.308871
HLA A*0212	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.349580	1.203805	-3.145776	22365.594114
HLA B*1509	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.297638	1.151838	-3.145800	19844.402389
HLA B*1509	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.441135	1.295300	-3.145836	27614.371979
HLA A*2501	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.475565	1.329702	-3.145863	29892.657347
HLA B*5401	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.485423	1.339557	-3.145866	30578.977755
HLA A*2501	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.421930	1.275786	-3.146144	26419.858076
HLA A*3002	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.449943	1.303793	-3.146151	28180.155808
HLA B*0702	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.067696	0.921448	-3.146249	11686.817899
HLA B*0801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.172845	1.026553	-3.146292	14888.300602
HLA A*0201	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.385537	1.239243	-3.146294	24296.121885
HLA A*1101	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.381447	1.235042	-3.146404	24068.360302
HLA A*0212	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.336625	1.190075	-3.146550	21708.278213
HLA A*2602	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-3.858822	0.712255	-3.146568	7224.742309
HLA A*0201	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.395762	1.249052	-3.146710	24874.932811
HLA B*0801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.337156	1.190433	-3.146723	21734.835744
HLA A*2301	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.541848	1.394918	-3.146930	34821.557697
HLA A*6802	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.378832	1.231855	-3.146976	23923.875156
HLA A*2601	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.396065	1.249052	-3.147013	24892.298481
HLA B*1501	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.337450	1.190433	-3.147017	21749.538596
HLA B*1502	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.273537	1.126421	-3.147116	18773.143833
HLA A*0211	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.542039	1.394918	-3.147120	34836.819883
HLA A*0202	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.375643	1.228391	-3.147252	23748.887831
HLA B*3501	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-3.895667	0.748391	-3.147276	7864.425183
HLA B*1501	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-3.936750	0.789472	-3.147278	8644.703056
HLA A*0216	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.339123	1.191820	-3.147303	21833.475915
HLA A*3201	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.469468	1.322138	-3.147330	29475.936371
HLA B*5301	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.469489	1.322138	-3.147351	29477.371560
HLA A*0206	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.382812	1.235408	-3.147404	24144.129677
HLA B*4501	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.465281	1.317518	-3.147763	29193.141215
HLA A*0212	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.239246	1.091476	-3.147770	17347.874592
HLA B*4002	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.607178	1.459325	-3.147853	40474.172172
HLA A*0301	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.363534	1.215498	-3.148036	23095.854270
HLA B*3501	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.225638	1.077535	-3.148103	16812.722964
HLA B*1801	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.428227	1.280105	-3.148122	26805.696747
HLA B*5101	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.441199	1.293038	-3.148160	27618.405822
HLA A*6901	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.269014	1.120820	-3.148194	18578.654095
HLA A*2601	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.386134	1.237896	-3.148238	24329.530422
HLA B*2705	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-3.755548	0.607235	-3.148314	5695.716948
HLA A*0216	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-3.911860	0.763388	-3.148472	8163.184942
HLA B*3501	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.111448	0.962975	-3.148474	12925.530796
HLA B*1509	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.052208	0.903619	-3.148589	11277.386682
HLA A*0203	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.108981	0.960386	-3.148596	12852.316961
HLA A*2601	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.380479	1.231855	-3.148623	24014.774692
HLA A*2501	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.104043	0.955413	-3.148630	12706.993566
HLA A*6801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.240116	1.091476	-3.148640	17382.633897
HLA B*1801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.409685	1.260962	-3.148723	25685.319038
HLA B*1517	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.212072	1.062990	-3.149082	16295.666591

HLA B*0802	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.412180	1.263086	-3.149094	25833.313690
HLA B*5801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.331308	1.182210	-3.149099	21444.133107
HLA B*1502	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.412335	1.263086	-3.149249	25842.539190
HLA A*6901	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.398363	1.249052	-3.149311	25024.349460
HLA B*1509	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.488886	1.339557	-3.149329	30823.794734
HLA B*1801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-3.899567	0.750232	-3.149335	7935.369068
HLA A*2602	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.523938	1.374504	-3.149434	33414.738801
HLA B*1509	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.241408	1.091915	-3.149493	17434.431887
HLA A*2601	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.377563	1.228069	-3.149494	23854.087366
HLA B*4001	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.384907	1.235408	-3.149499	24260.921670
HLA A*0216	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.082545	0.932998	-3.149547	12093.305448
HLA A*0216	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.425448	1.275786	-3.149662	26634.690793
HLA B*4403	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.609128	1.459325	-3.149803	40656.318254
HLA B*5801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.353645	1.203805	-3.149840	22575.898726
HLA B*2705	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.410834	1.260962	-3.149872	25753.357857
HLA A*2602	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.578451	1.428368	-3.150083	37883.563299
HLA A*0203	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.411081	1.260962	-3.150118	25767.990907
HLA A*0216	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.183531	1.033365	-3.150166	15259.158587
HLA A*6801	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.560325	1.410054	-3.150271	36334.948157
HLA B*3501	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.223152	1.072837	-3.150315	16716.767479
HLA B*4601	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.378735	1.228391	-3.150344	23918.569298
HLA A*3001	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.273546	1.123169	-3.150377	18773.550080
HLA A*2902	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.025250	0.874608	-3.150643	10598.648300
HLA A*0250	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.206504	1.055834	-3.150669	16088.066434
HLA A*2501	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.454476	1.303793	-3.150683	28475.774596
HLA A*3001	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.223646	1.072837	-3.150808	16735.769801
HLA B*4402	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.434369	1.283502	-3.150866	27187.461163
HLA A*0201	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.387938	1.236980	-3.150958	24430.824914
HLA B*1517	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.272825	1.121826	-3.150999	18742.396171
HLA B*3501	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.383657	1.232655	-3.151002	24191.197640
HLA B*1501	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.412039	1.260962	-3.151077	25824.929728
HLA B*4402	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.400341	1.249052	-3.151289	25138.598553
HLA A*0101	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.388323	1.236980	-3.151343	24452.510093
HLA B*4002	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.452504	1.301147	-3.151358	28346.818868
HLA A*0203	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.277855	1.126421	-3.151434	18960.743406
HLA B*1801	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.481283	1.329702	-3.151581	30288.876919
HLA A*3002	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.441598	1.289436	-3.152162	27643.817633
HLA A*8001	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.384907	1.232655	-3.152252	24260.921670
HLA A*2601	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.252887	1.100487	-3.152400	17901.415955
HLA B*4403	1:147-155	9	AAPDGFDVV	1.259209	0.218589	-4.630250	1.477798	-3.152452	42682.506733
HLA A*3101	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.334779	1.182210	-3.152569	21616.166837
HLA A*0212	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.384632	1.231855	-3.152777	24245.570408
HLA B*7301	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.506651	1.353717	-3.152933	32110.758181
HLA A*8001	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.363292	1.210159	-3.153133	23082.988416
HLA A*2402	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.388467	1.235042	-3.153424	24460.580832
HLA A*6901	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.245430	1.091915	-3.153516	17596.654965
HLA B*1509	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.335751	1.182210	-3.153542	21664.634694
HLA A*2902	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.231138	1.077535	-3.153603	17027.002556
HLA A*3001	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.187135	1.033365	-3.153770	15386.317736
HLA B*5401	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.476086	1.322138	-3.153949	29928.579858
HLA B*0702	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.382360	1.228391	-3.153969	24119.064221
HLA B*0801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.326797	1.172675	-3.154122	21222.545975
HLA B*2705	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.382572	1.228391	-3.154181	24130.810412
HLA A*2402	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.417436	1.263086	-3.154350	26147.845820
HLA A*8001	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.417450	1.263086	-3.154364	26148.694575
HLA A*1101	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.458223	1.303793	-3.154430	28722.548744
HLA A*6801	1:203-211	9	GAQWTPANI	1.276445	0.182880	-4.613808	1.459325	-3.154483	41096.820306
HLA A*0101	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.392395	1.237896	-3.154499	24682.838654
HLA B*3801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.443882	1.289353	-3.154529	27789.563081
HLA A*0201	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.087554	0.932998	-3.154556	12233.595717
HLA B*3501	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.438793	1.284024	-3.154769	27465.830411
HLA B*0803	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.382882	1.228069	-3.154813	24148.048507
HLA A*0201	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.383211	1.228391	-3.154820	24166.344792
HLA B*5101	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.390278	1.235408	-3.154870	24562.819587
HLA A*0101	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.365064	1.210159	-3.154904	23177.337525

HLA A*3301	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.581280	1.426359	-3.154921	38131.123504
HLA A*2602	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.610557	1.455494	-3.155062	40790.265698
HLA B*0801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.392992	1.237896	-3.155096	24716.778948
HLA A*1101	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.438635	1.283502	-3.155133	27455.876880
HLA A*0250	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.012319	0.857166	-3.155153	10287.714788
HLA B*5101	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.390201	1.235042	-3.155158	24558.434868
HLA B*1801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.472731	1.317518	-3.155213	29698.262733
HLA A*0212	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.255777	1.100487	-3.155290	18020.932105
HLA B*1502	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.431138	1.275786	-3.155352	26985.974897
HLA B*4402	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.450822	1.295300	-3.155522	28237.230396
HLA A*0203	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.431357	1.275786	-3.155571	26999.555488
HLA A*0206	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.550579	1.394918	-3.155661	35528.664348
HLA A*0216	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.256379	1.100487	-3.155892	18045.907154
HLA B*0802	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.459783	1.303793	-3.155990	28825.910453
HLA B*5701	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.395370	1.239243	-3.156127	24852.469664
HLA A*2902	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.219135	1.062990	-3.156145	16562.835264
HLA B*5101	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.315703	1.159455	-3.156248	20687.271535
HLA A*2601	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.393269	1.236980	-3.156289	24732.562360
HLA B*3901	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.395541	1.239243	-3.156298	24862.286387
HLA B*7301	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.495859	1.339557	-3.156302	31322.713302
HLA B*0702	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.389038	1.232655	-3.156383	24492.757932
HLA A*0212	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.391895	1.235408	-3.156487	24654.412842
HLA A*3101	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.321744	1.165167	-3.156577	20977.017516
HLA B*3801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.469940	1.313175	-3.156764	29508.005575
HLA A*2301	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.392209	1.235408	-3.156802	24672.291926
HLA B*5701	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.391888	1.235042	-3.156845	24654.012712
HLA B*4002	1:118-126	9	TELKVLGGK	0.614308	0.199612	-3.970836	0.813920	-3.156916	9350.533884
HLA B*7301	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.567025	1.410054	-3.156971	36899.907383
HLA B*1503	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.339205	1.182210	-3.156995	21837.610390
HLA B*1501	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.288113	1.131046	-3.157067	19413.918965
HLA B*5701	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.394232	1.236980	-3.157252	24787.481416
HLA B*7301	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.583782	1.426359	-3.157423	38351.451293
HLA B*0803	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.304806	1.147258	-3.157548	20174.663674
HLA B*4001	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.385626	1.228069	-3.157557	24301.117093
HLA B*1501	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.394554	1.236980	-3.157574	24805.859587
HLA A*2501	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.396857	1.239243	-3.157614	24937.721836
HLA B*1517	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.296792	1.138932	-3.157860	19805.791833
HLA A*6901	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.395792	1.237896	-3.157897	24876.682290
HLA B*0801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.230753	1.072837	-3.157916	17011.902527
HLA B*5701	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.418916	1.260962	-3.157954	26237.115736
HLA B*1509	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.461867	1.303793	-3.158074	28964.566059
HLA B*4403	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.568249	1.410054	-3.158195	37004.058408
HLA B*1503	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.170951	1.012736	-3.158215	14823.523422
HLA B*0802	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.442439	1.284024	-3.158415	27697.408408
HLA B*5101	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.390290	1.231855	-3.158435	24563.484006
HLA A*8001	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.386535	1.228069	-3.158466	24352.047867
HLA A*0219	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.165806	1.007289	-3.158517	14648.935668
HLA B*1502	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.614170	1.455494	-3.158676	41131.073276
HLA A*3001	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.285113	1.126421	-3.158692	19280.261508
HLA B*4501	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.366130	1.207422	-3.158708	23234.333108
HLA A*0202	1:237-245	9	DSAVAAALV	0.764846	0.042930	-3.966546	0.807776	-3.158770	9258.619764
HLA A*8001	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.419760	1.260962	-3.158797	26288.121671
HLA B*1501	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.141404	0.982586	-3.158818	13848.550547
HLA B*0802	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.445005	1.286148	-3.158856	27861.517858
HLA A*3301	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.515478	1.356576	-3.158901	32770.085549
HLA B*5801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.349355	1.190433	-3.158922	22353.981573
HLA B*4501	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.532878	1.373907	-3.158971	34109.696964
HLA A*2501	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.391707	1.232655	-3.159052	24643.744940
HLA A*3001	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.176280	1.017185	-3.159095	15006.522921
HLA B*0802	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.420248	1.260962	-3.159286	26317.719211
HLA B*4801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.422405	1.263068	-3.159337	26448.745414
HLA B*5101	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.387428	1.228069	-3.159359	24402.161274
HLA B*0801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.040922	0.881518	-3.159404	10988.073251
HLA A*3101	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.306726	1.147258	-3.159468	20264.030605
HLA A*0216	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.387922	1.228391	-3.159531	24429.899755

HLA B*5701	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.397501	1.237896	-3.159605	24974.714672
HLA A*0301	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.367063	1.207422	-3.159641	23284.287715
HLA B*1501	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.300380	1.140721	-3.159658	19970.083176
HLA B*1501	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.300100	1.140437	-3.159664	19957.231037
HLA A*1101	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.471014	1.311116	-3.159897	29581.049044
HLA A*2601	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.399218	1.239243	-3.159975	25073.675951
HLA A*2402	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.463819	1.303793	-3.160027	29095.072814
HLA A*2601	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.351883	1.191820	-3.160063	22484.484472
HLA A*0202	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.057838	0.897730	-3.160108	11424.516730
HLA A*0203	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.399371	1.239243	-3.160128	25082.494478
HLA B*1517	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.398048	1.237896	-3.160152	25006.215253
HLA A*2601	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.395562	1.235408	-3.160154	24863.496937
HLA A*0301	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.364013	1.203805	-3.160208	23121.357327
HLA B*5701	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.392106	1.231855	-3.160251	24666.419753
HLA A*0201	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.398189	1.237896	-3.160293	25014.333422
HLA B*4402	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.395835	1.235408	-3.160427	24879.104850
HLA B*1501	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.350574	1.190075	-3.160499	22416.833767
HLA A*8001	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.211442	1.050933	-3.160509	16272.057433
HLA A*0206	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.399782	1.239243	-3.160539	25106.252088
HLA A*2603	1:163-171	9	VAAFEAFDR	0.865161	0.637959	-4.663692	1.503120	-3.160572	46099.104284
HLA A*3301	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.534666	1.373907	-3.160758	34250.413511
HLA B*0702	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.364591	1.203805	-3.160786	23152.148470
HLA A*0206	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-3.924223	0.763388	-3.160835	8398.904167
HLA A*2403	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.352658	1.191820	-3.160839	22524.661052
HLA A*6802	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.436718	1.275786	-3.160932	27334.940878
HLA B*1509	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.422008	1.260962	-3.161046	26424.575137
HLA B*5701	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.326466	1.165167	-3.161299	21206.363709
HLA B*1501	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.300894	1.139224	-3.161670	19993.757067
HLA A*2301	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.501287	1.339557	-3.161730	31716.604433
HLA A*2902	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.397205	1.235408	-3.161797	24957.696558
HLA B*1801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.454934	1.293038	-3.161895	28505.830349
HLA A*0203	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.271028	1.109115	-3.161913	18664.989828
HLA A*3301	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.442066	1.280105	-3.161961	27673.594106
HLA A*2501	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.455098	1.293038	-3.162060	28516.627330
HLA A*2501	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.448221	1.286148	-3.162073	28068.630115
HLA B*1501	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.344294	1.182210	-3.162084	22095.004680
HLA B*4601	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.399225	1.236980	-3.162245	25074.082891
HLA A*2301	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.431862	1.269596	-3.162266	27030.977648
HLA A*0211	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.518903	1.356576	-3.162327	33029.585551
HLA B*5801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.301336	1.138932	-3.162404	20014.102245
HLA B*4601	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.303159	1.140721	-3.162438	20098.299536
HLA B*3801	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.446093	1.283502	-3.162590	27931.392267
HLA A*3101	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.399794	1.236980	-3.162813	25106.931207
HLA A*0202	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.271756	1.108898	-3.162858	18696.318504
HLA A*1101	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-3.917484	0.754547	-3.162937	8269.596185
HLA A*0219	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.354883	1.191820	-3.163064	22640.354714
HLA A*3301	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.512003	1.348830	-3.163173	32508.930860
HLA B*4601	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.395038	1.231855	-3.163183	24833.519569
HLA B*1801	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.519834	1.356576	-3.163257	33100.421213
HLA B*4801	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.412366	1.249052	-3.163314	25844.356723
HLA A*0211	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.412394	1.249052	-3.163342	25846.034559
HLA B*4001	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.401441	1.237896	-3.163545	25202.325803
HLA B*0801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.355548	1.191820	-3.163729	22675.043613
HLA B*5401	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.126964	0.962975	-3.163990	13395.668318
HLA B*4501	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.207340	1.043307	-3.164034	16119.080628
HLA A*2402	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.503829	1.339557	-3.164272	31902.802001
HLA B*4601	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.336973	1.172675	-3.164298	21725.666201
HLA A*1101	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.448404	1.284024	-3.164381	28080.476772
HLA B*3901	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.448141	1.283502	-3.164639	28063.467752
HLA A*2402	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.400242	1.235408	-3.164834	25132.887326
HLA B*4001	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.393243	1.228391	-3.164852	24731.090599
HLA B*4402	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.434465	1.269596	-3.164869	27193.492159
HLA A*2603	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.191486	1.026553	-3.164933	15541.249863
HLA B*1801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.451160	1.286148	-3.165012	28259.236447
HLA A*2603	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.589475	1.424271	-3.165204	38857.477597

HLA B*0801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.355316	1.190075	-3.165240	22662.902587
HLA A*0216	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.402366	1.236980	-3.165386	25256.101759
HLA A*3301	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.547238	1.381752	-3.165486	35256.395828
HLA B*5801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.355659	1.190075	-3.165583	22680.809811
HLA A*1101	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.460939	1.295300	-3.165639	28902.737582
HLA A*2602	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.292138	1.126421	-3.165717	19594.666686
HLA A*0206	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.414837	1.249052	-3.165786	25991.861555
HLA A*8001	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.414941	1.249052	-3.165889	25998.049267
HLA A*0216	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.297008	1.131046	-3.165962	19815.651823
HLA A*3001	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.281570	1.115576	-3.165994	19123.610816
HLA B*4601	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.305001	1.138932	-3.166069	20183.724552
HLA A*3001	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.279594	1.113445	-3.166149	19036.801432
HLA A*0216	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.292610	1.126421	-3.166189	19615.985274
HLA B*1502	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.258178	1.091915	-3.166264	18120.844105
HLA A*3201	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.633042	0.466612	-3.166429	4295.775251
HLA A*3101	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.325961	1.159455	-3.166506	21181.712372
HLA B*1503	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.357075	1.190433	-3.166642	22754.919126
HLA B*4002	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.593081	1.426359	-3.166722	39181.500590
HLA B*0702	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.254248	1.087303	-3.166945	17957.576933
HLA A*2902	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.298019	1.131046	-3.166973	19861.801687
HLA B*4001	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.357632	1.190433	-3.167199	22784.112914
HLA A*6802	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.428185	1.260962	-3.167223	26803.086589
HLA A*0202	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.223115	1.055834	-3.167280	16715.320568
HLA A*0212	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.395715	1.228391	-3.167324	24872.241544
HLA A*2301	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.521088	1.353717	-3.167371	33196.182640
HLA B*0803	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.506972	1.339557	-3.167415	32134.566045
HLA B*5401	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.562463	1.394918	-3.167545	36514.266104
HLA B*4801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.404582	1.236980	-3.167601	25385.275617
HLA B*4001	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.332782	1.165167	-3.167615	21516.995121
HLA B*0803	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.396178	1.228391	-3.167787	24898.763219
HLA B*3801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.485364	1.317518	-3.167846	30574.842313
HLA A*0211	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.405002	1.236980	-3.168022	25409.869866
HLA B*5301	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.592339	1.424271	-3.168068	39114.576057
HLA A*6901	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.101285	0.932998	-3.168287	12626.544528
HLA B*5301	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.522077	1.353717	-3.168360	33271.875213
HLA B*1502	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.517195	1.348830	-3.168365	32899.935664
HLA A*0101	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.360224	1.191820	-3.168404	22920.474608
HLA A*3002	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.449730	1.281231	-3.168499	28166.286134
HLA A*8001	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.431580	1.263068	-3.168512	27013.435192
HLA B*5401	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.841638	0.673013	-3.168625	6944.455960
HLA B*0802	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.397094	1.228391	-3.168703	24951.351501
HLA A*2402	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.203219	1.034513	-3.168706	15966.850941
HLA B*0803	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.405745	1.236980	-3.168764	25453.345824
HLA B*4403	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.248125	1.079304	-3.168821	17706.184194
HLA A*1101	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.444622	1.275786	-3.168836	27836.960068
HLA A*2301	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.543342	1.374504	-3.168839	34941.574216
HLA A*2402	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.269348	1.100487	-3.168861	18592.931780
HLA B*3801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.491123	1.322138	-3.168985	30982.953386
HLA A*2601	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.309717	1.140721	-3.168995	20404.066351
HLA A*2603	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.550548	1.381432	-3.169117	35526.165756
HLA A*0219	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.418207	1.249052	-3.169155	26194.284888
HLA A*6901	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.372974	1.203805	-3.169169	23603.383424
HLA B*0801	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.408463	1.239243	-3.169220	25613.164118
HLA B*0802	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.458780	1.289436	-3.169344	28759.398798
HLA B*0702	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.359566	1.190075	-3.169491	22885.781667
HLA B*0801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.225328	1.055834	-3.169494	16800.721194
HLA A*3002	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.247049	1.077535	-3.169514	17662.367369
HLA A*6901	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.376959	1.207422	-3.169537	23820.945083
HLA B*0803	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.453578	1.284024	-3.169554	28416.987961
HLA A*0212	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.283492	1.113845	-3.169647	19208.425853
HLA A*0101	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.360320	1.190433	-3.169887	22925.559058
HLA B*0802	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.463159	1.293038	-3.170121	29050.876701
HLA B*3901	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.459562	1.289436	-3.170126	28811.255352
HLA B*7301	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-3.777366	0.607235	-3.170131	5989.157255
HLA B*3801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.474122	1.303793	-3.170329	29793.528474

HLA A*0212	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.419562	1.249052	-3.170511	26276.178255
HLA A*0203	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.203915	1.033365	-3.170550	15992.439576
HLA B*4402	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.398678	1.228069	-3.170609	25042.496817
HLA A*3001	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.837367	0.666703	-3.170664	6876.490769
HLA A*2501	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.458566	1.287816	-3.170750	28745.244033
HLA A*0219	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.407742	1.236980	-3.170761	25570.660159
HLA A*0219	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.296738	1.125828	-3.170910	19803.327602
HLA A*2402	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.221879	1.050933	-3.170946	16667.823035
HLA B*4801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.408888	1.237896	-3.170993	25638.256553
HLA B*5101	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.262969	1.091915	-3.171054	18321.837376
HLA A*2501	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.406170	1.235042	-3.171128	25478.281691
HLA B*1801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.474980	1.303793	-3.171187	29852.417182
HLA A*6901	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.285059	1.113845	-3.171214	19277.862664
HLA B*1502	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.336463	1.165167	-3.171297	21700.176408
HLA A*6802	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.406720	1.235408	-3.171312	25510.555429
HLA B*5801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.363168	1.191820	-3.171348	23076.370915
HLA A*6901	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.134426	0.962975	-3.171452	13627.818789
HLA B*5401	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.508004	1.336347	-3.171657	32210.974451
HLA B*0702	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.407077	1.235408	-3.171669	25531.541467
HLA A*3201	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.546174	1.374504	-3.171670	35170.099477
HLA A*3101	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.344405	1.172675	-3.171729	22100.623376
HLA A*2403	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.420782	1.249052	-3.171730	26350.058403
HLA A*3201	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.596072	1.424271	-3.171801	39452.266596
HLA A*2402	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.546329	1.374504	-3.171825	35182.659298
HLA A*6901	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.285393	1.113445	-3.171948	19292.677690
HLA B*0802	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.473133	1.301147	-3.171986	29725.749042
HLA A*3101	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.078823	0.906788	-3.172036	11990.117470
HLA A*2403	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.201086	1.028966	-3.172120	15888.611227
HLA B*1503	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.263646	1.091476	-3.172170	18350.405929
HLA B*4001	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.379734	1.207422	-3.172312	23973.626211
HLA B*4601	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.411567	1.239243	-3.172324	25796.863279
HLA B*4002	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.627828	1.455494	-3.172333	42445.103651
HLA B*3801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.546383	1.373907	-3.172475	35187.037259
HLA A*3101	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.281412	1.108898	-3.172514	19116.680478
HLA A*2601	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.345196	1.172675	-3.172521	22140.952496
HLA A*0101	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.380042	1.207422	-3.172620	23990.622233
HLA A*6801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.228490	1.055834	-3.172656	16923.505685
HLA A*0219	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.408374	1.235408	-3.172966	25607.899212
HLA B*1501	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.217030	1.044058	-3.172972	16482.745150
HLA B*0802	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.436053	1.263068	-3.172985	27293.123141
HLA B*4801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.401671	1.228391	-3.173280	25215.690841
HLA A*3101	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.377140	1.203805	-3.173335	23830.870037
HLA A*2501	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.474554	1.301147	-3.173408	29823.200302
HLA A*0206	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.225986	1.052564	-3.173422	16826.189689
HLA B*7301	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.614464	1.440990	-3.173474	41158.897001
HLA A*0219	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.401969	1.228391	-3.173578	25233.021383
HLA B*0801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.381010	1.207422	-3.173588	24044.153951
HLA B*5301	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.178738	1.005094	-3.173644	15091.681712
HLA B*4601	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.095115	0.921448	-3.173667	12448.435317
HLA B*1801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.300091	1.126421	-3.173670	19956.799176
HLA B*4601	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.355950	1.182210	-3.173740	22696.029798
HLA B*0801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.314876	1.140721	-3.174155	20647.914642
HLA B*3501	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.402277	1.228069	-3.174208	25250.910249
HLA A*3101	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.313603	1.139224	-3.174378	20587.460329
HLA A*0301	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.364859	1.190433	-3.174426	23166.431437
HLA A*0211	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.455688	1.281231	-3.174457	28555.375852
HLA A*2501	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.300462	1.125828	-3.174634	19973.864791
HLA A*0206	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.230520	1.055834	-3.174686	17002.793748
HLA A*6802	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-3.938103	0.763388	-3.174716	8671.682796
HLA A*0250	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.366605	1.191820	-3.174785	23259.737410
HLA A*3201	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.378928	1.203805	-3.175123	23929.182190
HLA B*0803	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.486656	1.311116	-3.175540	30665.951370
HLA B*0702	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.284446	1.108898	-3.175547	19250.661895
HLA B*3801	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.414823	1.239243	-3.175580	25991.017890
HLA B*1501	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.032792	0.857166	-3.175626	10784.309118

HLA A*2902	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.267245	1.091476	-3.175769	18503.125169
HLA A*0206	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.103399	0.927581	-3.175818	12688.171821
HLA A*2501	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.438887	1.263068	-3.175819	27471.774538
HLA B*4801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.411024	1.235042	-3.175982	25764.645477
HLA B*5801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.301832	1.125828	-3.176004	20036.961119
HLA B*1501	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.379908	1.203805	-3.176103	23983.225537
HLA A*3101	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.386296	1.210159	-3.176137	24338.613902
HLA B*2705	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.408043	1.231855	-3.176187	25588.373099
HLA B*3501	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.366266	1.190075	-3.176191	23241.624572
HLA A*0216	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.358410	1.182210	-3.176200	22824.948368
HLA B*4001	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.366313	1.190075	-3.176238	23244.139400
HLA B*0702	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.228974	1.052564	-3.176411	16942.376381
HLA B*5101	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.465786	1.289353	-3.176433	29227.116276
HLA A*2301	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.506352	1.329702	-3.176650	32088.703871
HLA A*3002	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.571759	1.394918	-3.176841	37304.350965
HLA A*0301	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.368729	1.191820	-3.176909	23373.768692
HLA A*8001	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.413923	1.236980	-3.176943	25937.220578
HLA B*5801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.316197	1.139224	-3.176972	20710.787218
HLA A*2902	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.316002	1.138932	-3.177069	20701.489731
HLA B*3801	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.458357	1.281231	-3.177126	28731.407100
HLA A*0212	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.416510	1.239243	-3.177267	26092.171139
HLA A*0301	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.367451	1.190075	-3.177375	23305.081287
HLA A*6802	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.405898	1.228391	-3.177507	25462.297884
HLA A*3001	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.198431	1.020917	-3.177514	15791.777652
HLA B*3901	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.359808	1.182210	-3.177598	22898.537604
HLA B*4001	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.269564	1.091915	-3.177649	18602.187968
HLA B*5401	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.555043	1.377330	-3.177712	35895.739317
HLA A*6802	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-3.952139	0.774258	-3.177881	8956.518075
HLA B*0803	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.409934	1.231855	-3.178079	25700.052463
HLA A*3002	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.195367	1.017185	-3.178183	15680.766652
HLA A*3301	1:278-286	9	ATGANLVTV	1.225117	0.184937	-4.588258	1.410054	-3.178204	38748.738842
HLA B*3501	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.415187	1.236980	-3.178207	26012.821352
HLA B*1801	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.388375	1.210159	-3.178216	24455.420544
HLA B*1502	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.555828	1.377330	-3.178497	35960.658068
HLA B*1801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.213256	1.034513	-3.178743	16340.158725
HLA A*6802	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.427807	1.249052	-3.178755	26779.751475
HLA B*7301	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.591455	1.412655	-3.178800	39035.093248
HLA B*0802	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.414264	1.235408	-3.178856	25957.574596
HLA A*2301	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.492091	1.313175	-3.178915	31052.087512
HLA B*4801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.344257	1.165167	-3.179090	22093.092259
HLA A*0219	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.223345	1.044058	-3.179287	16724.184864
HLA B*5401	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.553210	1.373907	-3.179303	35744.588710
HLA B*0801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.416419	1.236980	-3.179438	26086.666645
HLA B*4002	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.561384	1.381752	-3.179632	36423.708581
HLA B*5701	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.408038	1.228391	-3.179647	25588.096240
HLA A*2902	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.442738	1.263086	-3.179651	27716.444615
HLA A*0203	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.775176	0.595350	-3.179826	5959.035825
HLA B*4001	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.390046	1.210159	-3.179886	24549.667778
HLA A*3201	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.475226	1.295300	-3.179927	29869.379317
HLA B*0801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.305774	1.125828	-3.179946	20219.680614
HLA A*2403	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.345279	1.165167	-3.180112	22145.145196
HLA A*2601	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.383944	1.203805	-3.180139	24207.169257
HLA B*1517	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.464285	1.284024	-3.180261	29126.254933
HLA A*3001	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.267642	1.087303	-3.180339	18520.049780
HLA B*0802	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.418251	1.237896	-3.180356	26196.977482
HLA A*3002	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.353067	1.172675	-3.180392	22545.873965
HLA A*6802	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.353123	1.172675	-3.180448	22548.801451
HLA B*1517	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.208867	1.028301	-3.180566	16175.861988
HLA A*0206	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.417643	1.236980	-3.180662	26160.296995
HLA A*2603	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.185908	1.005151	-3.180758	15342.928651
HLA A*0202	1:208-216	9	PANIANALI	0.995189	0.008861	-4.185039	1.004050	-3.180989	15312.248056
HLA A*6901	1:294-302	9	EALSGVSAP	0.479426	0.006871	-3.667391	0.486297	-3.181094	4649.336956
HLA B*1509	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.444267	1.263068	-3.181199	27814.229529
HLA B*1517	1:208-216	9	PANIANALI	0.995189	0.008861	-4.185250	1.004050	-3.181200	15319.705252
HLA B*5401	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.562878	1.381432	-3.181447	36549.247098

HLA B*4801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.409549	1.228069	-3.181480	25677.260928
HLA A*2301	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.470849	1.289353	-3.181496	29569.849051
HLA B*2705	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.444718	1.263068	-3.181650	27843.135143
HLA A*6802	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.254593	1.072837	-3.181756	17971.863443
HLA A*6801	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.495119	1.313175	-3.181944	31269.381249
HLA B*0803	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.417001	1.235042	-3.181959	26121.689376
HLA B*1801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.410042	1.228069	-3.181973	25706.448843
HLA A*2902	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.413961	1.231855	-3.182106	25939.465755
HLA B*0702	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.303965	1.121826	-3.182139	20135.628403
HLA A*0201	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.389815	1.207422	-3.182393	24536.655751
HLA A*3002	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.417802	1.235408	-3.182394	26169.922418
HLA B*5101	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.347565	1.165167	-3.182398	22262.020637
HLA B*0702	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.421674	1.239243	-3.182431	26404.283461
HLA A*2402	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.463671	1.281231	-3.182440	29085.158233
HLA A*6802	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.084768	0.902116	-3.182652	12155.354665
HLA A*0219	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.443619	1.260962	-3.182656	27772.730274
HLA B*4601	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.386637	1.203805	-3.182832	24357.713427
HLA B*0702	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.152104	0.969193	-3.182910	14193.969747
HLA B*5401	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.116129	0.933159	-3.182969	13065.576012
HLA A*0219	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.373195	1.190075	-3.183120	23615.389495
HLA A*2501	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.411595	1.228069	-3.183526	25798.538032
HLA B*7301	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-3.241974	0.058419	-3.183556	1745.719536
HLA B*0803	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.473013	1.289353	-3.183660	29717.548709
HLA A*0206	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.391133	1.207422	-3.183711	24611.236338
HLA B*3901	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-3.961819	0.778023	-3.183796	9158.388974
HLA A*2601	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.399512	1.215498	-3.184014	25090.637411
HLA B*4403	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.639620	1.455494	-3.184125	43613.371792
HLA A*0203	1:208-216	9	PANIANALI	0.995189	0.008861	-4.188187	1.004050	-3.184137	15423.653708
HLA A*2402	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.579097	1.394918	-3.184179	37939.965361
HLA B*5301	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.323802	1.139224	-3.184577	21076.664852
HLA A*0101	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.374957	1.190075	-3.184882	23711.401623
HLA B*4402	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.400463	1.215498	-3.184965	25145.671393
HLA A*0301	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.332234	1.147258	-3.184976	21489.889945
HLA A*2601	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.332267	1.147258	-3.185009	21491.517618
HLA A*3002	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.448144	1.263086	-3.185057	28063.619572
HLA A*0201	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.211659	1.026553	-3.185106	16280.158211
HLA A*3301	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.448235	1.263068	-3.185167	28069.541219
HLA A*0216	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.446194	1.260962	-3.185231	27937.890570
HLA B*1502	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.375789	1.190433	-3.185356	23756.854856
HLA A*2902	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.300944	1.115576	-3.185367	19996.028640
HLA B*1503	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.413923	1.228391	-3.185532	25937.220578
HLA A*0301	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.367810	1.182210	-3.185600	23324.379192
HLA B*4403	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.612102	1.426359	-3.185744	40935.725839
HLA B*5101	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.489723	1.303793	-3.185930	30883.216115
HLA A*6801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.326920	1.140721	-3.186198	21228.517019
HLA A*2501	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.396380	1.210159	-3.186220	24910.350076
HLA A*2403	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.316690	1.130410	-3.186280	20734.329631
HLA B*3901	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.229588	1.043287	-3.186301	16966.315593
HLA B*0801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.390375	1.203805	-3.186570	24568.268358
HLA A*0211	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.418434	1.231855	-3.186579	26208.034189
HLA A*0219	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.418582	1.231855	-3.186727	26216.968012
HLA A*0250	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.113723	0.926967	-3.186756	12993.396406
HLA A*0301	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.308612	1.121826	-3.186786	20352.251895
HLA A*2902	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.221606	1.034513	-3.187093	16657.366471
HLA A*3001	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.279042	1.091915	-3.187127	19012.614868
HLA A*3301	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.628168	1.440990	-3.187179	42478.412093
HLA A*2902	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.352386	1.165167	-3.187219	22510.530200
HLA B*4801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.419160	1.231855	-3.187305	26251.881638
HLA B*3501	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.422372	1.235042	-3.187330	26446.742303
HLA A*0212	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.424362	1.236980	-3.187382	26568.204001
HLA A*1101	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.450479	1.263068	-3.187411	28214.936199
HLA B*0702	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.360137	1.172675	-3.187461	22915.887170
HLA B*3801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.498627	1.311116	-3.187511	31522.965648
HLA B*3901	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.422929	1.235408	-3.187521	26480.672575
HLA A*0301	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.347076	1.159455	-3.187621	22236.984233

HLA A*3101	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.318088	1.130410	-3.187678	20801.178566
HLA B*1801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.509905	1.322138	-3.187767	32352.257957
HLA A*8001	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.416266	1.228391	-3.187875	26077.495070
HLA B*0803	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.475701	1.287816	-3.187884	29902.038345
HLA B*4601	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.170524	0.982586	-3.187937	14808.935366
HLA A*0101	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.391819	1.203805	-3.188015	24650.145127
HLA B*4501	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.309858	1.121826	-3.188031	20410.690450
HLA B*0801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.340105	1.151838	-3.188267	21882.904555
HLA A*2301	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.469592	1.281231	-3.188361	29484.389045
HLA B*4501	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.601018	1.412655	-3.188363	39904.109644
HLA A*0212	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.370691	1.182210	-3.188481	23479.592859
HLA B*2705	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.395950	1.207422	-3.188528	24885.700791
HLA B*0702	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.420420	1.231855	-3.188564	26328.114708
HLA B*1801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.404063	1.215498	-3.188564	25354.943485
HLA B*3901	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.231878	1.043307	-3.188572	17056.043265
HLA A*3002	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.100636	0.911989	-3.188647	12607.705531
HLA B*5701	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.396133	1.207422	-3.188711	24896.204060
HLA A*0101	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.310560	1.121826	-3.188734	20443.732619
HLA A*0201	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.121913	0.933159	-3.188754	13240.762417
HLA B*1509	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.276114	1.087303	-3.188812	18884.887091
HLA B*1517	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.417255	1.228391	-3.188864	26136.955903
HLA B*4402	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.421620	1.232655	-3.188965	26400.998248
HLA B*2705	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.276669	1.087303	-3.189366	18909.013464
HLA A*2403	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.371602	1.182210	-3.189392	23528.929155
HLA A*0201	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.379567	1.190075	-3.189492	23964.419658
HLA B*0702	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.328726	1.139224	-3.189502	21317.015956
HLA B*5401	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.354669	1.165167	-3.189503	22629.211612
HLA B*4501	1:435-443	9	TAAGLDNQI	1.153463	0.272896	-4.616007	1.426359	-3.189649	41305.448241
HLA A*0211	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.519425	1.329702	-3.189723	33069.277762
HLA B*5801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.311667	1.121826	-3.189840	20495.890854
HLA A*0216	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.379999	1.190075	-3.189924	23988.286188
HLA A*3101	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.380392	1.190433	-3.189959	24009.968234
HLA A*3001	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.117581	0.927581	-3.190000	13109.331405
HLA A*0301	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.316046	1.125828	-3.190218	20703.617703
HLA B*1517	1:237-245	9	DSAVAAALV	0.764846	0.042930	-3.998025	0.807776	-3.190248	9954.619141
HLA A*2301	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.277559	1.087303	-3.190257	18947.823295
HLA A*6901	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.211231	1.020917	-3.190314	16264.136659
HLA B*4601	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.382177	1.191820	-3.190358	24108.888814
HLA B*4402	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.451372	1.260962	-3.190410	28272.998938
HLA A*3101	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.173038	0.982586	-3.190451	14894.906680
HLA B*2705	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.246967	1.056396	-3.190571	17659.023385
HLA B*1502	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.263439	1.072837	-3.190602	18341.671926
HLA A*0250	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.863648	0.673013	-3.190635	7305.470705
HLA A*1101	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.363348	1.172675	-3.190673	23085.985644
HLA B*3501	1:9-17	9	VPETPARPV	0.601332	-0.092772	-3.699311	0.508560	-3.190751	5003.928847
HLA A*2602	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.483971	1.293038	-3.190933	30476.913419
HLA A*2402	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.520773	1.329702	-3.191072	33172.126613
HLA A*0201	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.974821	0.783681	-3.191141	9436.721429
HLA A*3101	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.398600	1.207422	-3.191178	25038.026470
HLA B*1501	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.146644	0.955413	-3.191231	14016.632026
HLA A*6802	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.430478	1.239243	-3.191235	26944.982554
HLA B*7301	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.615563	1.424271	-3.191292	41263.236282
HLA B*5301	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.568698	1.377330	-3.191368	37042.314049
HLA A*2902	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.428542	1.236980	-3.191561	26825.135916
HLA B*1509	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.318001	1.126421	-3.191580	20797.015296
HLA B*1502	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.278922	1.087303	-3.191619	19007.369928
HLA B*4402	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.364450	1.172675	-3.191775	23144.634656
HLA B*5701	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.395950	1.203805	-3.192145	24885.700791
HLA A*3101	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.271462	1.079304	-3.192158	18683.679652
HLA A*0101	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.279488	1.087303	-3.192185	19032.167581
HLA B*5701	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.402378	1.210159	-3.192219	25256.784931
HLA B*0803	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.427663	1.235408	-3.192255	26770.915528
HLA A*8001	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.424191	1.231855	-3.192335	26557.713707
HLA B*4001	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.333362	1.140721	-3.192640	21545.766265
HLA A*0250	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.587729	1.394918	-3.192811	38701.601601

HLA A*0219	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.313650	1.120820	-3.192829	20589.687967
HLA A*0212	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.155825	0.962975	-3.192851	14316.124266
HLA A*2402	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.425520	1.232655	-3.192865	26639.157981
HLA B*4601	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.403097	1.210159	-3.192938	25298.630298
HLA B*5401	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.549515	1.356576	-3.192938	35441.701571
HLA B*1501	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.226319	1.033365	-3.192955	16839.120606
HLA B*5401	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.486008	1.293038	-3.192970	30620.197303
HLA A*0301	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.358205	1.165167	-3.193039	22814.208097
HLA A*3301	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.432381	1.239243	-3.193138	27063.314820
HLA A*2601	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.400604	1.207422	-3.193182	25153.834836
HLA B*4601	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.383296	1.190075	-3.193220	24171.051791
HLA B*5301	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.566191	1.372792	-3.193400	36829.108724
HLA B*4601	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.315358	1.121826	-3.193532	20670.826445
HLA B*7301	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.230572	1.036964	-3.193608	17004.817500
HLA B*4403	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.606288	1.412655	-3.193633	40391.271052
HLA B*0802	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.428685	1.235042	-3.193643	26833.989759
HLA B*1509	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.477301	1.283502	-3.193799	30012.404653
HLA B*3901	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.315797	1.121826	-3.193971	20691.748653
HLA A*3001	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.211236	1.017228	-3.194008	16264.312634
HLA A*0212	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.345864	1.151838	-3.194025	22174.996189
HLA B*1517	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.433354	1.239243	-3.194111	27123.996295
HLA A*2403	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.401586	1.207422	-3.194164	25210.780411
HLA A*6802	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-3.405649	0.211398	-3.194251	2544.772689
HLA A*6802	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.308187	1.113845	-3.194342	20332.332929
HLA B*3501	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.867389	0.673013	-3.194376	7368.661114
HLA A*2602	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.075896	0.881518	-3.194378	11909.567212
HLA B*3501	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.294948	1.100487	-3.194461	19721.859675
HLA B*1503	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.353925	1.159455	-3.194470	22590.437246
HLA B*7301	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-3.647406	0.452913	-3.194493	4440.238549
HLA B*4501	1:186-194	9	PHGQQVLSR	1.083686	0.371808	-4.650021	1.455494	-3.194526	44670.502079
HLA A*0203	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.367246	1.172675	-3.194571	23294.115090
HLA B*5101	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.484204	1.289436	-3.194767	30493.240587
HLA B*3501	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.402249	1.207422	-3.194827	25249.271047
HLA B*4002	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.543702	1.348830	-3.194872	34970.507786
HLA B*4601	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.286377	1.091476	-3.194901	19336.458844
HLA B*4601	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.402406	1.207422	-3.194984	25258.424622
HLA B*4402	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.008936	0.813920	-3.195016	10207.882377
HLA A*0250	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.426925	1.231855	-3.195070	26725.478238
HLA A*2602	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.577135	1.381752	-3.195383	37768.967282
HLA B*4001	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.286899	1.091476	-3.195422	19359.695793
HLA A*0212	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.212678	1.017185	-3.195494	16318.427171
HLA A*0202	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.458676	1.263086	-3.195590	28752.553866
HLA A*0206	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.273368	1.077535	-3.195832	18765.832892
HLA A*2602	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.535420	1.339557	-3.195863	34309.943577
HLA A*0206	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.327129	1.131046	-3.196083	21238.740590
HLA B*0802	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.309529	1.113445	-3.196084	20395.237562
HLA A*3001	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.116185	0.920085	-3.196100	13067.272521
HLA B*4403	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.431155	1.235042	-3.196112	26986.996854
HLA A*6901	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.053285	0.857166	-3.196118	11305.363638
HLA A*0216	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.309982	1.113845	-3.196137	20416.543526
HLA A*2403	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.434477	1.237896	-3.196581	27194.227737
HLA A*2501	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.480663	1.284024	-3.196639	30245.648897
HLA B*2705	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.335592	1.138932	-3.196659	21656.666338
HLA A*0212	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.322615	1.125828	-3.196787	21019.162114
HLA A*6901	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.386965	1.190075	-3.196890	24376.168569
HLA A*3101	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.323001	1.126026	-3.196975	21037.819049
HLA A*2601	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.387501	1.190433	-3.197068	24406.254020
HLA A*2602	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.260213	1.062990	-3.197223	18205.938784
HLA B*5701	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.412822	1.215498	-3.197323	25871.495092
HLA A*2902	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.357291	1.159455	-3.197837	22766.247291
HLA A*2602	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.484011	1.286148	-3.197863	30479.716452
HLA B*4002	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.638887	1.440990	-3.197897	43539.819509
HLA A*3002	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.248886	1.050933	-3.197953	17737.246881
HLA B*0801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.218890	1.020890	-3.198001	16553.519163
HLA B*1517	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.461141	1.263068	-3.198073	28916.187723

HLA A*1101	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.461233	1.263086	-3.198146	28922.289268
HLA B*4402	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.408372	1.210159	-3.198212	25607.760677
HLA A*0216	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.437475	1.239243	-3.198232	27382.599414
HLA A*2402	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.402037	1.203805	-3.198233	25236.980421
HLA B*3901	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.461327	1.263086	-3.198240	28928.548600
HLA B*4002	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.493571	1.295300	-3.198271	31158.100730
HLA A*2902	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.426700	1.228391	-3.198309	26711.601982
HLA A*0202	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.593241	1.394918	-3.198323	39195.917037
HLA A*6901	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.215554	1.017185	-3.198369	16426.841518
HLA A*0203	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.436347	1.237896	-3.198451	27311.585979
HLA B*0803	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.484619	1.286148	-3.198471	30522.453385
HLA B*4501	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.402418	1.203805	-3.198613	25259.107857
HLA B*1509	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.488160	1.289436	-3.198724	30772.311004
HLA A*6801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.225943	1.027198	-3.198745	16824.551268
HLA A*0201	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.329878	1.131046	-3.198832	21373.599039
HLA A*3001	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.292986	1.094025	-3.198961	19632.971874
HLA A*0219	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.381188	1.182210	-3.198978	24054.041775
HLA B*3801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.538601	1.339557	-3.199044	34562.186276
HLA A*0211	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.434456	1.235408	-3.199048	27192.903710
HLA A*0216	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.308230	1.109115	-3.199115	20334.312947
HLA A*8001	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-3.994016	0.794851	-3.199166	9863.167928
HLA B*5801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.358659	1.159455	-3.199204	22838.041048
HLA B*0803	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.492283	1.293038	-3.199245	31065.865613
HLA A*2403	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.409408	1.210159	-3.199248	25668.927612
HLA B*5301	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.510429	1.311116	-3.199312	32391.311445
HLA A*2402	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.340190	1.140721	-3.199468	21887.166797
HLA B*4001	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.338442	1.138932	-3.199509	21799.248932
HLA A*0301	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.329967	1.130410	-3.199557	21377.993385
HLA B*3501	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.227926	1.028301	-3.199625	16901.546914
HLA B*1517	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.313683	1.113845	-3.199838	20591.247457
HLA A*2603	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.487688	1.287816	-3.199871	30738.867757
HLA A*2603	1:211-219	9	IANALIEQV	1.224006	0.188649	-4.612629	1.412655	-3.199974	40985.362442
HLA B*4001	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.321812	1.121826	-3.199986	20980.308791
HLA B*1503	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.169189	0.969193	-3.199996	14763.500060
HLA A*0202	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.539635	1.339557	-3.200078	34644.554412
HLA B*2705	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.330709	1.130410	-3.200299	21414.570855
HLA B*1801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.183061	0.982586	-3.200474	15242.657444
HLA A*6901	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.113314	0.912830	-3.200484	12981.171208
HLA B*4402	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.429308	1.228391	-3.200917	26872.487108
HLA B*1501	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.360402	1.159455	-3.200947	22929.900335
HLA B*4402	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.391197	1.190075	-3.201122	24614.831490
HLA B*5801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.352971	1.151838	-3.201133	22540.873721
HLA B*4801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.391230	1.190075	-3.201155	24616.695850
HLA A*6901	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.295185	1.094025	-3.201160	19732.638620
HLA B*5801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.348605	1.147258	-3.201347	22315.437354
HLA A*2403	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.433309	1.231855	-3.201454	27121.208420
HLA A*2601	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.366656	1.165167	-3.201490	23262.505892
HLA A*0101	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.374266	1.172675	-3.201591	23673.718439
HLA A*6901	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.274458	1.072837	-3.201621	18812.997842
HLA B*4001	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.383977	1.182210	-3.201767	24209.002740
HLA A*3101	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.391932	1.190075	-3.201857	24656.546977
HLA A*0202	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.162554	0.960386	-3.202169	14539.664471
HLA A*1101	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.463216	1.260962	-3.202253	29054.648835
HLA B*5101	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.384543	1.182210	-3.202333	24240.586618
HLA A*1101	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.430483	1.228069	-3.202414	26945.274094
HLA B*4801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.409941	1.207422	-3.202519	25700.469570
HLA A*0212	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.440449	1.237896	-3.202554	27570.784334
HLA B*0802	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.435238	1.232655	-3.202583	27241.935690
HLA B*1503	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.135794	0.933159	-3.202634	13670.794353
HLA A*2501	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.367869	1.165167	-3.202702	23327.533963
HLA A*0301	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.343427	1.140721	-3.202706	22050.941542
HLA B*5401	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.231110	1.028301	-3.202809	17025.897221
HLA B*4001	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.375577	1.172675	-3.202902	23745.290696
HLA A*0219	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.442190	1.239243	-3.202947	27681.529931
HLA A*3301	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.631335	1.428368	-3.202968	42789.319484

HLA A*3101	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.343780	1.140721	-3.203058	22068.842777
HLA B*2705	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.440101	1.236980	-3.203121	27548.718245
HLA A*2603	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.584931	1.381752	-3.203179	38453.041911
HLA B*1502	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.598316	1.394918	-3.203398	39656.621968
HLA A*6802	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.441535	1.237896	-3.203639	27639.780078
HLA B*1509	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.395513	1.191820	-3.203693	24860.672413
HLA B*5801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.295613	1.091915	-3.203698	19752.076941
HLA B*5101	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.419393	1.215498	-3.203895	26265.945361
HLA B*3801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.497004	1.293038	-3.203965	31405.345428
HLA B*1509	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.394423	1.190433	-3.203990	24798.345696
HLA A*3201	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.533787	1.329702	-3.204085	34181.184758
HLA A*0301	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.343448	1.139224	-3.204224	22052.015207
HLA B*1502	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.408094	1.203805	-3.204290	25591.418746
HLA A*3301	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.493742	1.289353	-3.204389	31170.408176
HLA A*3101	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.238906	1.034513	-3.204392	17334.271666
HLA B*3801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.490702	1.286148	-3.204554	30952.964941
HLA B*1517	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.412051	1.207422	-3.204629	25825.628288
HLA A*2402	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.494093	1.289353	-3.204739	31195.543945
HLA B*0801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.433138	1.228391	-3.204746	27110.499775
HLA A*8001	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.420420	1.215498	-3.204922	26328.114708
HLA B*5401	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.485071	1.280105	-3.204966	30554.173489
HLA A*0250	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.486248	1.281231	-3.205017	30637.098456
HLA B*5101	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.454114	1.249052	-3.205062	28452.060655
HLA B*4601	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.352459	1.147258	-3.205201	22514.305680
HLA B*3501	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.118060	0.912830	-3.205230	13123.807078
HLA B*1801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.370409	1.165167	-3.205242	23464.355167
HLA A*3201	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-3.720109	0.514746	-3.205363	5249.389121
HLA A*2603	1:206-214	9	WTPANIANA	1.064045	-0.280364	-3.989289	0.783681	-3.205609	9756.392497
HLA A*6802	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.019104	0.813260	-3.205844	10449.709763
HLA B*5801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.210113	1.004050	-3.206062	16222.308642
HLA A*6802	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.396345	1.190075	-3.206269	24908.328724
HLA B*1801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.496010	1.289436	-3.206573	31333.560133
HLA A*0212	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.414217	1.207422	-3.206795	25954.766196
HLA B*3501	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.446053	1.239243	-3.206810	27928.823588
HLA A*2602	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.347426	1.140437	-3.206989	22254.916103
HLA B*0803	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.470142	1.263086	-3.207056	29521.737383
HLA A*2603	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.510863	1.303793	-3.207070	32423.745852
HLA A*2902	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.128943	0.921448	-3.207495	13456.826470
HLA B*4801	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.417727	1.210159	-3.207568	26165.392366
HLA B*1501	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.263437	1.055834	-3.207602	18341.572700
HLA B*3501	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.212749	1.005094	-3.207655	16321.075812
HLA A*2602	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.495476	1.287816	-3.207660	31295.104734
HLA A*2601	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.397839	1.190075	-3.207764	24994.178155
HLA B*0801	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-3.713121	0.505350	-3.207771	5165.607435
HLA B*0802	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.444958	1.236980	-3.207977	27858.503467
HLA A*2402	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.494128	1.286148	-3.207979	31198.075514
HLA B*0803	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.497426	1.289436	-3.207990	31435.942222
HLA A*2402	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.483811	1.275786	-3.208025	30465.703864
HLA B*4601	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.141202	0.933159	-3.208043	13842.109001
HLA A*3001	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.168546	0.960386	-3.208160	14741.632194
HLA A*6802	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.412018	1.203805	-3.208213	25823.672369
HLA A*2402	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.418742	1.210159	-3.208583	26226.614287
HLA A*0101	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.339012	1.130410	-3.208602	21827.925137
HLA B*2705	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.484565	1.275786	-3.208779	30518.655790
HLA A*2902	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.111030	0.902116	-3.208914	12913.090015
HLA A*2602	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.135888	0.926967	-3.208921	13673.752972
HLA A*3002	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.242287	1.033365	-3.208922	17469.742658
HLA A*6801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.334765	1.125828	-3.208936	21615.465202
HLA B*4601	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.334809	1.125828	-3.208981	21617.687124
HLA A*0206	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.252312	1.043307	-3.209005	17877.704726
HLA B*5101	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.138881	0.929716	-3.209165	13768.320711
HLA B*1509	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.437757	1.228391	-3.209366	27400.381605
HLA A*6802	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-3.985342	0.775707	-3.209635	9668.122149
HLA A*2902	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.458695	1.249052	-3.209644	28753.798278
HLA B*4001	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.356979	1.147258	-3.209721	22749.872521

HLA A*2301	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.485529	1.275786	-3.209743	30586.422961
HLA B*1501	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.142917	0.933159	-3.209758	13896.882608
HLA B*3801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.301681	1.091915	-3.209767	20030.024864
HLA B*5101	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.485569	1.275786	-3.209783	30589.236066
HLA B*2705	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.445263	1.235408	-3.209855	27878.102842
HLA B*3501	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.447789	1.237896	-3.209893	28040.703952
HLA B*5701	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.399979	1.190075	-3.209904	25117.663732
HLA B*5101	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.400104	1.190075	-3.210029	25124.866605
HLA B*3901	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.349501	1.138932	-3.210568	22361.480649
HLA A*2301	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.443264	1.232655	-3.210609	27750.052182
HLA A*3002	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.486426	1.275786	-3.210640	30649.697538
HLA B*4801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.383474	1.172675	-3.210799	24180.991801
HLA A*6801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.506162	1.295300	-3.210862	32074.645649
HLA B*1503	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.110706	0.899837	-3.210869	12903.453155
HLA A*3001	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.191641	0.980728	-3.210913	15546.799899
HLA A*2403	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.401107	1.190075	-3.211032	25182.972703
HLA B*4403	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.652227	1.440990	-3.211237	44898.000477
HLA A*3301	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.533385	1.322138	-3.211248	34149.578671
HLA B*3901	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.350563	1.139224	-3.211338	22416.227413
HLA B*1503	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.124258	0.912830	-3.211428	13312.443543
HLA A*2602	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.421597	1.210159	-3.211438	26399.570022
HLA B*5301	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.606389	1.394918	-3.211470	40400.668174
HLA B*1801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.447096	1.235408	-3.211688	27995.988998
HLA A*0250	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.447117	1.235408	-3.211709	27997.352128
HLA B*1502	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.568317	1.356576	-3.211741	37009.864311
HLA A*0202	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.123797	0.911989	-3.211808	13298.335331
HLA B*5401	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.475125	1.263068	-3.212057	29862.431754
HLA B*1801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.447124	1.235042	-3.212082	27997.806519
HLA B*4001	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.363959	1.151838	-3.212121	23118.480574
HLA B*7301	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.561140	1.348830	-3.212310	36403.221329
HLA A*2501	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.217739	1.005151	-3.212589	16509.696447
HLA B*5701	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.404432	1.191820	-3.212612	25376.487920
HLA B*3901	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.156347	0.943730	-3.212618	14333.328194
HLA B*3501	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.118915	0.906227	-3.212688	13149.675936
HLA B*1801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.292058	1.079304	-3.212754	19591.062848
HLA B*7301	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.594676	1.381752	-3.212925	39325.691240
HLA A*0201	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.385772	1.172675	-3.213097	24309.269374
HLA B*3501	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.403553	1.190433	-3.213120	25325.195617
HLA A*0202	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-3.976508	0.763388	-3.213120	9473.447772
HLA B*1509	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.338984	1.125828	-3.213156	21826.508143
HLA B*3801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.514799	1.301147	-3.213652	32718.890929
HLA A*2601	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.395992	1.182210	-3.213782	24888.124229
HLA B*0702	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.334607	1.120820	-3.213787	21607.631824
HLA B*1517	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.176985	0.962975	-3.214010	15030.897783
HLA B*5301	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.570735	1.356576	-3.214159	37216.464448
HLA B*0802	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.424393	1.210159	-3.214233	26570.072570
HLA A*0206	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.221569	1.007289	-3.214280	16655.924702
HLA B*5801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.354871	1.140437	-3.214435	22639.742313
HLA B*4001	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.373926	1.159455	-3.214471	23655.155253
HLA B*4501	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.655479	1.440990	-3.214489	45235.426298
HLA B*3501	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.424693	1.210159	-3.214534	26588.477809
HLA B*5401	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.532107	1.317518	-3.214589	34049.224897
HLA A*2603	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.379783	1.165167	-3.214616	23976.349954
HLA B*5101	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.241514	1.026553	-3.214961	17438.676729
HLA A*0301	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.366812	1.151838	-3.214973	23270.813315
HLA B*1501	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.341550	1.126421	-3.215129	21955.832020
HLA A*3001	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.292737	1.077535	-3.215202	19621.716608
HLA B*4601	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.405663	1.190433	-3.215230	25448.526788
HLA B*0801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.346350	1.131046	-3.215304	22199.842703
HLA A*6802	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.367220	1.151838	-3.215382	23292.728927
HLA A*3002	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.443868	1.228391	-3.215477	27788.661065
HLA B*1509	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.356239	1.140721	-3.215517	22711.137134
HLA B*4601	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.354827	1.139224	-3.215602	22637.415341
HLA A*3101	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.407834	1.191820	-3.216014	25576.055771
HLA A*3101	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.233269	1.017185	-3.216084	17110.755442

HLA A*0250	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.545798	1.329702	-3.216096	35139.670035
HLA B*0802	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.448076	1.231855	-3.216220	28059.217107
HLA A*0216	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.389012	1.172675	-3.216337	24491.300441
HLA B*4403	1:99-107	9	MAQALGGIV	1.150311	0.231441	-4.598090	1.381752	-3.216338	39636.031674
HLA A*8001	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.381681	1.165167	-3.216515	24081.384541
HLA B*3801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.486111	1.269596	-3.216516	30627.486853
HLA B*1517	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.329965	1.113445	-3.216520	21377.877733
HLA B*5101	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.408346	1.191820	-3.216526	25606.236836
HLA B*2705	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.138209	0.921448	-3.216761	13747.034447
HLA B*1503	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.018080	0.801202	-3.216878	10425.090956
HLA A*2301	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.355912	1.138932	-3.216980	22694.065355
HLA A*6801	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.598584	1.381432	-3.217152	39681.086836
HLA B*3501	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.348253	1.131046	-3.217207	22297.336093
HLA A*8001	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.407695	1.190433	-3.217262	25567.893620
HLA A*3001	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.273701	1.056396	-3.217305	18780.254423
HLA B*1502	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.547031	1.329702	-3.217329	35239.615302
HLA B*1801	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.500871	1.283502	-3.217369	31686.248722
HLA B*3501	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.445780	1.228391	-3.217389	27911.302433
HLA A*0202	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.573994	1.356576	-3.217417	37496.769113
HLA A*0219	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.244051	1.026553	-3.217498	17540.863574
HLA B*4801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.377199	1.159455	-3.217744	23834.093315
HLA A*6802	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-3.966142	0.748391	-3.217751	9250.008617
HLA A*0101	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.365024	1.147258	-3.217766	23175.206047
HLA A*3001	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.115546	0.897730	-3.217816	13048.058303
HLA B*5301	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.487509	1.269596	-3.217914	30726.232021
HLA B*1517	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.478950	1.260962	-3.217988	30126.600735
HLA A*2603	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.457293	1.239243	-3.218050	28661.081829
HLA B*5301	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.501616	1.283502	-3.218113	31740.635196
HLA A*3002	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.467214	1.249052	-3.218163	29323.408752
HLA A*3301	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.599643	1.381432	-3.218212	39778.021337
HLA B*5801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.349334	1.131046	-3.218288	22352.893206
HLA B*0803	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.450956	1.232655	-3.218301	28245.939075
HLA B*5301	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.592903	1.374504	-3.218399	39165.394365
HLA A*8001	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.408543	1.190075	-3.218468	25617.875740
HLA B*5301	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.592421	1.373907	-3.218514	39121.982952
HLA A*2902	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.365945	1.147258	-3.218687	23224.405312
HLA A*3001	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.262128	1.043307	-3.218821	18286.387075
HLA B*1801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.391641	1.172675	-3.218966	24640.012264
HLA B*1501	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.013921	0.794851	-3.219070	10325.741876
HLA A*1101	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.450933	1.231855	-3.219077	28244.411042
HLA A*3002	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.345060	1.125828	-3.219232	22134.006340
HLA B*2705	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.378886	1.159455	-3.219431	23926.852128
HLA B*5101	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.500673	1.281231	-3.219443	31671.852790
HLA A*2902	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.119690	0.900174	-3.219516	13173.172539
HLA B*5801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.345972	1.126421	-3.219551	22180.515233
HLA B*4801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.358494	1.138932	-3.219562	22829.394096
HLA B*0702	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.457302	1.236980	-3.220322	28661.702049
HLA A*2301	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.504355	1.284024	-3.220331	31941.485734
HLA A*0216	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.263641	1.043307	-3.220334	18350.207383
HLA A*6901	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.203013	0.982586	-3.220426	15959.251407
HLA B*4501	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.615361	1.394918	-3.220443	41244.043008
HLA A*1101	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.469503	1.249052	-3.220451	29478.328392
HLA A*2902	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.248757	1.028301	-3.220456	17731.970057
HLA A*3002	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.483609	1.263068	-3.220541	30451.532978
HLA B*4402	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.385906	1.165167	-3.220739	24316.766626
HLA B*4801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.412580	1.191820	-3.220760	25857.083030
HLA A*0219	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.372657	1.151838	-3.220819	23586.151339
HLA B*7301	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.615838	1.394918	-3.220920	41289.362405
HLA B*3501	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.120762	0.899837	-3.220925	13205.709679
HLA B*3901	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.458890	1.237896	-3.220995	28766.712230
HLA B*3801	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.470121	1.249052	-3.221069	29520.300034
HLA B*4801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.403360	1.182210	-3.221150	25313.963575
HLA B*3501	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.413000	1.191820	-3.221181	25882.134385
HLA A*2602	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.522373	1.301147	-3.221227	33294.562586
HLA A*0219	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.459304	1.237896	-3.221408	28794.115225

HLA B*1801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.484497	1.263086	-3.221411	30513.868192
HLA A*1101	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.437028	1.215498	-3.221530	27354.467878
HLA B*4501	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.543819	1.322138	-3.221682	34979.968394
HLA A*0250	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.578366	1.356576	-3.221790	37876.185966
HLA B*4002	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.646198	1.424271	-3.221927	44279.042569
HLA B*1502	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.284974	1.062990	-3.221984	19274.108550
HLA A*2403	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.084171	0.862117	-3.222054	12138.663319
HLA A*6802	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.353173	1.131046	-3.222127	22551.363313
HLA B*3801	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.517451	1.295300	-3.222151	32919.341751
HLA A*3101	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.374020	1.151838	-3.222182	23660.274677
HLA B*1501	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.314009	1.091476	-3.222533	20606.737375
HLA B*5101	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.131203	0.908582	-3.222621	13527.042566
HLA A*2403	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.382121	1.159455	-3.222666	24105.758783
HLA B*0802	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.426625	1.203805	-3.222820	26706.978164
HLA A*0216	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.353279	1.130410	-3.222868	22556.853999
HLA A*1101	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.460845	1.237896	-3.222949	28896.483834
HLA A*0216	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.006638	0.783681	-3.222957	10154.016407
HLA A*0206	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.498752	1.275786	-3.222966	31532.005339
HLA A*2603	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.504226	1.281231	-3.222995	31931.983153
HLA A*0212	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.249584	1.026553	-3.223031	17765.768881
HLA B*4501	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.275644	1.052564	-3.223081	18864.465112
HLA B*0802	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.370359	1.147258	-3.223101	23461.689587
HLA B*3901	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.382607	1.159455	-3.223152	24132.768666
HLA A*2601	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.353633	1.130410	-3.223223	22575.288069
HLA B*4501	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.037144	0.813920	-3.223224	10892.901439
HLA A*0301	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.363929	1.140437	-3.223492	23116.854742
HLA A*1101	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.460626	1.236980	-3.223646	28881.949101
HLA B*5701	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.364410	1.140721	-3.223689	23142.506186
HLA B*3901	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-3.526351	0.302627	-3.223724	3360.094082
HLA B*1801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-3.999448	0.775634	-3.223814	9987.307847
HLA A*2301	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.427623	1.203805	-3.223818	26768.453571
HLA A*8001	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.431267	1.207422	-3.223845	26994.005604
HLA B*5101	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.324342	1.100487	-3.223855	21102.906331
HLA B*4001	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.349714	1.125828	-3.223886	22372.491914
HLA B*2705	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.434066	1.210159	-3.223906	27168.494313
HLA B*3901	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-3.950128	0.726094	-3.224034	8915.137536
HLA B*1509	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.431472	1.207422	-3.224050	27006.713602
HLA A*2902	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.231364	1.007289	-3.224075	17035.847815
HLA B*5701	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.414652	1.190433	-3.224219	25980.755494
HLA A*0219	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.315722	1.091476	-3.224246	20688.166881
HLA A*0202	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.042754	0.818458	-3.224296	11034.537737
HLA B*3501	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.473424	1.249052	-3.224372	29745.696544
HLA B*5801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.347612	1.123169	-3.224442	22264.429469
HLA B*4801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.350309	1.125828	-3.224481	22403.134153
HLA A*0202	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.355691	1.131046	-3.224645	22682.527686
HLA A*0216	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.316201	1.091476	-3.224725	20711.011305
HLA B*5801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.350903	1.126026	-3.224877	22433.818360
HLA A*2602	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.581479	1.356576	-3.224903	38148.661773
HLA B*4402	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.032736	0.807656	-3.225080	10782.909003
HLA A*2603	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.598050	1.372792	-3.225259	39632.386591
HLA A*3001	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.158269	0.932998	-3.225271	14396.897872
HLA B*0802	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.453454	1.228069	-3.225384	28408.841293
HLA B*2705	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.407615	1.182210	-3.225405	25563.191191
HLA A*3201	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.620352	1.394918	-3.225433	41720.695262
HLA A*8001	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.377354	1.151838	-3.225516	23842.604861
HLA A*3101	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.351378	1.125828	-3.225550	22458.347384
HLA B*0803	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.463458	1.237896	-3.225562	29070.843136
HLA A*3001	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.252791	1.027198	-3.225593	17897.445763
HLA A*0250	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.757860	0.532233	-3.225627	5726.117979
HLA B*1801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.326241	1.100487	-3.225753	21195.353057
HLA B*5401	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.511972	1.286148	-3.225824	32506.644634
HLA B*5801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.356265	1.130410	-3.225855	22712.488686
HLA B*4801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.429672	1.203805	-3.225867	26895.030021
HLA B*1517	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.457969	1.231855	-3.226114	28705.771978
HLA A*2501	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.475170	1.249052	-3.226118	29865.501408

HLA A*2603	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.537262	1.311116	-3.226146	34455.773201
HLA A*3101	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.247049	1.020890	-3.226159	17662.367369
HLA B*3801	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.514035	1.287816	-3.226219	32661.414661
HLA A*0219	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.313532	1.087303	-3.226229	20584.119324
HLA B*1503	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.892956	0.666703	-3.226253	7815.480422
HLA A*1101	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.208910	0.982586	-3.226323	16177.437238
HLA B*3901	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.489415	1.263068	-3.226347	30861.337073
HLA B*3801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.515849	1.289436	-3.226413	32798.108164
HLA B*4002	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.548735	1.322138	-3.226597	35378.102458
HLA B*5701	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.156375	0.929716	-3.226659	14334.258725
HLA A*2902	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.357193	1.130410	-3.226783	22761.075038
HLA A*2602	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.548948	1.322138	-3.226811	35395.523383
HLA A*8001	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.409039	1.182210	-3.226829	25647.134898
HLA A*2403	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.417344	1.190433	-3.226911	26142.329581
HLA A*2603	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.462342	1.235408	-3.226934	28996.235768
HLA A*2501	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.458834	1.231855	-3.226978	28762.977479
HLA B*1502	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.365992	1.138932	-3.227059	23226.918277
HLA A*1101	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.021928	0.794851	-3.227077	10517.882364
HLA A*2902	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.417591	1.190433	-3.227158	26157.183645
HLA B*3501	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.459325	1.231855	-3.227470	28795.517216
HLA A*0206	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.319401	1.091915	-3.227487	20864.179206
HLA B*4002	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.148551	0.920891	-3.227660	14078.340144
HLA B*2705	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.431768	1.203805	-3.227963	27025.128897
HLA A*8001	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.419804	1.191820	-3.227985	26290.823910
HLA B*1517	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.418256	1.190075	-3.228181	26197.260929
HLA B*5801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.256531	1.028301	-3.228230	18052.253983
HLA A*2902	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.354084	1.125828	-3.228256	22598.749174
HLA B*4001	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.367570	1.139224	-3.228346	23311.512148
HLA A*0219	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.337478	1.109115	-3.228364	21750.950593
HLA B*3801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.461056	1.232655	-3.228401	28910.556670
HLA B*5801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.342335	1.113845	-3.228490	21995.539941
HLA A*0202	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.532307	1.303793	-3.228514	34064.885712
HLA B*4601	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.388030	1.159455	-3.228575	24435.980011
HLA A*3201	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.359707	1.131046	-3.228661	22893.211445
HLA B*5301	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.158565	0.929716	-3.228849	14406.714805
HLA A*1101	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.464308	1.235408	-3.228900	29127.830674
HLA A*2902	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.419095	1.190075	-3.229019	26247.905386
HLA B*7301	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.602968	1.373907	-3.229060	40083.690272
HLA A*3001	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.211668	0.982586	-3.229082	16280.510511
HLA A*2301	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.517120	1.287816	-3.229303	32894.240637
HLA A*0202	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.091576	0.862117	-3.229460	12347.426300
HLA B*1517	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.159528	0.929716	-3.229812	14438.705150
HLA A*2403	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.370559	1.140721	-3.229838	23472.480705
HLA A*2603	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.499616	1.269596	-3.230021	31594.843020
HLA B*1501	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.282768	1.052564	-3.230204	19176.446543
HLA B*0802	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.445782	1.215498	-3.230284	27911.453430
HLA A*3201	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.382147	1.151838	-3.230308	24107.193330
HLA A*6802	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.437829	1.207422	-3.230407	27404.977214
HLA B*1502	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.518271	1.287816	-3.230455	32981.553869
HLA B*3901	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.395687	1.165167	-3.230520	24870.626923
HLA B*5101	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.440787	1.210159	-3.230628	27592.271006
HLA B*4002	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.612102	1.381432	-3.230671	40935.725839
HLA B*4402	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.946270	0.715584	-3.230687	8836.294731
HLA A*2403	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.353866	1.123169	-3.230697	22587.382158
HLA A*8001	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.369671	1.138932	-3.230739	23424.529980
HLA A*3001	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.146005	0.915104	-3.230901	13996.021861
HLA B*4501	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.655204	1.424271	-3.230933	45206.803277
HLA B*1517	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.467915	1.236980	-3.230934	29370.720523
HLA A*2403	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.251943	1.020890	-3.231053	17862.526698
HLA B*1801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.459560	1.228391	-3.231169	28811.099486
HLA A*6901	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.191646	0.960386	-3.231260	15546.968113
HLA A*3002	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.561053	1.329702	-3.231351	36395.935375
HLA A*0301	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.362535	1.131046	-3.231489	23042.813215
HLA B*5101	1:208-216	9	PANIANALI	0.995189	0.008861	-4.235800	1.004050	-3.231749	17210.741412
HLA A*8001	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.287721	1.055834	-3.231886	19396.387352

HLA B*1509	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.464874	1.232655	-3.232219	29165.831820
HLA B*0702	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.899046	0.666703	-3.232343	7925.844447
HLA B*1502	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.899083	0.666703	-3.232380	7926.530524
HLA A*2402	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.460490	1.228069	-3.232421	28872.888130
HLA B*1501	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.341649	1.109115	-3.232534	21960.821288
HLA B*3901	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.464574	1.231855	-3.232718	29145.642470
HLA A*2301	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.522174	1.289436	-3.232737	33279.255915
HLA B*5101	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.465424	1.232655	-3.232769	29202.776636
HLA B*5701	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.415065	1.182210	-3.232855	26005.504604
HLA A*2602	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.423326	1.190433	-3.232893	26504.894164
HLA A*2301	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.250080	1.017185	-3.232895	17786.059847
HLA A*0212	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.320219	1.087303	-3.232916	20903.495972
HLA A*0101	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.371865	1.138932	-3.232933	23543.189831
HLA B*2705	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.358983	1.126026	-3.232957	22855.097489
HLA A*3101	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.364030	1.131046	-3.232984	23122.232931
HLA B*7301	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.546401	1.313175	-3.233226	35188.560156
HLA A*2301	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.537163	1.303793	-3.233371	34447.945210
HLA B*1509	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.359418	1.126026	-3.233392	22877.982995
HLA B*0702	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.440856	1.207422	-3.233434	27596.600208
HLA A*0201	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.347325	1.113845	-3.233480	22249.739650
HLA B*0803	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.355522	1.121826	-3.233696	22673.694289
HLA A*8001	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.437550	1.203805	-3.233745	27387.340203
HLA B*3801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.496841	1.263068	-3.233773	31393.624555
HLA A*2501	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.364946	1.131046	-3.233900	23171.069031
HLA A*8001	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.374649	1.140721	-3.233928	23694.603413
HLA B*1517	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.254908	1.020917	-3.233991	17984.896422
HLA B*0803	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.449520	1.215498	-3.234022	28152.727891
HLA A*0301	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.149129	0.915104	-3.234025	14097.088533
HLA A*3301	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.503730	1.269596	-3.234135	31895.554018
HLA A*2301	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.529450	1.295300	-3.234150	33841.527887
HLA A*2402	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.522054	1.287816	-3.234237	33270.075290
HLA B*5801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.350036	1.115576	-3.234460	22389.079541
HLA B*4002	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.608430	1.373907	-3.234523	40591.046691
HLA A*2602	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.407249	1.172675	-3.234573	25541.626423
HLA A*2603	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.574177	1.339557	-3.234620	37512.595015
HLA B*3801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.470069	1.235408	-3.234661	29516.786809
HLA A*2601	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.373649	1.138932	-3.234716	23640.059403
HLA B*1801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.466592	1.231855	-3.234736	29281.400228
HLA A*2301	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.426679	1.191820	-3.234859	26710.301452
HLA B*1503	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.438682	1.203805	-3.234877	27458.847706
HLA A*0202	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.147734	0.912830	-3.234904	14051.860612
HLA A*0212	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.242279	1.007289	-3.234990	17469.459132
HLA B*1503	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.386895	1.151838	-3.235057	24372.212719
HLA A*0206	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.361532	1.126421	-3.235111	22989.645227
HLA A*6801	1:401-409	9	PFPGPGLGI	1.372989	0.068001	-4.676128	1.440990	-3.235139	47438.211949
HLA A*0211	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.474423	1.239243	-3.235180	29814.166619
HLA A*2402	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.524631	1.289436	-3.235195	33468.108536
HLA A*2403	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.407935	1.172675	-3.235259	25582.006099
HLA A*0101	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.366330	1.131046	-3.235284	23245.019654
HLA A*6901	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.358480	1.123169	-3.235311	22828.653081
HLA B*3901	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.382598	1.147258	-3.235340	24132.246450
HLA A*0101	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.361854	1.126421	-3.235433	23006.690429
HLA A*0201	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.195842	0.960386	-3.235456	15697.911923
HLA A*0101	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.387341	1.151838	-3.235503	24397.277282
HLA B*7301	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.612871	1.377330	-3.235540	41008.206611
HLA B*4501	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.484643	1.249052	-3.235591	30524.104660
HLA A*0201	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.356420	1.120820	-3.235599	22720.599689
HLA B*4501	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.531034	1.295300	-3.235734	33965.148315
HLA A*0301	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.362214	1.126421	-3.235793	23025.741250
HLA B*0801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.329828	1.094025	-3.235803	21371.170972
HLA B*4801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.357766	1.121826	-3.235940	22791.139790
HLA B*4001	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.163607	0.927581	-3.236026	14574.945981
HLA B*5701	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.248997	1.012736	-3.236260	17741.757412
HLA A*2601	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.358180	1.121826	-3.236353	22812.850492
HLA B*7301	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.617809	1.381432	-3.236378	41477.196525

HLA A*2501	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.264973	1.028301	-3.236672	18406.581356
HLA B*0702	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.446835	1.210159	-3.236676	27979.182517
HLA B*1502	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.522998	1.286148	-3.236850	33342.508967
HLA B*5101	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.328463	1.091476	-3.236987	21304.103726
HLA B*5701	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.376308	1.139224	-3.237084	23785.275194
HLA A*0201	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.137011	0.899837	-3.237174	13709.158057
HLA A*6901	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.274150	1.036964	-3.237187	18799.669879
HLA A*3301	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.550400	1.313175	-3.237225	35514.059684
HLA A*2603	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.427729	1.190433	-3.237296	26774.971011
HLA B*1517	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.452812	1.215498	-3.237314	28366.915250
HLA B*4801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.427769	1.190433	-3.237336	26777.433567
HLA A*2501	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.475325	1.237896	-3.237429	29876.166869
HLA A*0206	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.331454	1.094025	-3.237429	21451.326957
HLA B*4403	1:244-252	9	LVQRAIGDR	0.665293	0.758978	-4.661808	1.424271	-3.237537	45899.525938
HLA B*1509	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.346460	1.108898	-3.237562	22205.488059
HLA A*2902	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.143852	0.906227	-3.237625	13926.836720
HLA B*1517	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.159228	0.921448	-3.237780	14428.710301
HLA A*0201	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.389630	1.151838	-3.237792	24526.171485
HLA A*0201	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.293646	1.055834	-3.237812	19662.840199
HLA B*1502	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.559984	1.322138	-3.237846	36306.456967
HLA A*2601	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.364298	1.126421	-3.237877	23136.497443
HLA A*2301	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.539113	1.301147	-3.237967	34602.971438
HLA B*3801	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.498984	1.260962	-3.238022	31548.897743
HLA A*3101	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.364509	1.126421	-3.238088	23147.765116
HLA A*3101	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.378538	1.140437	-3.238101	23907.702436
HLA B*1517	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.243294	1.005151	-3.238144	17510.334263
HLA A*0211	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.428253	1.190075	-3.238178	26807.291969
HLA A*3002	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.522277	1.284024	-3.238253	33287.178489
HLA B*5801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.359192	1.120820	-3.238372	22866.104414
HLA A*0301	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.275414	1.036964	-3.238451	18854.466406
HLA B*2705	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.379280	1.140721	-3.238559	23948.608205
HLA B*1502	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.473986	1.235408	-3.238578	29784.181519
HLA B*5701	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.364486	1.125828	-3.238657	23146.512881
HLA B*1801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.471317	1.232655	-3.238662	29601.700144
HLA B*1509	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.398123	1.159455	-3.238668	25010.544615
HLA A*2501	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.475717	1.236980	-3.238737	29903.170733
HLA B*1801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.446259	1.207422	-3.238837	27942.122835
HLA A*2602	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.552024	1.313175	-3.238848	35647.067981
HLA A*0219	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.446353	1.207422	-3.238931	27948.170041
HLA B*5801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.154129	0.915104	-3.239025	14260.315408
HLA B*4402	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.429496	1.190433	-3.239063	26884.119800
HLA B*1517	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.316610	1.077535	-3.239075	20730.516188
HLA B*5801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.352527	1.113445	-3.239082	22517.838154
HLA B*4001	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.365148	1.126026	-3.239122	23181.851890
HLA A*2601	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.370214	1.131046	-3.239168	23453.821548
HLA B*3801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.474289	1.235042	-3.239246	29804.974430
HLA A*0101	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.348154	1.108898	-3.239256	22292.270372
HLA A*6801	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.613219	1.373907	-3.239311	41041.053537
HLA B*2705	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.330825	1.091476	-3.239348	21420.248279
HLA A*0211	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.145643	0.906227	-3.239416	13984.366311
HLA A*2403	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.370474	1.131046	-3.239428	23467.909744
HLA A*0201	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.365912	1.126421	-3.239491	23222.646398
HLA A*3101	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.267861	1.028301	-3.239559	18529.369927
HLA A*2603	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.614085	1.374504	-3.239582	41123.063532
HLA B*3901	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.365851	1.126026	-3.239825	23219.380197
HLA A*2902	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.340323	1.100487	-3.239836	21893.917045
HLA A*2902	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.422151	1.182210	-3.239942	26433.296772
HLA A*3201	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.475052	1.235042	-3.240010	29857.424048
HLA B*0702	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.257626	1.017185	-3.240442	18097.821280
HLA A*1101	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.422656	1.182210	-3.240447	26464.059918
HLA A*2601	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.167465	0.926967	-3.240498	14704.992528
HLA B*2705	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.366384	1.125828	-3.240556	23247.912153
HLA A*2601	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.379959	1.139224	-3.240735	23986.080132
HLA B*4801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.142960	0.902116	-3.240844	13898.235924
HLA B*5401	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.456393	1.215498	-3.240895	28601.757905

HLA A*0202	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.570796	1.329702	-3.241094	37221.699577
HLA A*3002	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.270064	1.028966	-3.241099	18623.635742
HLA B*5801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.350299	1.109115	-3.241185	22402.649364
HLA A*0301	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.356791	1.115576	-3.241215	22740.028708
HLA A*2403	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.363095	1.121826	-3.241268	23072.501181
HLA B*0803	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.502236	1.260962	-3.241274	31785.999899
HLA A*2403	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.328588	1.087303	-3.241285	21310.213003
HLA A*1101	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.363130	1.121826	-3.241304	23074.373552
HLA B*5701	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.400759	1.159455	-3.241304	25162.817684
HLA A*0101	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.381780	1.140437	-3.241343	24086.856823
HLA A*2501	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.456884	1.215498	-3.241386	28634.115254
HLA B*2705	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.388706	1.147258	-3.241448	24474.082118
HLA B*1502	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.525533	1.284024	-3.241509	33537.707366
HLA B*1501	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.357120	1.115576	-3.241544	22757.258176
HLA A*0101	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.362444	1.120820	-3.241624	23037.952024
HLA A*6801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-3.799202	0.557541	-3.241660	6297.988017
HLA A*0206	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.350586	1.108898	-3.241688	22417.440138
HLA B*4601	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.382130	1.140437	-3.241694	24106.280426
HLA A*0101	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.364899	1.123169	-3.241730	23168.562108
HLA B*5701	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.389249	1.147258	-3.241991	24504.686115
HLA A*3301	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.614788	1.372792	-3.241996	41189.636253
HLA B*0802	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.432299	1.190075	-3.242224	27058.190971
HLA B*5301	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.559756	1.317518	-3.242238	36287.409816
HLA B*1509	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.355684	1.113445	-3.242240	22682.159559
HLA A*0219	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.356220	1.113845	-3.242375	22710.154237
HLA A*2601	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.394275	1.151838	-3.242437	24789.895289
HLA A*3101	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.333928	1.091476	-3.242452	21573.875595
HLA A*0301	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.229717	0.987241	-3.242476	16971.364568
HLA B*4501	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.351392	1.108898	-3.242494	22459.076378
HLA A*0212	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.958121	0.715584	-3.242537	9080.734864
HLA B*0702	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.315635	1.072837	-3.242798	20684.026230
HLA A*3001	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.271789	1.028966	-3.242823	18697.734588
HLA A*8001	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.149759	0.906788	-3.242972	14117.542024
HLA A*2501	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.373465	1.130410	-3.243055	23630.086080
HLA B*1501	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.363938	1.120820	-3.243118	23117.354986
HLA A*2603	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.544275	1.301147	-3.243129	35016.699789
HLA B*0801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.255885	1.012736	-3.243149	18025.417260
HLA B*5401	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.512764	1.269596	-3.243168	32565.962615
HLA B*0803	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.446995	1.203805	-3.243190	27989.477182
HLA A*2501	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.433647	1.190433	-3.243214	27142.344725
HLA A*0212	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.316551	1.072837	-3.243714	20727.712632
HLA B*3501	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.403184	1.159455	-3.243729	25303.694728
HLA B*0802	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.408926	1.165167	-3.243759	25640.475851
HLA A*0216	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.224520	0.980728	-3.243792	16769.484096
HLA A*3002	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.447660	1.203805	-3.243855	28032.361852
HLA A*0206	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.504907	1.260962	-3.243945	31982.119534
HLA A*0201	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.353084	1.109115	-3.243969	22546.727776
HLA B*5301	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.476688	1.232655	-3.244032	29970.057610
HLA A*3001	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.287488	1.043287	-3.244202	19386.001835
HLA B*1509	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.409424	1.165167	-3.244257	25669.899693
HLA B*5101	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.472682	1.228391	-3.244291	29694.888974
HLA B*1502	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.188037	0.943730	-3.244307	15418.314456
HLA B*4402	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.426606	1.182210	-3.244396	26705.822335
HLA A*0219	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.213590	0.969193	-3.244397	16352.716127
HLA A*0219	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.776910	0.532233	-3.244676	5982.874821
HLA B*4402	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.144858	0.900174	-3.244684	13959.120733
HLA B*0702	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.383756	1.138932	-3.244824	24196.694875
HLA A*0301	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.368256	1.123169	-3.245087	23348.366156
HLA A*6901	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.385542	1.140437	-3.245105	24296.384765
HLA A*2601	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.279643	1.034513	-3.245130	19038.964281
HLA B*0802	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.437094	1.191820	-3.245275	27358.611761
HLA B*5301	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.529344	1.284024	-3.245320	33833.290338
HLA A*2301	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.473438	1.228069	-3.245369	29746.662085
HLA A*2602	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.575091	1.329702	-3.245389	37591.621402
HLA B*1517	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.200851	0.955413	-3.245438	15880.017989

HLA A*2902	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.000036	0.754547	-3.245489	10000.824543
HLA A*3201	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.436140	1.190433	-3.245707	27298.586840
HLA B*3501	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.367688	1.121826	-3.245862	23317.818635
HLA A*0216	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.149519	0.903619	-3.245900	14109.753991
HLA B*4002	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.640902	1.394918	-3.245984	43742.387396
HLA A*2402	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.369286	1.123169	-3.246116	23403.756443
HLA A*0301	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.367000	1.120820	-3.246179	23280.886897
HLA B*4402	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.405869	1.159455	-3.246415	25460.644959
HLA A*2501	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.438288	1.191820	-3.246468	27433.902757
HLA A*0301	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.273687	1.027198	-3.246489	18779.644838
HLA B*1502	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.387240	1.140721	-3.246519	24391.602520
HLA A*2403	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.355419	1.108898	-3.246521	22668.297796
HLA A*3201	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.355583	1.108898	-3.246685	22676.883730
HLA A*0101	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.372810	1.126026	-3.246784	23594.446698
HLA B*4501	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.628234	1.381432	-3.246802	42484.847078
HLA A*6801	1:388-396	9	RELGLPEEI	1.155087	0.273281	-4.675238	1.428368	-3.246870	47341.046752
HLA B*5801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.355778	1.108898	-3.246880	22687.068409
HLA B*1502	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.539983	1.293038	-3.246944	34672.304153
HLA B*4403	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.387461	1.140437	-3.247024	24404.009526
HLA B*0801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.387626	1.140437	-3.247189	24413.252885
HLA B*4001	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.347856	1.100487	-3.247369	22276.959596
HLA B*1501	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.149989	0.902388	-3.247601	14125.028694
HLA B*4402	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.356873	1.109115	-3.247759	22744.334852
HLA A*2601	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.388375	1.140437	-3.247938	24455.420544
HLA A*0250	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.339417	1.091476	-3.247941	21848.245494
HLA A*0212	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.368823	1.120820	-3.248002	23378.827219
HLA B*5401	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.551836	1.303793	-3.248043	35631.643585
HLA B*4801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.151770	0.903619	-3.248151	14183.070066
HLA A*0211	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.342196	1.094025	-3.248171	21988.520449
HLA A*0250	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.362101	1.113845	-3.248256	23019.762824
HLA B*3901	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.230845	0.982586	-3.248258	17015.492174
HLA A*2602	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.517865	1.269596	-3.248269	32950.700516
HLA A*2402	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.549510	1.301147	-3.248363	35441.318102
HLA B*1801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-3.939288	0.690895	-3.248392	8695.359132
HLA A*2403	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.395750	1.147258	-3.248492	24874.259967
HLA A*6802	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.362040	1.113445	-3.248595	23016.525159
HLA A*1101	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.408104	1.159455	-3.248649	25591.972539
HLA B*7301	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.585142	1.336347	-3.248795	38471.768872
HLA A*3201	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.605428	1.356576	-3.248851	40311.374675
HLA A*0211	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.282590	1.033365	-3.249225	19168.563738
HLA A*0219	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.343399	1.094025	-3.249374	22049.510071
HLA B*4501	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.626820	1.377330	-3.249489	42346.709476
HLA B*0801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.358680	1.109115	-3.249565	22839.153036
HLA A*0212	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.375991	1.126421	-3.249570	23767.910316
HLA A*0301	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.363623	1.113845	-3.249778	23100.602707
HLA B*5401	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.337123	1.087303	-3.249821	21733.189644
HLA B*3501	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.210258	0.960386	-3.249872	16227.750730
HLA B*0801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.267161	1.017228	-3.249933	18499.521925
HLA B*4403	1:303-311	9	EGKRKIIGR	1.019538	0.375380	-4.644998	1.394918	-3.250080	44156.804260
HLA B*5401	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.539520	1.289353	-3.250167	34635.371893
HLA A*2601	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.337793	1.087303	-3.250490	21766.724121
HLA B*4501	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.590100	1.339557	-3.250542	38913.434946
HLA A*0301	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.359556	1.108898	-3.250658	22885.286434
HLA A*0250	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.023300	0.772641	-3.250659	10551.164850
HLA A*0203	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.391122	1.140437	-3.250685	24610.570626
HLA B*3501	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.454497	1.203805	-3.250692	28477.161087
HLA B*4001	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.323666	1.072837	-3.250828	21070.052589
HLA A*0201	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.351328	1.100487	-3.250841	22455.796088
HLA B*4002	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.590421	1.339557	-3.250864	38942.286516
HLA A*2301	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.543989	1.293038	-3.250950	34993.596166
HLA B*4002	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.628300	1.377330	-3.250969	42491.283039
HLA B*5101	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.441431	1.190433	-3.250998	27633.201623
HLA A*8001	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.398346	1.147258	-3.251088	25023.401825
HLA A*6901	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.360275	1.109115	-3.251161	22923.202709
HLA A*0301	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.307034	1.055834	-3.251199	20278.396722

HLA B*4601	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.403057	1.151838	-3.251219	25296.303738
HLA B*0802	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.377763	1.126421	-3.251342	23865.058965
HLA B*7301	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.607930	1.356576	-3.251353	40544.300307
HLA A*2603	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.479476	1.228069	-3.251407	30163.130736
HLA A*8001	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.390647	1.139224	-3.251423	24583.690943
HLA A*0301	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.364904	1.113445	-3.251459	23168.812789
HLA B*5101	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.307299	1.055834	-3.251465	20290.797050
HLA A*3001	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.655930	0.404390	-3.251541	4528.248319
HLA B*2705	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.390788	1.139224	-3.251564	24591.671941
HLA A*3001	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.280275	1.028547	-3.251728	19066.691098
HLA B*5701	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.343260	1.091476	-3.251784	22042.473355
HLA B*5401	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.541345	1.289436	-3.251909	34781.267540
HLA B*4403	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.538077	1.286148	-3.251929	34520.515414
HLA A*1101	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.392686	1.140721	-3.251965	24699.402105
HLA B*4601	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.378575	1.126421	-3.252154	23909.771933
HLA B*4403	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.601011	1.348830	-3.252181	39903.462019
HLA A*0211	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.528003	1.275786	-3.252217	33728.938981
HLA B*5701	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.352740	1.100487	-3.252253	22528.926413
HLA B*4601	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.383366	1.131046	-3.252320	24174.974991
HLA A*0212	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.036030	0.783681	-3.252349	10865.004691
HLA A*0212	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-3.551496	0.299099	-3.252397	3560.374043
HLA B*4801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.719272	0.466612	-3.252660	5239.288944
HLA B*1502	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.592402	1.339557	-3.252845	39120.289824
HLA B*4601	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.383272	1.130410	-3.252862	24169.744200
HLA B*3801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.443045	1.190075	-3.252970	27736.094096
HLA B*1801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.281953	1.028966	-3.252987	19140.481681
HLA B*1501	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.379200	1.126026	-3.253175	23944.203593
HLA B*1509	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.400475	1.147258	-3.253217	25146.351579
HLA B*3901	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.481619	1.228391	-3.253228	30312.317889
HLA A*2902	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.460662	1.207422	-3.253240	28884.292918
HLA A*0301	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.236032	0.982586	-3.253446	17219.961593
HLA B*1517	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.393901	1.140437	-3.253464	24768.580875
HLA A*8001	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.412953	1.159455	-3.253498	25879.334147
HLA B*0702	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.155031	0.901531	-3.253500	14289.970543
HLA A*2501	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.488919	1.235408	-3.253511	30826.129368
HLA A*0211	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.376905	1.123169	-3.253736	23817.981288
HLA B*1801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.457544	1.203805	-3.253739	28677.677333
HLA B*0803	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.463970	1.210159	-3.253810	29105.148230
HLA A*2501	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.345643	1.091476	-3.254167	22163.722415
HLA A*2603	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.517357	1.263086	-3.254271	32912.218922
HLA B*3501	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.187313	0.932998	-3.254316	15392.645145
HLA A*2602	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.517486	1.263086	-3.254400	32922.013209
HLA A*0301	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.281133	1.026553	-3.254580	19104.377564
HLA A*0202	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.283586	1.028966	-3.254620	19212.582921
HLA A*2402	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.538683	1.284024	-3.254659	34568.731112
HLA A*6801	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.544132	1.289436	-3.254696	35005.146071
HLA A*6801	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.558621	1.303793	-3.254828	36192.715440
HLA A*2402	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.376679	1.121826	-3.254853	23805.614646
HLA A*3001	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.189625	0.934761	-3.254864	15474.803774
HLA B*5801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.307475	1.052564	-3.254912	20299.031543
HLA B*3801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.538944	1.284024	-3.254920	34589.495789
HLA B*4801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.375747	1.120820	-3.254926	23754.541574
HLA A*3101	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.283933	1.028966	-3.254968	19227.971897
HLA A*3301	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.629620	1.374504	-3.255116	42620.668327
HLA A*0201	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.395691	1.140437	-3.255255	24870.896019
HLA B*4801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.402521	1.147258	-3.255263	25265.121128
HLA A*0216	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.364526	1.108898	-3.255627	23148.641720
HLA B*4403	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.543488	1.287816	-3.255672	34953.296045
HLA A*0201	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.364772	1.108898	-3.255874	23161.794772
HLA A*8001	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.382323	1.126421	-3.255902	24116.976608
HLA B*5701	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.394907	1.138932	-3.255974	24825.997299
HLA A*0301	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.319035	1.062990	-3.256045	20846.578462
HLA B*0801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-3.491452	0.235291	-3.256162	3100.646012
HLA A*0216	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.379388	1.123169	-3.256219	23954.568675
HLA B*5101	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.403489	1.147258	-3.256231	25321.496711

HLA B*4501	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.396692	1.140437	-3.256256	24928.279902
HLA A*3101	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.369732	1.113445	-3.256287	23427.825039
HLA A*0216	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.494285	1.237896	-3.256390	31209.385699
HLA A*0301	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.307339	1.050933	-3.256406	20292.663242
HLA B*4801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.343906	1.087303	-3.256604	22075.290778
HLA A*2501	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.403889	1.147258	-3.256631	25344.795126
HLA B*5701	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.378512	1.121826	-3.256686	23906.279760
HLA A*2601	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.372380	1.115576	-3.256804	23571.099525
HLA B*1501	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.131522	0.874608	-3.256915	13536.998681
HLA B*4402	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-3.518222	0.261282	-3.256940	3297.784099
HLA B*5401	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.540450	1.283502	-3.256948	34709.651344
HLA B*5701	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.365996	1.108898	-3.257098	23227.169588
HLA B*1501	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.300448	1.043307	-3.257141	19973.216464
HLA A*6802	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-3.884549	0.627189	-3.257361	7665.654164
HLA A*3101	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.366619	1.109115	-3.257504	23260.492418
HLA B*1509	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.495404	1.237896	-3.257508	31289.856780
HLA A*2301	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.518497	1.260962	-3.257534	32998.687266
HLA A*0101	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.270271	1.012736	-3.257535	18632.504012
HLA B*4402	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.396824	1.139224	-3.257599	24935.833163
HLA A*2301	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.520785	1.263086	-3.257699	33173.023913
HLA B*3801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.461519	1.203805	-3.257714	28941.384467
HLA B*1517	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.461578	1.203805	-3.257773	28945.298974
HLA A*0206	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.180274	0.922498	-3.257776	15145.171670
HLA B*4001	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.388213	1.130410	-3.257803	24446.293471
HLA A*3301	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.569086	1.311116	-3.257970	37075.393955
HLA A*6901	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.291381	1.033365	-3.258017	19560.562797
HLA B*4001	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.345361	1.087303	-3.258058	22149.338690
HLA A*2403	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.378930	1.120820	-3.258110	23929.311645
HLA A*2402	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.553419	1.295300	-3.258120	35761.803163
HLA B*1801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.371579	1.113445	-3.258134	23527.656300
HLA A*2403	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.384005	1.125828	-3.258177	24210.574407
HLA A*0202	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.507250	1.249052	-3.258198	32155.086238
HLA B*4002	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.571428	1.313175	-3.258253	37275.906267
HLA B*1501	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.358746	1.100487	-3.258259	22842.612902
HLA A*1101	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.397207	1.138932	-3.258275	24957.831576
HLA A*2501	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.440536	1.182210	-3.258326	27576.303617
HLA A*2603	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.450317	1.191820	-3.258497	28204.406027
HLA B*1503	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.293049	1.034513	-3.258536	19635.839813
HLA A*3201	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.474103	1.215498	-3.258605	29792.239065
HLA B*5701	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.410449	1.151838	-3.258610	25730.519049
HLA A*0301	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.367899	1.109115	-3.258785	23329.174613
HLA B*1517	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.441069	1.182210	-3.258860	27610.189357
HLA A*2601	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.384726	1.125828	-3.258898	24250.817609
HLA B*7301	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.581082	1.322138	-3.258945	38113.799487
HLA B*5301	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.548349	1.289353	-3.258996	35346.728154
HLA B*1509	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.487131	1.228069	-3.259062	30699.481365
HLA B*3901	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.466545	1.207422	-3.259123	29278.232216
HLA A*0101	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.372601	1.113445	-3.259156	23583.089175
HLA A*0216	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.466585	1.207422	-3.259163	29280.925004
HLA A*6901	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.385201	1.126026	-3.259175	24277.333330
HLA A*3101	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.133867	0.874608	-3.259260	13610.283533
HLA B*4801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.400019	1.140721	-3.259298	25119.973862
HLA B*4501	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.595663	1.336347	-3.259316	39415.146834
HLA B*4001	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.380220	1.120820	-3.259400	24000.488043
HLA A*3001	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.192618	0.933159	-3.259459	15581.827588
HLA B*5301	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.280489	1.020917	-3.259572	19076.079939
HLA B*1801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.406960	1.147258	-3.259702	25524.636260
HLA A*0203	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.014292	0.754590	-3.259703	10334.571706
HLA B*4001	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.390793	1.131046	-3.259747	24591.938019
HLA A*0301	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.166567	0.906788	-3.259780	14674.634898
HLA A*0212	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.315619	1.055834	-3.259784	20683.242957
HLA B*0702	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.373696	1.113845	-3.259851	23642.617343
HLA A*0201	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.277064	1.017185	-3.259879	18926.206948
HLA B*5101	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.499172	1.239243	-3.259929	31562.554781
HLA A*3002	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.497845	1.237896	-3.259949	31466.228365

HLA A*2902	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.451797	1.191820	-3.259978	28300.697132
HLA A*3002	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.267327	1.007289	-3.260038	18506.628996
HLA B*4501	1:496-504	9	ISTRITNEV	1.144524	0.204306	-4.608884	1.348830	-3.260054	40633.450286
HLA B*1801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.497957	1.237896	-3.260062	31474.400408
HLA B*1517	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.386545	1.126421	-3.260124	24352.574840
HLA B*1503	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.288494	1.028301	-3.260193	19430.940821
HLA A*6901	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.272966	1.012736	-3.260230	18748.480815
HLA A*3201	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.286786	1.026553	-3.260233	19354.669223
HLA A*8001	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.339602	1.079304	-3.260298	21857.585020
HLA B*5801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.354329	1.094025	-3.260304	22611.467451
HLA B*5401	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.193337	0.932998	-3.260340	15607.643514
HLA A*2501	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.450470	1.190075	-3.260394	28214.325647
HLA A*2902	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.303690	1.043287	-3.260404	20122.887448
HLA A*0101	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.374274	1.113845	-3.260429	23674.102659
HLA B*4403	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.614440	1.353717	-3.260723	41156.670410
HLA A*0219	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.387233	1.126421	-3.260812	24391.206655
HLA B*4403	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.597254	1.336347	-3.260906	39559.769288
HLA B*3501	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.376524	1.115576	-3.260948	23797.116305
HLA A*1101	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.452814	1.191820	-3.260995	28367.068713
HLA A*3101	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.376590	1.115576	-3.261014	23800.721291
HLA B*5301	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.496552	1.235408	-3.261144	31372.741672
HLA A*6801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-3.988349	0.727191	-3.261158	9735.302923
HLA A*3201	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.278346	1.017185	-3.261162	18982.193814
HLA A*0101	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.355189	1.094025	-3.261164	22656.282949
HLA A*2403	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.353133	1.091915	-3.261218	22549.289402
HLA A*3201	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.174109	0.912830	-3.261279	14931.696426
HLA A*6802	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.384506	1.123169	-3.261336	24238.488486
HLA B*2705	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.426528	1.165167	-3.261362	26701.055068
HLA A*6802	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.224477	0.962975	-3.261503	16767.851196
HLA B*2705	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.452013	1.190433	-3.261580	28314.786173
HLA B*4002	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-3.838824	0.577199	-3.261624	6899.594146
HLA A*0211	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.522667	1.260962	-3.261705	33317.085187
HLA B*1502	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.565703	1.303793	-3.261910	36787.689822
HLA A*2601	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.370841	1.108898	-3.261943	23487.723675
HLA B*4601	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.225027	0.962975	-3.262053	16789.091296
HLA A*2601	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.388455	1.126026	-3.262429	24459.919196
HLA A*2602	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.225427	0.962975	-3.262452	16804.539009
HLA B*2705	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.177615	0.915104	-3.262511	15052.706140
HLA A*0203	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.414506	1.151838	-3.262668	25972.042669
HLA A*3002	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.393718	1.131046	-3.262672	24758.131448
HLA A*3001	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.729446	0.466612	-3.262833	5363.467091
HLA A*0212	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.356873	1.094025	-3.262848	22744.334852
HLA A*0203	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.160788	0.897730	-3.263058	14480.633832
HLA B*5801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.206833	0.943730	-3.263103	16100.255901
HLA B*4601	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.383946	1.120820	-3.263126	24207.300215
HLA B*5701	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.389634	1.126421	-3.263213	24526.436855
HLA A*6802	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.268415	1.005094	-3.263321	18553.042108
HLA A*0203	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.190903	0.927581	-3.263323	15520.412888
HLA B*5701	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.384205	1.120820	-3.263384	24221.709972
HLA B*4403	1:248-256	9	AIGDRLTCV	1.133412	0.240495	-4.637315	1.373907	-3.263407	43382.524319
HLA B*4402	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.379212	1.115576	-3.263636	23944.851279
HLA B*4801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.389712	1.126026	-3.263686	24530.815860
HLA A*0206	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.276436	1.012736	-3.263700	18898.888904
HLA B*5801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.341550	1.077535	-3.264015	21955.832020
HLA B*5401	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.545278	1.281231	-3.264048	35097.682659
HLA A*8001	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.327054	1.062990	-3.264063	21235.064132
HLA A*1101	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.471561	1.207422	-3.264139	29618.359590
HLA B*4001	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.358203	1.094025	-3.264178	22814.084675
HLA B*4601	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.937309	0.673013	-3.264296	8655.840743
HLA B*5101	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.468159	1.203805	-3.264354	29387.249976
HLA B*0702	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.454849	1.190433	-3.264416	28500.279208
HLA A*0212	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.233617	0.969193	-3.264424	17124.460887
HLA B*4402	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.386254	1.121826	-3.264427	24336.243972
HLA A*2501	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.373425	1.108898	-3.264527	23627.912965
HLA B*0802	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.416449	1.151838	-3.264611	26088.501348

HLA A*6802	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-3.950993	0.686294	-3.264699	8932.903820
HLA A*0301	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.365188	1.100487	-3.264701	23183.983979
HLA A*0202	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.454835	1.190075	-3.264760	28499.354123
HLA A*8001	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.386590	1.121826	-3.264763	24355.078119
HLA B*1501	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.378293	1.113445	-3.264849	23894.255065
HLA A*6801	1:441-449	9	NQIWQCPVV	1.157076	0.154040	-4.575972	1.311116	-3.264856	37667.961251
HLA B*5401	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.472390	1.207422	-3.264968	29674.975543
HLA B*5401	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.379010	1.113845	-3.265165	23933.713517
HLA A*3101	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.309411	1.044058	-3.265354	20389.721510
HLA B*7301	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.551568	1.286148	-3.265420	35609.675350
HLA A*6801	1:269-277	9	AQVQRDFVA	1.417756	-0.044964	-4.638243	1.372792	-3.265451	43475.327826
HLA A*0212	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.298850	1.033365	-3.265486	19899.875484
HLA B*4402	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.417389	1.151838	-3.265551	26145.016834
HLA B*4801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.404800	1.139224	-3.265576	25398.050662
HLA B*5801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.338481	1.072837	-3.265644	21801.253860
HLA A*0219	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.438461	1.172675	-3.265786	27444.887619
HLA B*1517	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.457777	1.191820	-3.265957	28693.040609
HLA A*3201	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.529147	1.263068	-3.266079	33817.918946
HLA B*4601	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.379529	1.113445	-3.266085	23962.345430
HLA B*1509	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.498075	1.231855	-3.266220	31482.915211
HLA A*0201	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.389409	1.123169	-3.266240	24513.702372
HLA B*4402	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.339113	1.072837	-3.266276	21833.003453
HLA B*4601	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.358219	1.091915	-3.266305	22814.948643
HLA B*4801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.381938	1.115576	-3.266361	24095.588989
HLA A*2601	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.389606	1.123169	-3.266437	24524.844683
HLA A*6802	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-3.565536	0.299099	-3.266437	3677.360007
HLA B*0803	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.353857	1.087303	-3.266554	22586.893382
HLA B*7301	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.229378	0.962750	-3.266628	16958.148615
HLA B*4403	1:175-183	9	GVQYHPEVM	1.214367	0.167065	-4.648125	1.381432	-3.266693	44475.905562
HLA A*6901	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.235919	0.969193	-3.266726	17215.490586
HLA B*5701	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.380272	1.113445	-3.266827	24003.344693
HLA B*3501	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.322674	1.055834	-3.266840	21022.005090
HLA B*2705	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.439657	1.172675	-3.266982	27520.564929
HLA B*4002	1:503-511	9	EVAEVNRVV	1.178358	0.175359	-4.620706	1.353717	-3.266989	41754.790541
HLA A*3101	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.387816	1.120820	-3.266996	24423.953141
HLA A*3002	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.200170	0.933159	-3.267010	15855.123872
HLA A*2602	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.570888	1.303793	-3.267095	37229.553651
HLA A*2902	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.393652	1.126421	-3.267231	24754.381447
HLA A*2601	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.388178	1.120820	-3.267357	24444.309775
HLA B*1502	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.556951	1.289436	-3.267514	36053.770044
HLA A*0203	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.983190	0.715584	-3.267606	9620.330684
HLA B*4001	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.381195	1.113445	-3.267751	24054.432167
HLA A*3002	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.528766	1.260962	-3.267804	33788.293836
HLA A*1101	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.394298	1.126421	-3.267877	24791.236431
HLA B*2705	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-3.422330	0.154429	-3.267901	2644.419425
HLA B*3901	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.471862	1.203805	-3.268057	29638.876394
HLA B*5301	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.549388	1.281231	-3.268157	35431.349357
HLA A*3001	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-3.502147	0.233980	-3.268167	3177.949877
HLA A*2501	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.440905	1.172675	-3.268230	27599.735572
HLA B*4601	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.296574	1.028301	-3.268272	19795.829655
HLA A*1101	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.433481	1.165167	-3.268314	27131.921295
HLA A*2301	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.301710	1.033365	-3.268345	20031.325229
HLA B*4801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.391547	1.123169	-3.268378	24634.680852
HLA A*1101	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.472320	1.203805	-3.268515	29670.159784
HLA B*7301	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.558017	1.289436	-3.268581	36142.430170
HLA A*0203	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.076469	0.807776	-3.268693	11925.298375
HLA B*3501	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.224360	0.955413	-3.268947	16763.316199
HLA B*1502	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.501634	1.232655	-3.268979	31742.008932
HLA A*3001	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.168823	0.899837	-3.268986	14751.045768
HLA A*3201	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.555142	1.286148	-3.268993	35903.896306
HLA B*0702	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.451238	1.182210	-3.269028	28264.281916
HLA A*0203	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.082940	0.813884	-3.269056	12104.301583
HLA A*0203	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.392273	1.123169	-3.269104	24675.895997
HLA A*0250	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.312506	1.043307	-3.269199	20535.513441
HLA A*0202	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.191791	0.922498	-3.269293	15552.183645

HLA A*2402	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.562333	1.293038	-3.269295	36503.403122
HLA B*1501	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.421150	1.151838	-3.269312	26372.448401
HLA A*0212	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.442059	1.172675	-3.269383	27673.144977
HLA A*1101	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.383239	1.113845	-3.269394	24167.913690
HLA B*4402	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.395936	1.126421	-3.269515	24884.893031
HLA B*4601	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.385156	1.115576	-3.269580	24274.838042
HLA A*2501	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.196584	0.926967	-3.269618	15724.770847
HLA A*2603	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.176031	0.906227	-3.269804	14997.919923
HLA B*1501	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.094452	0.824605	-3.269847	12429.458603
HLA B*5301	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.565289	1.295300	-3.269989	36752.679443
HLA B*5701	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.357313	1.087303	-3.270010	22767.355784
HLA B*5301	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.563407	1.293038	-3.270369	36593.762845
HLA A*0301	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.362383	1.091915	-3.270468	23034.711800
HLA A*3101	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.333533	1.062990	-3.270543	21554.276841
HLA A*2403	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.409809	1.139224	-3.270585	25692.684694
HLA A*2501	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.409607	1.138932	-3.270675	25680.733941
HLA B*5701	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.411165	1.140437	-3.270728	25773.009867
HLA A*3002	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.283485	1.012736	-3.270748	19208.114110
HLA B*1801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.364775	1.094025	-3.270750	23161.920075
HLA B*7301	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.588290	1.317518	-3.270773	38751.673723
HLA B*2705	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.462619	1.191820	-3.270799	29014.751915
HLA B*0803	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.410216	1.139224	-3.270992	25716.742012
HLA B*4002	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.392818	1.121826	-3.270992	24706.886016
HLA B*0802	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.461465	1.190433	-3.271032	28937.783588
HLA A*0301	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.362902	1.091476	-3.271426	23062.268237
HLA A*0219	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.304797	1.033365	-3.271432	20174.227108
HLA A*0101	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.387085	1.115576	-3.271509	24382.894987
HLA B*1801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.461618	1.190075	-3.271543	28947.961141
HLA B*2705	1:494-502	9	ERISTRITN	1.065751	-0.517476	-3.819859	0.548275	-3.271584	6604.782219
HLA B*0702	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.431164	1.159455	-3.271709	26987.580847
HLA B*7301	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.506829	1.235042	-3.271787	32123.963284
HLA A*0201	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.397841	1.126026	-3.271815	24994.313371
HLA A*2403	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.398245	1.126421	-3.271824	25017.581427
HLA B*0801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.385730	1.113845	-3.271885	24306.902301
HLA B*5401	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.535032	1.263086	-3.271946	34279.331098
HLA A*0250	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.397886	1.125828	-3.272058	24996.882616
HLA A*2301	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.169838	0.897730	-3.272108	14785.560342
HLA A*1101	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.482345	1.210159	-3.272186	30363.032025
HLA A*3201	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.556243	1.284024	-3.272220	35995.108701
HLA A*3101	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.259743	0.987241	-3.272502	18186.251015
HLA B*0802	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.445209	1.172675	-3.272534	27874.634256
HLA B*5301	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.437707	1.165167	-3.272541	27397.268888
HLA B*1501	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.395724	1.123169	-3.272555	24872.779774
HLA B*4402	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.398530	1.125828	-3.272702	25033.963212
HLA B*5101	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.395915	1.123169	-3.272745	24883.681440
HLA B*4001	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.386601	1.113845	-3.272756	24355.736919
HLA B*4601	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.381712	1.108898	-3.272814	24083.078209
HLA A*0101	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.382024	1.109115	-3.272910	24100.412587
HLA A*0206	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.868314	0.595350	-3.272964	7384.384139
HLA B*5301	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.562418	1.289436	-3.272982	36510.513072
HLA B*0702	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.464827	1.191820	-3.273008	29162.676312
HLA A*0301	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.367119	1.094025	-3.273094	23287.311081
HLA B*1517	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.463552	1.190433	-3.273119	29077.134619
HLA A*2601	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.386984	1.113845	-3.273139	24377.223570
HLA B*4402	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.412112	1.138932	-3.273180	25829.261102
HLA A*2902	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.394005	1.120820	-3.273184	24774.477369
HLA A*3002	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.425044	1.151838	-3.273205	26609.918716
HLA B*3801	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.501618	1.228391	-3.273227	31740.806910
HLA A*2301	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.522319	1.249052	-3.273268	33290.420086
HLA B*4601	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.346124	1.072837	-3.273287	22188.316222
HLA B*5801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.352632	1.079304	-3.273328	22523.320677
HLA A*0206	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.256062	0.982586	-3.273475	18032.732407
HLA B*4601	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.374137	1.100487	-3.273650	23666.675516
HLA B*0802	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.433199	1.159455	-3.273744	27114.313328
HLA A*8001	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.361194	1.087303	-3.273891	22971.742715

HLA B*1801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.389512	1.115576	-3.273936	24519.538189
HLA A*0101	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.302243	1.028301	-3.273942	20055.939705
HLA B*0802	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.456165	1.182210	-3.273955	28586.752806
HLA B*4403	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.506000	1.231855	-3.274144	32062.674984
HLA B*1501	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.186984	0.912830	-3.274155	15380.991409
HLA B*5101	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.512068	1.237896	-3.274173	32513.855585
HLA A*2603	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.631030	1.356576	-3.274454	42759.236952
HLA A*6802	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.327025	1.052564	-3.274462	21233.685625
HLA B*4501	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.604234	1.329702	-3.274532	40200.742091
HLA B*7301	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.512451	1.237896	-3.274556	32542.539335
HLA B*7301	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.570399	1.295300	-3.275099	37187.684398
HLA A*2501	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.482634	1.207422	-3.275212	30383.242807
HLA A*2403	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.384407	1.109115	-3.275292	24232.981755
HLA B*1801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.512287	1.236980	-3.275307	32530.218061
HLA B*7301	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.605063	1.329702	-3.275362	40277.586432
HLA B*4403	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.592928	1.317518	-3.275410	39167.725120
HLA A*0250	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.457755	1.182210	-3.275546	28691.643607
HLA B*4002	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.593100	1.317518	-3.275582	39183.196367
HLA A*6901	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.391176	1.115576	-3.275599	24613.633047
HLA B*1501	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.030166	0.754547	-3.275619	10719.279711
HLA A*3301	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.615187	1.339557	-3.275630	41227.535010
HLA B*5401	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.507708	1.231855	-3.275852	32189.025450
HLA B*4402	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.390015	1.113845	-3.276170	24547.941296
HLA A*2601	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.389703	1.113445	-3.276258	24530.285030
HLA B*5301	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.580135	1.303793	-3.276343	38030.794857
HLA B*5701	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.399533	1.123169	-3.276364	25091.859079
HLA B*4001	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.385267	1.108898	-3.276368	24281.011064
HLA B*1509	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.480221	1.203805	-3.276416	30214.902920
HLA B*4601	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.402481	1.126026	-3.276456	25262.797649
HLA B*4001	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.402991	1.126421	-3.276570	25292.472223
HLA A*6801	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.598710	1.322138	-3.276573	39692.680724
HLA A*2602	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.428424	1.151838	-3.276586	26817.880847
HLA A*0219	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.191758	0.915104	-3.276654	15551.005791
HLA A*0203	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.329441	1.052564	-3.276877	21352.102899
HLA A*0216	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.370904	1.094025	-3.276879	23491.154707
HLA A*2602	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.540112	1.263068	-3.277044	34682.622221
HLA A*8001	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.407580	1.130410	-3.277170	25561.116864
HLA A*0203	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.403339	1.126026	-3.277313	25312.731093
HLA B*1501	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.371384	1.094025	-3.277359	23517.094264
HLA B*4001	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.400588	1.123169	-3.277418	25152.882298
HLA A*1101	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.416663	1.139224	-3.277439	26101.347876
HLA A*6801	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.617013	1.339557	-3.277456	41401.199030
HLA B*5801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.310861	1.033365	-3.277496	20457.894107
HLA B*0702	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.417953	1.140437	-3.277516	26178.984875
HLA A*0301	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.364836	1.087303	-3.277533	23165.178193
HLA B*4001	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.298521	1.020890	-3.277632	19884.809333
HLA B*1501	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.159181	0.881518	-3.277663	14427.149231
HLA B*0803	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.469634	1.191820	-3.277815	29487.260316
HLA B*3901	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.487982	1.210159	-3.277822	30759.661520
HLA A*3101	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.369817	1.091915	-3.277902	23432.388193
HLA A*0203	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.298881	1.020917	-3.277964	19901.275063
HLA B*1509	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.180091	0.902116	-3.277975	15138.782190
HLA B*1502	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.152630	0.874608	-3.278023	14211.180641
HLA B*0802	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.485498	1.207422	-3.278076	30584.271938
HLA B*3801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.391707	1.113445	-3.278262	24643.744940
HLA B*0802	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.408703	1.130410	-3.278293	25627.301584
HLA B*2705	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.430140	1.151838	-3.278301	26923.999939
HLA A*2902	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.417546	1.139224	-3.278322	26154.495142
HLA A*6801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.260913	0.982586	-3.278327	18235.313105
HLA B*3501	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.295570	1.017228	-3.278343	19750.153617
HLA B*7301	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.558494	1.280105	-3.278390	36182.143861
HLA A*0101	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.341508	1.062990	-3.278517	21953.694109
HLA A*8001	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.322728	1.044058	-3.278671	21024.620967
HLA B*2705	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.073523	0.794851	-3.278672	11844.670937
HLA A*2402	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.122218	0.843518	-3.278701	13250.077730

HLA A*3001	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.054525	0.775707	-3.278818	11337.702687
HLA B*5701	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.370749	1.091915	-3.278835	23482.768624
HLA A*0203	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.171731	0.892605	-3.279126	14850.171627
HLA B*4002	1:42-50	9	EVIPHTASI	1.080334	0.256013	-4.615512	1.336347	-3.279164	41258.325525
HLA B*1801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.410089	1.130410	-3.279679	25709.230374
HLA A*3101	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.393624	1.113845	-3.279779	24752.774478
HLA A*3001	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.284892	1.005094	-3.279798	19270.459418
HLA A*0250	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.469933	1.190075	-3.279858	29507.526674
HLA A*0201	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.352748	1.072837	-3.279910	22529.292053
HLA A*8001	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.185213	0.905240	-3.279972	15318.379263
HLA B*5801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.684387	0.404390	-3.279998	4834.896670
HLA A*2501	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.483879	1.203805	-3.280075	30470.483905
HLA A*0216	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.243078	0.962975	-3.280104	17501.621367
HLA B*5401	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.515226	1.235042	-3.280184	32751.121808
HLA B*5301	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.371684	1.091476	-3.280208	23533.384688
HLA A*0202	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-3.995957	0.715584	-3.280374	9907.340790
HLA A*0101	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.359681	1.079304	-3.280377	22891.849139
HLA A*0212	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.309376	1.028966	-3.280410	20388.066985
HLA A*1101	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.470511	1.190075	-3.280436	29546.822398
HLA A*8001	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.381059	1.100487	-3.280572	24046.885706
HLA A*0201	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.396178	1.115576	-3.280601	24898.763219
HLA A*0250	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.517590	1.236980	-3.280609	32929.850737
HLA B*4001	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.421066	1.140437	-3.280629	26367.312708
HLA B*5101	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.453341	1.172675	-3.280665	28401.465194
HLA B*4601	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.403903	1.123169	-3.280734	25345.617815
HLA B*4001	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.315323	1.034513	-3.280809	20669.149110
HLA A*0101	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.325092	1.044058	-3.281034	21139.356212
HLA A*6901	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.155713	0.874608	-3.281105	14312.407214
HLA B*5701	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.407187	1.126026	-3.281162	25538.034064
HLA B*3501	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.318201	1.036964	-3.281237	20806.580807
HLA B*5801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.344254	1.062990	-3.281264	22092.972738
HLA B*0803	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.394773	1.113445	-3.281328	24818.343044
HLA B*1503	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.214356	0.932998	-3.281358	16381.581614
HLA A*0211	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.036199	0.754590	-3.281609	10869.237566
HLA B*4601	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.359227	1.077535	-3.281692	22867.960036
HLA B*1801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.407535	1.125828	-3.281707	25558.489626
HLA A*3002	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.211433	0.929716	-3.281717	16271.705317
HLA A*0219	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.286901	1.005151	-3.281750	19359.800527
HLA A*3101	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.318795	1.036964	-3.281832	20835.078312
HLA B*1509	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.359401	1.077535	-3.281866	22877.116640
HLA A*0219	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.215051	0.932998	-3.282054	16407.834901
HLA B*5101	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.489504	1.207422	-3.282082	30867.682069
HLA A*2301	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.492281	1.210159	-3.282122	31065.697550
HLA A*0212	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.391025	1.108898	-3.282127	24605.112473
HLA B*4402	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.422887	1.140721	-3.282165	26478.094066
HLA A*0201	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.395640	1.113445	-3.282195	24867.936122
HLA A*0101	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.382774	1.100487	-3.282287	24142.039895
HLA A*0202	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.454969	1.172675	-3.282294	28508.143644
HLA A*8001	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.408146	1.125828	-3.282318	25594.464756
HLA B*3901	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.396244	1.113845	-3.282399	24902.535093
HLA B*4501	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.571947	1.289436	-3.282511	37320.499452
HLA B*1801	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.531586	1.249052	-3.282534	34008.356481
HLA A*0203	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.030950	0.748391	-3.282559	10738.665918
HLA A*0201	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.376809	1.094025	-3.282784	23812.698915
HLA A*3201	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.374309	1.091476	-3.282833	23676.023851
HLA A*6901	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.335408	1.052564	-3.282845	21647.529773
HLA A*6901	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.180800	0.897730	-3.283070	15163.535943
HLA A*0206	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.312057	1.028966	-3.283091	20514.305284
HLA A*0201	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.198271	0.915104	-3.283167	15785.969360
HLA B*5701	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.413679	1.130410	-3.283269	25922.631663
HLA A*0211	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.455972	1.172675	-3.283297	28574.074223
HLA B*1517	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.339334	1.055834	-3.283500	21844.109005
HLA B*3801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.511592	1.228069	-3.283522	32478.168224
HLA B*4801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.056221	0.772641	-3.283580	11382.073672
HLA A*8001	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.399176	1.115576	-3.283599	25071.234445

HLA B*4403	1:410-418	9	RIVGEVTAK	0.975253	0.402077	-4.661028	1.377330	-3.283698	45817.160561
HLA A*3301	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.571546	1.287816	-3.283729	37285.990556
HLA B*4601	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.392888	1.109115	-3.283774	24710.896187
HLA B*5301	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.569943	1.286148	-3.283795	37148.675709
HLA A*3201	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.361511	1.077535	-3.283976	22988.525912
HLA A*2402	1:208-216	9	PANIANALI	0.995189	0.008861	-4.288113	1.004050	-3.284063	19413.918965
HLA A*1101	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.474564	1.190433	-3.284131	29823.845670
HLA B*1801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.062161	0.778023	-3.284138	11538.806496
HLA A*0101	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.339987	1.055834	-3.284153	21876.986151
HLA A*3101	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.289307	1.005151	-3.284156	19467.346138
HLA B*3801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.522129	1.237896	-3.284233	33275.835386
HLA B*4501	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.597449	1.313175	-3.284273	39577.536436
HLA A*2301	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.516199	1.231855	-3.284343	32824.556507
HLA B*0803	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.425314	1.140721	-3.284592	26626.478888
HLA B*1509	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.494866	1.210159	-3.284706	31251.116885
HLA A*6802	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.425152	1.140437	-3.284715	26616.541549
HLA B*1503	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.187121	0.902388	-3.284732	15385.818314
HLA A*8001	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.302032	1.017185	-3.284847	20046.177045
HLA A*3002	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.060291	0.775312	-3.284979	11489.224094
HLA A*1101	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.313342	1.028301	-3.285041	20575.101317
HLA B*5401	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.560863	1.275786	-3.285077	36379.990133
HLA B*3501	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.092855	0.807776	-3.285078	12383.818049
HLA B*1509	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.424043	1.138932	-3.285110	26548.663769
HLA B*0702	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.416282	1.131046	-3.285236	26078.482623
HLA B*4801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.437461	1.151838	-3.285622	27381.710608
HLA B*7301	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.524934	1.239243	-3.285691	33491.473268
HLA B*2705	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.377643	1.091915	-3.285728	23858.475400
HLA A*2902	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.185584	0.899837	-3.285747	15331.478436
HLA A*3002	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.475849	1.190075	-3.285774	29912.231384
HLA A*6801	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.578860	1.293038	-3.285821	37919.240671
HLA B*1801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.468147	1.182210	-3.285937	29386.455078
HLA B*5401	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.468166	1.182210	-3.285956	29387.726925
HLA B*4402	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.399516	1.113445	-3.286072	25090.908887
HLA A*2902	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.330160	1.044058	-3.286102	21387.479000
HLA B*4002	1:139-147	9	MSHGDAVTA	1.492894	-0.205078	-4.574010	1.287816	-3.286194	37498.189114
HLA A*0202	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.525458	1.239243	-3.286215	33531.901940
HLA B*1501	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.359216	1.072837	-3.286378	22867.341479
HLA B*4601	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.313084	1.026553	-3.286531	20562.860968
HLA A*3002	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.314909	1.028301	-3.286608	20649.478542
HLA B*1503	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.267576	0.980728	-3.286849	18517.244633
HLA B*4402	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.434209	1.147258	-3.286951	27177.461484
HLA B*4801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.400451	1.113445	-3.287007	25144.991226
HLA B*0803	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.313579	1.026553	-3.287026	20586.346600
HLA A*6901	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.364636	1.077535	-3.287101	23154.528353
HLA A*2603	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.438967	1.151838	-3.287128	27476.828058
HLA A*2403	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.427713	1.140437	-3.287276	26773.957082
HLA A*6801	1:100-108	9	AQALGGIVA	1.487590	-0.113086	-4.661865	1.374504	-3.287361	45905.485797
HLA B*5301	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.515506	1.228069	-3.287437	32772.213009
HLA A*2403	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.413674	1.126026	-3.287649	25922.351188
HLA B*4002	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.644279	1.356576	-3.287702	44083.766406
HLA B*4402	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.408705	1.120820	-3.287885	25627.440226
HLA B*2705	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.194122	0.906227	-3.287895	15635.870506
HLA B*5701	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.360745	1.072837	-3.287908	22948.018529
HLA A*2403	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.343773	1.055834	-3.287938	22068.484610
HLA A*0202	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.180721	0.892605	-3.288115	15160.747076
HLA A*2902	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.343977	1.055834	-3.288143	22078.873816
HLA B*1509	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.019678	0.731526	-3.288152	10463.512623
HLA A*0101	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.380077	1.091915	-3.288162	23992.569111
HLA A*0219	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.305415	1.017185	-3.288230	20202.951445
HLA B*3501	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.411431	1.123169	-3.288261	25788.770175
HLA B*4801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.388814	1.100487	-3.288327	24480.173371
HLA B*0702	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.397472	1.109115	-3.288358	24973.093399
HLA B*4402	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.388920	1.100487	-3.288433	24486.133673
HLA B*4402	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.375768	1.087303	-3.288465	23755.698187
HLA B*0803	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.389031	1.100487	-3.288543	24492.360426

HLA B*5301	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.589735	1.301147	-3.288589	38880.818431
HLA A*0216	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.215634	0.926967	-3.288667	16429.863287
HLA B*0803	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.478800	1.190075	-3.288725	30116.171720
HLA B*4403	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.645479	1.356576	-3.288903	44205.802526
HLA A*0212	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.380861	1.091915	-3.288947	24035.960546
HLA A*3201	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.517350	1.228391	-3.288959	32911.684772
HLA B*3501	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.189141	0.900174	-3.288967	15457.567684
HLA B*3901	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.479601	1.190433	-3.289168	30171.780473
HLA A*3201	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.436500	1.147258	-3.289242	27321.191590
HLA A*0212	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.332608	1.043307	-3.289301	21508.382908
HLA B*0803	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.479737	1.190433	-3.289304	30181.249066
HLA B*3901	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.419748	1.130410	-3.289338	26287.410601
HLA B*0803	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.428399	1.138932	-3.289466	26816.284995
HLA A*3101	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.412650	1.123169	-3.289481	25861.279889
HLA A*0211	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.079138	0.789472	-3.289666	11998.812559
HLA A*8001	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.403344	1.113445	-3.289899	25313.004973
HLA B*4402	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.345868	1.055834	-3.290034	22175.236119
HLA B*4403	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.583072	1.293038	-3.290034	38288.844366
HLA B*4501	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.574067	1.284024	-3.290043	37503.058095
HLA A*0212	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.318431	1.028301	-3.290130	20817.614738
HLA B*0803	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.449659	1.159455	-3.290204	28161.715210
HLA B*5101	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.442150	1.151838	-3.290312	27678.984230
HLA B*5701	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.421388	1.131046	-3.290342	26386.862213
HLA B*0801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.413524	1.123169	-3.290355	25913.377570
HLA A*0301	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.363207	1.072837	-3.290370	23078.493303
HLA A*3301	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.573895	1.283502	-3.290393	37488.250240
HLA A*2301	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.437771	1.147258	-3.290513	27401.271018
HLA A*2902	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.416621	1.126026	-3.290595	26098.806303
HLA B*4801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.421017	1.130410	-3.290606	26364.317350
HLA B*5401	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.527589	1.236980	-3.290609	33696.839576
HLA A*8001	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.431070	1.140437	-3.290633	26981.741486
HLA A*0212	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.368400	1.077535	-3.290864	23356.072464
HLA A*3002	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.194536	0.903619	-3.290916	15650.765141
HLA A*8001	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.382840	1.091915	-3.290925	24145.697133
HLA B*5401	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.519035	1.228069	-3.290966	33039.593505
HLA A*2601	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.400127	1.109115	-3.291013	25126.225869
HLA B*5701	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.400144	1.109115	-3.291029	25127.177397
HLA A*2301	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.519479	1.228391	-3.291088	33073.392744
HLA B*1503	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.354110	1.062990	-3.291120	22600.094038
HLA A*2501	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.417624	1.126421	-3.291203	26159.164825
HLA B*4501	1:299-307	9	VSAPEGKRK	1.115540	0.241036	-4.647810	1.356576	-3.291234	44443.675544
HLA A*0211	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.272111	0.980728	-3.291383	18711.597640
HLA A*0202	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.567352	1.275786	-3.291566	36927.665611
HLA A*2402	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.552531	1.260962	-3.291569	35688.747213
HLA A*0301	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.166351	0.874608	-3.291744	14667.333006
HLA A*0101	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.364704	1.072837	-3.291867	23158.161277
HLA A*3101	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.385894	1.094025	-3.291869	24316.108879
HLA B*1502	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.407700	1.115576	-3.292123	25568.170261
HLA A*0211	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-3.919416	0.627189	-3.292227	8306.452379
HLA B*1502	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.423373	1.131046	-3.292327	26507.762090
HLA A*2402	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.372091	1.079304	-3.292787	23555.420147
HLA B*1502	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.406316	1.113445	-3.292871	25486.828874
HLA B*7301	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.596772	1.303793	-3.292979	39515.920744
HLA B*3501	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.431930	1.138932	-3.292998	27035.218784
HLA B*4001	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.408679	1.115576	-3.293103	25625.915213
HLA A*2301	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.483189	1.190075	-3.293113	30422.058895
HLA A*0250	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.196796	0.903619	-3.293176	15732.428945
HLA A*0203	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.370716	1.077535	-3.293181	23480.990143
HLA A*0211	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.068956	0.775707	-3.293249	11720.755353
HLA A*2501	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.372608	1.079304	-3.293304	23583.471924
HLA A*8001	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.424376	1.131046	-3.293330	26569.066401
HLA B*7301	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.562977	1.269596	-3.293382	36557.552591
HLA A*8001	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.414217	1.120820	-3.293397	25954.766196
HLA B*0802	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.432684	1.138932	-3.293752	27082.208242
HLA A*6802	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.387959	1.094025	-3.293934	24432.014455

HLA B*0802	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.385422	1.091476	-3.293946	24289.682212
HLA B*5401	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.320557	1.026553	-3.294004	20919.786642
HLA B*0801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.227090	0.932998	-3.294092	16869.027203
HLA A*2902	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.417283	1.123169	-3.294114	26138.652735
HLA B*2705	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.420678	1.126421	-3.294257	26343.786911
HLA A*3002	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.328907	1.034513	-3.294394	21325.897653
HLA A*0219	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.322855	1.028301	-3.294554	21030.763871
HLA A*3001	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.113093	0.818458	-3.294635	12974.571577
HLA A*6901	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.070483	0.775707	-3.294776	11762.043094
HLA B*3501	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.446664	1.151838	-3.294825	27968.135107
HLA B*1502	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.543946	1.249052	-3.294895	34990.188725
HLA B*7301	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.558024	1.263086	-3.294938	36143.016754
HLA B*4801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.426089	1.131046	-3.295043	26674.056624
HLA B*4002	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.624816	1.329702	-3.295114	42151.745041
HLA B*4402	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.338472	1.043307	-3.295165	21800.782096
HLA B*4001	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.358241	1.062990	-3.295250	22816.059507
HLA B*0802	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.421113	1.125828	-3.295285	26370.165748
HLA B*3501	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.070990	0.775634	-3.295356	11775.795499
HLA A*3002	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.157512	0.862117	-3.295396	14371.840533
HLA B*1801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.426472	1.131046	-3.295426	26697.588499
HLA A*3001	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.061329	0.765882	-3.295448	11516.729666
HLA B*5301	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.558553	1.263068	-3.295485	36187.037726
HLA A*3101	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.322716	1.027198	-3.295518	21024.052270
HLA A*0211	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.373103	1.077535	-3.295568	23610.407512
HLA A*0219	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.368647	1.072837	-3.295809	23369.343378
HLA B*0702	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.044333	0.748391	-3.295942	11074.726205
HLA B*4501	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.251485	0.955413	-3.296072	17843.692948
HLA B*0803	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.503552	1.207422	-3.296130	31882.442806
HLA B*0802	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.396753	1.100487	-3.296266	24931.786489
HLA B*5701	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.410183	1.113845	-3.296338	25714.794340
HLA A*6802	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.339703	1.043307	-3.296397	21862.670237
HLA A*3002	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.209239	0.912830	-3.296409	16189.694419
HLA A*0211	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.503848	1.207422	-3.296426	31904.182755
HLA B*4801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.436953	1.140437	-3.296516	27349.732779
HLA B*2705	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.409981	1.113445	-3.296536	25702.833302
HLA B*0702	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.448426	1.151838	-3.296587	28081.844016
HLA A*0250	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.469343	1.172675	-3.296668	29467.486121
HLA B*0801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.412281	1.115576	-3.296705	25839.323869
HLA B*4001	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.374276	1.077535	-3.296740	23674.230733
HLA B*5701	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.412361	1.115576	-3.296785	25844.077094
HLA A*0301	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.110720	0.813920	-3.296800	12903.872000
HLA A*3101	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.240694	0.943730	-3.296964	17405.782676
HLA A*3001	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.200597	0.903619	-3.296978	15870.742512
HLA A*3001	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.252403	0.955413	-3.296991	17881.477064
HLA A*2902	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.092028	0.794851	-3.297177	12360.258219
HLA B*1509	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-3.716303	0.419078	-3.297225	5203.584377
HLA B*1509	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.412826	1.115576	-3.297250	25871.775017
HLA A*0201	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-3.964079	0.666703	-3.297376	9206.176343
HLA B*1801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.487932	1.190433	-3.297499	30756.167185
HLA B*4501	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.195391	0.897730	-3.297661	15681.614987
HLA A*0212	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-3.731114	0.433361	-3.297753	5384.107898
HLA B*4501	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.601563	1.303793	-3.297770	39954.224507
HLA A*2501	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.437056	1.139224	-3.297832	27356.243751
HLA B*4403	1:247-255	9	RAIGDRLTC	1.196232	0.143325	-4.637526	1.339557	-3.297969	43403.651980
HLA A*0101	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.350544	1.052564	-3.297980	22415.257279
HLA A*2402	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.370876	1.072837	-3.298039	23489.629742
HLA A*0211	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.258561	0.960386	-3.298176	18136.830329
HLA B*2705	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.392320	1.094025	-3.298295	24678.566018
HLA A*0211	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.225413	0.926967	-3.298446	16803.993554
HLA B*4402	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.428861	1.130410	-3.298451	26844.879636
HLA A*0212	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.424553	1.126026	-3.298527	26579.848766
HLA A*0201	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.390464	1.091915	-3.298549	24573.319518
HLA B*1503	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.332074	1.033365	-3.298710	21481.985861
HLA B*4002	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.582302	1.283502	-3.298799	38220.963213
HLA A*3001	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.205588	0.906788	-3.298800	16054.158701

HLA B*5401	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.548093	1.249052	-3.299041	35325.891113
HLA A*2501	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.439768	1.140721	-3.299046	27527.563329
HLA B*1517	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.414638	1.115576	-3.299061	25979.912190
HLA B*4002	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.562162	1.263068	-3.299094	36488.989975
HLA A*6801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.378439	1.079304	-3.299135	23902.270856
HLA A*0250	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.259635	0.960386	-3.299249	18181.725840
HLA A*2601	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.391270	1.091915	-3.299355	24618.959905
HLA A*2902	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.355774	1.056396	-3.299378	22686.822941
HLA B*4402	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.408299	1.108898	-3.299400	25603.466447
HLA A*3201	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.421228	1.121826	-3.299402	26377.156998
HLA A*3002	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.481643	1.182210	-3.299433	30313.957796
HLA B*5801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.343523	1.044058	-3.299466	22055.833104
HLA A*2301	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.391173	1.091476	-3.299697	24613.499891
HLA A*0201	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.352365	1.052564	-3.299801	22509.434211
HLA A*0301	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.352395	1.052564	-3.299831	22511.017323
HLA B*4002	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.589402	1.289353	-3.300049	38850.961490
HLA A*0212	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.413505	1.113445	-3.300061	25912.256087
HLA B*3501	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.334645	1.034513	-3.300131	21609.502223
HLA B*5301	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.400661	1.100487	-3.300173	25157.100955
HLA A*2501	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.422121	1.121826	-3.300294	26431.437821
HLA A*2603	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.430713	1.130410	-3.300303	26959.563435
HLA B*0702	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.363311	1.062990	-3.300321	23083.987449
HLA B*5801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.356756	1.056396	-3.300360	22738.183467
HLA B*5101	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.421263	1.120820	-3.300443	26379.297547
HLA B*4402	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.392468	1.091915	-3.300553	24686.978475
HLA B*3501	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.409492	1.108898	-3.300594	25673.927277
HLA B*0802	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.421475	1.120820	-3.300654	26392.144491
HLA A*3301	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.618390	1.317518	-3.300872	41532.657169
HLA A*3301	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.604688	1.303793	-3.300895	40242.737952
HLA A*2601	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.028145	0.727191	-3.300954	10669.524046
HLA A*0201	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.334360	1.033365	-3.300996	21595.361346
HLA B*0801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.364328	1.062990	-3.301338	23138.124657
HLA A*0206	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.424583	1.123169	-3.301414	26581.718154
HLA A*2501	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.388817	1.087303	-3.301514	24480.305806
HLA A*6901	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.380826	1.079304	-3.301522	24034.010147
HLA B*1801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.393004	1.091476	-3.301528	24717.447533
HLA B*5401	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.422457	1.120820	-3.301636	26451.893467
HLA B*5701	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.395713	1.094025	-3.301688	24872.106988
HLA A*8001	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.410620	1.108898	-3.301722	25740.682601
HLA A*3101	1:208-216	9	PANIANALI	0.995189	0.008861	-4.305896	1.004050	-3.301846	20225.369498
HLA B*4402	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.393361	1.091476	-3.301885	24737.781127
HLA A*0301	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.309284	1.007289	-3.301995	20383.765849
HLA B*5801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.345342	1.043287	-3.302055	22148.380107
HLA A*2602	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.085740	0.783681	-3.302060	12182.609451
HLA B*0801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.428117	1.126026	-3.302091	26798.881869
HLA B*0802	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.394014	1.091915	-3.302099	24775.013483
HLA A*0219	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.394021	1.091915	-3.302106	24775.415577
HLA B*4001	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.354676	1.052564	-3.302113	22629.578880
HLA A*2602	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.467395	1.165167	-3.302229	29335.626298
HLA B*4403	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.632000	1.329702	-3.302299	42854.880048
HLA B*1501	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.065760	0.763388	-3.302372	11634.836948
HLA B*0802	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.443111	1.140721	-3.302390	27740.295792
HLA A*0219	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.265481	0.962975	-3.302506	18428.102682
HLA A*2403	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.394021	1.091476	-3.302545	24775.415577
HLA A*0212	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.443175	1.140437	-3.302738	27744.348030
HLA A*1101	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.346886	1.044058	-3.302828	22227.242098
HLA B*5101	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.441911	1.138932	-3.302978	27663.714939
HLA B*0801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.236192	0.933159	-3.303033	17226.297508
HLA A*2902	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.416898	1.113845	-3.303053	26115.472236
HLA B*5801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.354160	1.050933	-3.303226	22602.661728
HLA B*4002	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.572948	1.269596	-3.303353	37406.607937
HLA B*1501	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.359874	1.056396	-3.303477	22902.006466
HLA B*5101	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.425398	1.121826	-3.303572	26631.665060
HLA B*1509	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.320762	1.017185	-3.303577	20929.635074
HLA A*0201	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.381127	1.077535	-3.303592	24050.658641

HLA A*0203	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.395562	1.091915	-3.303648	24863.496937
HLA B*4402	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.381214	1.077535	-3.303679	24055.473244
HLA A*2602	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.519190	1.215498	-3.303692	33051.392487
HLA B*4801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.376618	1.072837	-3.303781	23802.266452
HLA B*5101	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.397839	1.094025	-3.303814	24994.178155
HLA B*3501	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.230812	0.926967	-3.303845	17014.203495
HLA B*0702	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.404340	1.100487	-3.303853	25371.134410
HLA A*3001	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.215878	0.911989	-3.303889	16439.109797
HLA A*2403	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.417739	1.113845	-3.303894	26166.100135
HLA A*2602	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.332232	1.028301	-3.303931	21489.773688
HLA B*7301	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.593433	1.289353	-3.304080	39213.308630
HLA A*3002	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.434557	1.130410	-3.304146	27199.230201
HLA A*3301	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.633894	1.329702	-3.304192	43042.151198
HLA A*2603	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.367209	1.062990	-3.304218	23292.098880
HLA A*2403	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.398281	1.094025	-3.304256	25019.611645
HLA B*0802	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.426178	1.121826	-3.304352	26679.540728
HLA A*2601	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.395839	1.091476	-3.304363	24879.374038
HLA A*0219	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.088048	0.783681	-3.304367	12247.501918
HLA A*3301	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.383770	1.079304	-3.304466	24197.480297
HLA B*2705	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.427992	1.123169	-3.304823	26791.199084
HLA A*0212	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.204798	0.899837	-3.304961	16025.003198
HLA B*4801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.431413	1.126421	-3.304992	27003.061266
HLA B*5301	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-3.768917	0.463883	-3.305034	5873.770426
HLA B*1502	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.544339	1.239243	-3.305096	35021.814947
HLA A*2403	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.357825	1.052564	-3.305261	22794.222437
HLA A*2902	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.326156	1.020890	-3.305266	21191.225537
HLA A*0219	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.428495	1.123169	-3.305326	26822.233653
HLA A*6801	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.594721	1.289353	-3.305368	39329.733652
HLA A*1101	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.226841	0.921448	-3.305393	16859.356462
HLA A*0301	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.361826	1.056396	-3.305430	23005.196914
HLA A*3001	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.232428	0.926967	-3.305461	17077.648422
HLA A*6901	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.348854	1.043307	-3.305548	22328.237772
HLA A*3101	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.378493	1.072837	-3.305656	23905.245140
HLA B*4403	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.509604	1.203805	-3.305799	32329.862880
HLA A*0216	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.323106	1.017228	-3.305879	21042.941224
HLA A*2902	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.419337	1.113445	-3.305892	26262.535282
HLA B*3901	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.383479	1.077535	-3.305943	24181.253435
HLA A*6801	1:98-106	9	AMAQALGGI	0.985073	0.332445	-4.623523	1.317518	-3.306005	42026.511498
HLA A*3002	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.206372	0.900174	-3.306198	16083.193232
HLA A*0201	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.078917	0.772641	-3.306276	11992.712359
HLA A*2403	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.419731	1.113445	-3.306287	26286.415136
HLA B*0803	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.478995	1.172675	-3.306319	30129.697544
HLA A*0301	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.334633	1.028301	-3.306332	21608.917706
HLA B*5401	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.287061	0.980728	-3.306333	19366.923775
HLA A*2602	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.428225	1.121826	-3.306398	26805.551732
HLA B*4801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.415559	1.109115	-3.306444	26035.065641
HLA B*1501	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.341014	1.034513	-3.306501	21928.767190
HLA A*2402	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.432992	1.126421	-3.306571	27101.408083
HLA B*1801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.079317	0.772641	-3.306676	12003.746904
HLA A*0250	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.567664	1.260962	-3.306702	36954.245191
HLA A*0211	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-3.710786	0.403979	-3.306807	5137.904296
HLA B*5401	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.343857	1.036964	-3.306893	22072.782999
HLA A*0201	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.233913	0.926967	-3.306946	17136.137687
HLA B*4001	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.416141	1.109115	-3.307027	26070.019095
HLA A*8001	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.398570	1.091476	-3.307094	25036.265644
HLA A*0202	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.568447	1.260962	-3.307484	37020.878009
HLA A*0201	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.386810	1.079304	-3.307506	24367.466546
HLA A*2602	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.545410	1.237896	-3.307514	35108.317246
HLA A*2301	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.545424	1.237896	-3.307529	35109.456857
HLA B*4501	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.596944	1.289353	-3.307591	39531.529529
HLA B*1801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.448315	1.140721	-3.307594	28074.704699
HLA B*5401	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.540258	1.232655	-3.307602	34694.257179
HLA B*1517	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.380471	1.072837	-3.307634	24014.384943
HLA A*2601	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.401798	1.094025	-3.307773	25223.058278
HLA B*5401	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.268173	0.960386	-3.307787	18542.706888

HLA A*0201	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-3.980855	0.673013	-3.307842	9568.736876
HLA A*0203	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.401871	1.094025	-3.307846	25227.288705
HLA B*1517	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.459877	1.151838	-3.308039	28832.148927
HLA A*2603	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.630299	1.322138	-3.308162	42687.356069
HLA A*2603	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.182976	0.874608	-3.308369	15239.689134
HLA B*1503	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.434477	1.126026	-3.308451	27194.227737
HLA A*0250	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.584343	1.275786	-3.308557	38401.070391
HLA A*2602	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.592083	1.283502	-3.308580	39091.517855
HLA A*2402	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.557759	1.249052	-3.308707	36120.928649
HLA A*0219	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-3.916347	0.607629	-3.308718	8247.971511
HLA A*2603	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.594986	1.286148	-3.308838	39353.783956
HLA B*4001	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.122834	0.813920	-3.308914	13268.871586
HLA A*3002	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.435106	1.126026	-3.309081	27233.683892
HLA B*3801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.524596	1.215498	-3.309098	33465.392765
HLA B*5801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.242258	0.933159	-3.309099	17468.608582
HLA A*3101	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.360033	1.050933	-3.309100	22910.433033
HLA B*0803	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.365136	1.055834	-3.309302	23181.224842
HLA A*6802	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.435377	1.126026	-3.309351	27250.632253
HLA A*0201	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.337662	1.028301	-3.309360	21760.130808
HLA A*0219	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.418376	1.108898	-3.309477	26204.489864
HLA A*2403	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.035574	0.726094	-3.309480	10853.607650
HLA B*3501	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.435593	1.126026	-3.309567	27264.198536
HLA B*0803	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.440019	1.130410	-3.309609	27543.502496
HLA B*4601	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.372911	1.062990	-3.309921	23599.936000
HLA A*0206	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.244730	0.934761	-3.309969	17568.309426
HLA A*2902	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.450413	1.140437	-3.309977	28210.662612
HLA B*4801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.292638	0.982586	-3.310052	19617.258759
HLA B*1801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-3.943578	0.633434	-3.310143	8781.681532
HLA B*5401	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.545614	1.235408	-3.310206	35124.845228
HLA A*0202	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.433558	1.123169	-3.310389	27136.765490
HLA A*3002	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.549740	1.239243	-3.310497	35460.112977
HLA A*1101	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.431378	1.120820	-3.310557	27000.870101
HLA A*2601	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.094443	0.783681	-3.310762	12429.189638
HLA B*0801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.390222	1.079304	-3.310918	24559.630622
HLA A*2501	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.293627	0.982586	-3.311041	19661.989227
HLA A*2601	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.390490	1.079304	-3.311186	24574.781890
HLA A*2603	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.192750	0.881518	-3.311232	15586.548877
HLA A*3101	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.367152	1.055834	-3.311318	23289.074892
HLA B*4001	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.223326	0.911989	-3.311337	16723.461072
HLA A*2603	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.641177	1.329702	-3.311476	43770.083211
HLA B*5801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.354820	1.043307	-3.311513	22637.047946
HLA A*0211	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.549503	1.237896	-3.311607	35440.742906
HLA A*0219	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.425128	1.113445	-3.311684	26615.101662
HLA A*2601	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.316838	1.005151	-3.311687	20741.397572
HLA B*4601	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.364410	1.052564	-3.311847	23142.506186
HLA A*0206	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.463758	1.151838	-3.311920	29090.980673
HLA A*0101	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.087681	0.775707	-3.311974	12237.170088
HLA A*0212	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.435297	1.123169	-3.312127	27245.620335
HLA A*0101	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.125414	0.813260	-3.312153	13347.924012
HLA B*5801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.346806	1.034513	-3.312292	22223.154079
HLA B*0803	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.494508	1.182210	-3.312299	31225.429556
HLA A*0212	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.427980	1.115576	-3.312404	26790.474407
HLA B*5701	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.256137	0.943730	-3.312407	18035.854440
HLA B*5701	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.368254	1.055834	-3.312420	23348.239845
HLA A*0202	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.412981	1.100487	-3.312494	25881.014253
HLA A*2403	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.355948	1.043307	-3.312641	22695.907016
HLA A*2403	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.428222	1.115576	-3.312646	26805.406717
HLA A*1101	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.459933	1.147258	-3.312675	28835.892660
HLA B*7301	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.596213	1.283502	-3.312711	39465.074618
HLA B*5701	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.365275	1.052564	-3.312711	23188.625087
HLA B*4501	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.224769	0.911989	-3.312779	16779.103285
HLA A*0101	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.340265	1.027198	-3.313066	21890.956154
HLA A*0212	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.273570	0.960386	-3.313184	18774.565736
HLA B*3501	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.221846	0.908582	-3.313264	16666.560687
HLA A*8001	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.390938	1.077535	-3.313403	24600.187861

HLA B*1502	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.505231	1.191820	-3.313412	32006.005170
HLA B*5801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.243245	0.929716	-3.313529	17508.345068
HLA B*5801	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.330787	1.017185	-3.313602	21418.394261
HLA A*2603	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.551530	1.237896	-3.313635	35606.593173
HLA B*1509	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.220042	0.906227	-3.313814	16597.458199
HLA A*0219	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.342955	1.028966	-3.313989	22026.976651
HLA A*0301	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.319188	1.005151	-3.314037	20853.910300
HLA B*1502	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.595304	1.281231	-3.314073	39382.535901
HLA A*0206	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.552012	1.237896	-3.314116	35646.103761
HLA B*5401	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.553389	1.239243	-3.314146	35759.288176
HLA A*0203	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.429766	1.115576	-3.314190	26900.850616
HLA B*4403	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.627388	1.313175	-3.314213	42402.185806
HLA A*3002	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.504849	1.190433	-3.314416	31977.794333
HLA B*5801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.090284	0.775707	-3.314577	12310.741889
HLA A*0101	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.392116	1.077535	-3.314580	24666.953529
HLA B*4601	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.349099	1.034513	-3.314585	22340.803809
HLA B*1501	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.358236	1.043287	-3.314949	22815.812644
HLA B*1509	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.454222	1.139224	-3.314997	28459.141971
HLA B*1501	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.212730	0.897730	-3.315000	16320.369466
HLA B*1503	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.090721	0.775634	-3.315087	12323.135677
HLA B*3801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.547090	1.231855	-3.315235	35244.381685
HLA B*4402	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.441274	1.126026	-3.315248	27623.187437
HLA B*4402	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.438483	1.123169	-3.315313	27446.223916
HLA B*1502	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.553309	1.237896	-3.315413	35752.711352
HLA A*2301	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.497645	1.182210	-3.315435	31451.762242
HLA A*3201	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.322749	1.007289	-3.315460	21025.644660
HLA A*8001	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.424618	1.109115	-3.315504	26583.875304
HLA B*2705	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.429390	1.113845	-3.315545	26877.575791
HLA A*0203	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.429087	1.113445	-3.315642	26858.825128
HLA B*4601	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.409708	1.094025	-3.315684	25686.708623
HLA A*8001	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.438945	1.123169	-3.315776	27475.490271
HLA A*2403	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.349268	1.033365	-3.315903	22349.507516
HLA B*0702	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.431502	1.115576	-3.315926	27008.613012
HLA A*2501	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.350464	1.034513	-3.315951	22411.134680
HLA B*1517	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.436904	1.120820	-3.316083	27346.625816
HLA B*4601	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.359375	1.043287	-3.316089	22875.755291
HLA A*2902	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.353224	1.036964	-3.316261	22554.047481
HLA B*0702	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.407742	1.091476	-3.316266	25570.660159
HLA B*1503	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.447378	1.131046	-3.316332	28014.169522
HLA B*4601	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.372218	1.055834	-3.316383	23562.302492
HLA B*5301	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.508380	1.191820	-3.316560	32238.867770
HLA B*3501	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.457149	1.140437	-3.316713	28651.625140
HLA A*0203	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.135761	0.819048	-3.316713	13669.758987
HLA A*2601	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.389663	1.072837	-3.316825	24528.029130
HLA B*5301	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.551958	1.235042	-3.316916	35641.668683
HLA B*5801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.329652	1.012736	-3.316916	21362.501556
HLA A*3101	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.417462	1.100487	-3.316975	26149.401893
HLA A*0206	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.111848	0.794851	-3.316997	12937.423631
HLA A*2403	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.219407	0.902388	-3.317019	16573.232486
HLA B*5401	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.545448	1.228391	-3.317057	35111.356291
HLA B*5701	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.394864	1.077535	-3.317329	24823.579911
HLA A*0219	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.360726	1.043307	-3.317420	22947.025381
HLA B*4801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.396925	1.079304	-3.317621	24941.634542
HLA B*4601	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.361027	1.043307	-3.317720	22962.920914
HLA A*3101	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.370329	1.052564	-3.317765	23460.039619
HLA B*1501	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.298512	0.980728	-3.317784	19884.379039
HLA B*4402	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.008846	0.690895	-3.317951	10205.784099
HLA A*0219	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.370662	1.052564	-3.318099	23478.068645
HLA A*0206	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.351726	1.033365	-3.318361	22476.336165
HLA A*2403	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.395912	1.077535	-3.318377	24883.546822
HLA B*0702	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.444406	1.126026	-3.318380	27823.108788
HLA A*0250	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.427381	1.108898	-3.318483	26753.541846
HLA B*3901	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.418989	1.100487	-3.318502	26241.516242
HLA B*1517	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.449582	1.131046	-3.318536	28156.688051
HLA B*7301	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.335740	1.017185	-3.318555	21664.048686

HLA A*2902	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.427553	1.108898	-3.318655	26764.109492
HLA A*6901	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.094325	0.775634	-3.318691	12425.828066
HLA A*3101	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.326107	1.007289	-3.318818	21188.818188
HLA A*2601	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.099992	0.781170	-3.318823	12589.030852
HLA A*0201	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.347870	1.028966	-3.318904	22277.682703
HLA A*1101	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.450066	1.131046	-3.319020	28188.084402
HLA B*2705	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.382022	1.062990	-3.319032	24100.282207
HLA B*2705	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.398358	1.079304	-3.319054	25024.078703
HLA B*0802	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.340157	1.020890	-3.319267	21885.509160
HLA B*2705	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.428166	1.108898	-3.319268	26801.926600
HLA A*2601	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.396873	1.077535	-3.319338	24938.666226
HLA B*0801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.362716	1.043307	-3.319410	23052.413962
HLA A*0216	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.225638	0.906227	-3.319411	16812.722964
HLA B*0801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.353955	1.034513	-3.319442	22592.026054
HLA A*1101	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.382494	1.062990	-3.319504	24126.502811
HLA B*1801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.411442	1.091915	-3.319528	25789.467757
HLA A*3002	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.529758	1.210159	-3.319598	33865.519725
HLA B*0802	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.460199	1.140437	-3.319762	28853.525934
HLA A*2602	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.595630	1.275786	-3.319844	39412.161705
HLA A*3301	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.354465	1.034513	-3.319952	22618.563445
HLA A*3201	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.356930	1.036964	-3.319966	22747.288107
HLA B*3901	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.451034	1.131046	-3.319988	28250.982169
HLA A*6901	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.371059	1.050933	-3.320126	23499.543784
HLA B*3801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.459384	1.139224	-3.320159	28799.411993
HLA B*5701	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.348474	1.028301	-3.320173	22308.677831
HLA B*5801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.327481	1.007289	-3.320192	21255.982469
HLA B*5801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.357169	1.036964	-3.320206	22759.843722
HLA B*5801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.347428	1.027198	-3.320230	22255.036500
HLA B*3801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.527681	1.207422	-3.320259	33703.949877
HLA B*3901	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.460709	1.140437	-3.320272	28887.418304
HLA A*2403	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.383293	1.062990	-3.320303	24170.921029
HLA B*1517	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.353697	1.033365	-3.320332	22578.585815
HLA B*1501	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.399639	1.079304	-3.320335	25097.968310
HLA B*0801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.376740	1.056396	-3.320344	23808.963311
HLA B*0702	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.443543	1.123169	-3.320374	27767.922774
HLA B*4402	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.451654	1.131046	-3.320608	28291.359352
HLA A*0250	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.006943	0.686294	-3.320649	10161.160092
HLA B*3901	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.383657	1.062990	-3.320667	24191.197640
HLA A*2603	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.610129	1.289436	-3.320693	40750.123375
HLA A*0301	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.364147	1.043287	-3.320861	23128.488213
HLA A*3301	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.333632	1.012736	-3.320896	21559.174859
HLA B*4801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.377318	1.056396	-3.320922	23840.670152
HLA B*5801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.349966	1.028966	-3.321000	22385.446162
HLA B*5701	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.328289	1.007289	-3.321000	21295.576723
HLA B*4402	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.364570	1.043287	-3.321283	23151.021243
HLA B*0802	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.338651	1.017185	-3.321466	21809.747365
HLA B*5701	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.254539	0.932998	-3.321541	17969.627389
HLA A*1101	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.430483	1.108898	-3.321584	26945.274094
HLA A*6801	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.554308	1.232655	-3.321652	35835.008662
HLA B*4002	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.094302	0.772641	-3.321661	12425.155861
HLA A*2402	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.233654	0.911989	-3.321665	17125.943214
HLA A*2501	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.435172	1.113445	-3.321728	27237.809479
HLA B*2705	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.033995	0.712255	-3.321741	10814.221587
HLA B*3901	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.378157	1.056396	-3.321761	23886.758855
HLA A*2403	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.358760	1.036964	-3.321796	22843.354370
HLA B*1503	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.236932	0.915104	-3.321828	17255.678128
HLA A*6802	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.413764	1.091915	-3.321849	25927.680743
HLA A*0301	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.356363	1.034513	-3.321850	22717.649898
HLA B*4002	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.549926	1.228069	-3.321857	35475.271203
HLA B*0801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.265624	0.943730	-3.321894	18434.185019
HLA A*2602	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.571076	1.249052	-3.322024	37245.669758
HLA B*3501	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.442876	1.120820	-3.322056	27725.292658
HLA B*0803	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.430978	1.108898	-3.322080	26976.049325
HLA B*1801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.430997	1.108898	-3.322099	26977.216850
HLA B*4402	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.072367	0.750232	-3.322135	11813.186304

HLA B*1503	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.366208	1.044058	-3.322150	23238.481419
HLA A*0301	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.365548	1.043307	-3.322241	23203.181609
HLA A*6802	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.343237	1.020890	-3.322347	22041.280914
HLA A*0203	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.277764	0.955413	-3.322351	18956.743383
HLA B*4402	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.356927	1.034513	-3.322414	22747.165047
HLA A*2902	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.416489	1.094025	-3.322464	26090.900768
HLA A*3301	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.606572	1.284024	-3.322548	40417.719696
HLA A*0101	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.365916	1.043307	-3.322610	23222.897663
HLA A*6802	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.438288	1.115576	-3.322711	27433.902757
HLA B*1502	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.495465	1.172675	-3.322789	31294.258230
HLA B*2705	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.375427	1.052564	-3.322863	23737.070718
HLA A*3301	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.330185	1.007289	-3.322896	21388.751781
HLA A*0101	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.343855	1.020917	-3.322937	22072.663588
HLA A*2902	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.238100	0.915104	-3.322996	17302.136155
HLA A*0202	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.530592	1.207422	-3.323170	33930.621310
HLA A*2602	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.584167	1.260962	-3.323205	38385.492636
HLA B*5401	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.495958	1.172675	-3.323283	31329.831112
HLA B*1503	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.310584	0.987241	-3.323343	20444.838632
HLA B*4801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.417384	1.094025	-3.323359	26144.733952
HLA B*5401	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.515391	1.191820	-3.323571	32763.526752
HLA B*0702	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.216245	0.892605	-3.323640	16452.989320
HLA A*0219	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.449671	1.126026	-3.323645	28162.476979
HLA A*3201	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-3.818590	0.494882	-3.323708	6585.515560
HLA B*7301	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-3.593561	0.269777	-3.323784	3922.480612
HLA B*1501	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.016449	0.692424	-3.324025	10386.023721
HLA A*3101	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.411400	1.087303	-3.324097	25786.956552
HLA A*2603	1:26-34	9	YAQLIARRV	1.199062	0.114113	-4.637355	1.313175	-3.324179	43386.514312
HLA A*2402	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.556095	1.231855	-3.324240	35982.842830
HLA A*0202	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.433356	1.109115	-3.324241	27124.143033
HLA B*4402	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.251891	0.927581	-3.324310	17860.400870
HLA B*4801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.415843	1.091476	-3.324367	26052.113685
HLA A*0212	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.257577	0.933159	-3.324418	18095.765345
HLA B*4402	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.380869	1.056396	-3.324472	24036.350645
HLA B*1509	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.353445	1.028966	-3.324479	22565.519798
HLA A*3002	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.556483	1.231855	-3.324628	36014.976596
HLA B*4601	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.358062	1.033365	-3.324697	22806.680577
HLA A*8001	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.438638	1.113845	-3.324793	27456.025414
HLA B*3801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.516685	1.191820	-3.324866	32861.335580
HLA A*2602	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.280294	0.955413	-3.324882	19067.516305
HLA B*1517	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.330073	1.005094	-3.324979	21383.198384
HLA A*2501	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.388074	1.062990	-3.325084	24438.491863
HLA B*5101	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.359674	1.034513	-3.325161	22891.477615
HLA A*2301	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.376165	1.050933	-3.325232	23777.427271
HLA A*0202	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.368663	1.043287	-3.325376	23370.228374
HLA B*4403	1:268-276	9	RAQVQRDFV	1.144633	0.177505	-4.647584	1.322138	-3.325447	44420.599742
HLA A*8001	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.381858	1.056396	-3.325462	24091.157345
HLA A*6801	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.560548	1.235042	-3.325505	36353.626920
HLA A*3101	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.368900	1.043287	-3.325614	23383.001328
HLA B*4501	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.563581	1.237896	-3.325685	36608.415424
HLA B*1502	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.562702	1.236980	-3.325722	36534.420553
HLA A*0101	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.352296	1.026553	-3.325743	22505.903056
HLA A*3002	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.343108	1.017228	-3.325880	22034.723641
HLA B*2705	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.381766	1.055834	-3.325932	24086.074992
HLA A*8001	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.452138	1.126026	-3.326112	28322.905869
HLA B*0803	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.452168	1.126026	-3.326143	28324.897848
HLA B*3901	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.354709	1.028547	-3.326162	22631.292874
HLA A*3001	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.247126	0.920891	-3.326235	17665.520849
HLA B*7301	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.518196	1.191820	-3.326376	32975.844713
HLA B*1517	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.333679	1.007289	-3.326390	21561.507641
HLA A*0212	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.230093	0.903619	-3.326473	16986.061040
HLA B*3501	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.333907	1.007289	-3.326618	21572.825210
HLA B*0801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.331821	1.005151	-3.326670	21469.438289
HLA A*3201	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.563851	1.236980	-3.326871	36631.197970
HLA A*2902	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.360254	1.033365	-3.326889	22922.086629
HLA B*4002	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.575986	1.249052	-3.326935	37669.183948

HLA B*1503	1:208-216	9	PANIANALI	0.995189	0.008861	-4.331015	1.004050	-3.326964	21429.636711
HLA B*4403	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.534567	1.207422	-3.327145	34242.632175
HLA A*2403	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.309942	0.982586	-3.327356	20414.665942
HLA B*5401	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.565256	1.237896	-3.327361	36749.895958
HLA A*2402	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.555788	1.228391	-3.327397	35957.350986
HLA B*4002	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-3.123560	-0.203931	-3.327492	1329.108477
HLA A*0201	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.370867	1.043307	-3.327560	23489.121442
HLA A*0301	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.361020	1.033365	-3.327655	22962.548237
HLA B*1517	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.240487	0.912830	-3.327657	17397.498272
HLA B*5801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.348648	1.020917	-3.327730	22317.610492
HLA B*3901	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.257645	0.929716	-3.327929	18098.604554
HLA A*2601	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.384360	1.056396	-3.327964	24230.359942
HLA A*2602	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.612046	1.284024	-3.328022	40930.411198
HLA B*2705	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.400870	1.072837	-3.328032	25169.216516
HLA B*0801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.228025	0.899837	-3.328188	16905.387641
HLA B*4601	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.407627	1.079304	-3.328323	25563.882670
HLA B*3901	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.480200	1.151838	-3.328362	30213.431823
HLA A*0212	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.379308	1.050933	-3.328375	23950.162967
HLA A*6901	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.345647	1.017228	-3.328420	22163.962223
HLA B*5301	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.518600	1.190075	-3.328525	33006.543048
HLA A*3001	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.291301	0.962750	-3.328551	19556.965232
HLA A*0216	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.442106	1.113445	-3.328661	27676.139312
HLA B*4403	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.612803	1.284024	-3.328779	41001.773470
HLA A*2301	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.536221	1.207422	-3.328799	34373.296024
HLA A*2403	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.408125	1.079304	-3.328821	25593.218617
HLA A*0216	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.406414	1.077535	-3.328879	25492.620531
HLA B*1509	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.501578	1.172675	-3.328903	31737.887902
HLA A*2301	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.494114	1.165167	-3.328947	31197.062862
HLA A*0202	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.104691	0.775707	-3.328984	12725.980924
HLA A*2501	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.449866	1.120820	-3.329046	28175.125356
HLA A*2602	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.437959	1.108898	-3.329060	27413.132611
HLA A*2601	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.381820	1.052564	-3.329256	24089.072147
HLA B*4001	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.385107	1.055834	-3.329273	24272.080391
HLA A*2301	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.385109	1.055834	-3.329275	24272.211701
HLA B*5801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.310029	0.980728	-3.329302	20418.752671
HLA B*4801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.438309	1.108898	-3.329410	27435.238519
HLA B*3501	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.234822	0.905240	-3.329582	17172.051951
HLA B*3901	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.364241	1.034513	-3.329728	23133.493657
HLA B*1801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.489224	1.159455	-3.329770	30847.816566
HLA B*4002	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.633628	1.303793	-3.329836	43015.846820
HLA A*2403	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.356446	1.026553	-3.329893	22721.951805
HLA A*3301	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.619393	1.289436	-3.329957	41628.709447
HLA B*0702	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.358278	1.028301	-3.329977	22818.034510
HLA A*3001	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.123191	0.793168	-3.330023	13279.787108
HLA A*3002	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.567061	1.236980	-3.330080	36902.901870
HLA A*2501	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.470523	1.140437	-3.330086	29547.621634
HLA B*7301	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.611428	1.281231	-3.330197	40872.216784
HLA A*0216	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.382816	1.052564	-3.330253	24144.390913
HLA B*1509	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.084946	0.754590	-3.330356	12160.353386
HLA B*5801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.347647	1.017228	-3.330419	22266.236264
HLA A*0203	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.409734	1.079304	-3.330430	25688.237253
HLA A*2402	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.351364	1.020890	-3.330474	22457.618412
HLA B*5801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.351392	1.020890	-3.330502	22459.076378
HLA A*0301	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.343274	1.012736	-3.330538	22043.188851
HLA A*0250	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.383117	1.052564	-3.330553	24161.115868
HLA B*7301	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.562416	1.231855	-3.330560	36510.315555
HLA A*0206	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.138416	0.807776	-3.330639	13753.580560
HLA B*0801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.383244	1.052564	-3.330680	24168.175183
HLA B*2705	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.461747	1.131046	-3.330701	28956.575711
HLA A*3301	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.540918	1.210159	-3.330758	34747.038764
HLA A*2402	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.469808	1.138932	-3.330876	29499.067367
HLA B*1501	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-3.861440	0.530534	-3.330906	7268.414526
HLA B*5401	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.253482	0.922498	-3.330983	17925.934433
HLA B*5401	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.490662	1.159455	-3.331207	30950.118386
HLA A*0250	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.109263	0.778023	-3.331241	12860.663224

HLA B*3801	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.490705	1.159455	-3.331250	30953.132393
HLA B*5801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.359810	1.028547	-3.331263	22898.661482
HLA A*3201	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.566689	1.235408	-3.331281	36871.372131
HLA B*3901	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-3.784217	0.452913	-3.331304	6084.386788
HLA B*7301	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.607105	1.275786	-3.331319	40467.384957
HLA A*6802	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.440456	1.109115	-3.331341	27571.231802
HLA A*6801	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.614882	1.283502	-3.331380	41198.550472
HLA B*5301	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.504066	1.172675	-3.331391	31920.238417
HLA B*0702	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.264416	0.932998	-3.331419	18382.996596
HLA A*6901	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.336621	1.005151	-3.331470	21708.043335
HLA B*4402	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.425671	1.094025	-3.331646	26648.382930
HLA B*1509	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.462074	1.130410	-3.331664	28978.358510
HLA A*6802	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.109837	0.778023	-3.331814	12877.650675
HLA B*4001	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.411130	1.079304	-3.331826	25770.918515
HLA B*7301	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.568863	1.236980	-3.331882	37056.344343
HLA B*0802	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.440790	1.108898	-3.331892	27592.420277
HLA B*0802	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.462976	1.131046	-3.331930	29038.620650
HLA A*0301	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.301299	0.969193	-3.332105	20012.369935
HLA A*6802	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.247415	0.915104	-3.332311	17677.279687
HLA B*5101	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.462750	1.130410	-3.332340	29023.543376
HLA B*0803	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.484180	1.151838	-3.332342	30491.590981
HLA B*1517	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.116067	0.783681	-3.332387	13063.738375
HLA B*4402	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.073293	0.740887	-3.332406	11838.392922
HLA A*2902	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.044775	0.712255	-3.332520	11085.995587
HLA B*4601	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.369589	1.036964	-3.332625	23420.095056
HLA A*2902	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.441878	1.109115	-3.332763	27661.619812
HLA A*0101	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.353723	1.020890	-3.332833	22579.929479
HLA B*0803	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.405743	1.072837	-3.332905	25453.208125
HLA B*0801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.254567	0.921448	-3.333120	17970.793991
HLA B*4601	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.350363	1.017185	-3.333178	22405.921891
HLA B*0801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.340481	1.007289	-3.333192	21901.854209
HLA A*3101	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.389632	1.056396	-3.333236	24526.304170
HLA B*3501	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.362489	1.028966	-3.333523	23040.320168
HLA A*0219	1:208-216	9	PANIANALI	0.995189	0.008861	-4.337586	1.004050	-3.333536	21756.364097
HLA B*3801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.480806	1.147258	-3.333548	30255.631706
HLA B*3801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.459600	1.126026	-3.333574	28813.749311
HLA A*2301	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.406471	1.072837	-3.333633	25495.930640
HLA B*7301	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.541188	1.207422	-3.333766	34768.662917
HLA B*4403	1:264-272	9	RAGERAQVQ	1.271733	0.032060	-4.637660	1.303793	-3.333868	43417.038154
HLA A*2301	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.455756	1.121826	-3.333930	28559.856165
HLA A*0216	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.459999	1.126026	-3.333973	28840.260962
HLA A*0203	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.339250	1.005094	-3.334156	21839.855148
HLA B*4001	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.390570	1.056396	-3.334173	24579.302499
HLA B*1501	1:208-216	9	PANIANALI	0.995189	0.008861	-4.338254	1.004050	-3.334203	21789.816452
HLA B*0803	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.413602	1.079304	-3.334298	25918.004204
HLA B*0801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.355346	1.020917	-3.334429	22664.496492
HLA A*0206	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.413844	1.079304	-3.334540	25932.450222
HLA B*2705	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.317136	0.982586	-3.334550	20755.652969
HLA A*1101	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.428643	1.094025	-3.334618	26831.376845
HLA A*0211	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.739154	0.404390	-3.334764	5484.710287
HLA A*3001	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.116598	0.781791	-3.334808	13079.720326
HLA B*0702	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.412349	1.077535	-3.334814	25843.378036
HLA B*4002	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.616057	1.281231	-3.334826	41310.141123
HLA A*3002	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.494290	1.159455	-3.334835	31209.723379
HLA A*0101	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.385842	1.050933	-3.334909	24313.215008
HLA B*5301	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.574161	1.239243	-3.334918	37511.174469
HLA A*0101	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.371889	1.036964	-3.334925	23544.463526
HLA B*1501	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-3.991084	0.656026	-3.335058	9796.800632
HLA B*2705	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.276699	0.941565	-3.335134	18910.343354
HLA A*2501	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.298352	0.962975	-3.335378	19877.065469
HLA B*1517	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.444514	1.109115	-3.335399	27830.033566
HLA A*1101	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.391279	1.055834	-3.335445	24619.492654
HLA B*5101	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.268657	0.933159	-3.335498	18563.383089
HLA A*3301	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.636706	1.301147	-3.335560	43321.780971
HLA B*3501	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.378961	1.043307	-3.335654	23930.994618

HLA A*0219	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.413214	1.077535	-3.335679	25894.879294
HLA B*1801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.456529	1.120820	-3.335709	28610.733789
HLA A*2602	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.192961	0.857166	-3.335795	15594.139660
HLA B*2705	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.476272	1.140437	-3.335835	29941.373505
HLA A*0219	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.476288	1.140437	-3.335851	29942.507383
HLA A*0216	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.415218	1.079304	-3.335914	26014.650860
HLA A*2501	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.408776	1.072837	-3.335938	25631.599812
HLA B*1502	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.564570	1.228391	-3.336179	36691.888430
HLA B*0802	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.413728	1.077535	-3.336193	25925.576841
HLA A*6802	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.353427	1.017228	-3.336199	22564.543204
HLA A*0301	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.353424	1.017185	-3.336239	22564.421133
HLA A*2902	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.341390	1.005151	-3.336240	21947.756559
HLA A*8001	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.409128	1.072837	-3.336291	25652.407870
HLA A*2402	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.518530	1.182210	-3.336320	33001.186630
HLA B*2705	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.365348	1.028966	-3.336382	23192.514297
HLA A*2402	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.526525	1.190075	-3.336450	33614.360519
HLA A*0201	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.357381	1.020917	-3.336463	22770.927961
HLA A*2603	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.629547	1.293038	-3.336509	42613.521161
HLA A*0101	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.365510	1.028966	-3.336544	23201.173270
HLA A*0250	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.575845	1.239243	-3.336602	37656.958765
HLA B*1503	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.161243	0.824605	-3.336638	14495.839503
HLA A*3002	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.457509	1.120820	-3.336688	28675.350281
HLA A*3201	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.475962	1.139224	-3.336737	29919.999842
HLA A*1101	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.424177	1.087303	-3.336874	26556.851675
HLA A*2301	1:208-216	9	PANIANALI	0.995189	0.008861	-4.340951	1.004050	-3.336900	21925.564355
HLA B*5101	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.451064	1.113845	-3.337219	28252.969090
HLA A*0301	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.358137	1.020917	-3.337220	22810.629130
HLA B*5701	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.388403	1.050933	-3.337470	24457.008209
HLA B*5701	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.358389	1.020917	-3.337471	22823.837071
HLA B*0802	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.460923	1.123169	-3.337753	28901.643078
HLA A*6901	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.086149	0.748391	-3.337758	12194.082593
HLA A*2501	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.429728	1.091915	-3.337814	26898.522227
HLA A*2603	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.429780	1.091915	-3.337866	26901.723814
HLA A*2902	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.350602	1.012736	-3.337866	22418.289086
HLA A*0216	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.358936	1.020917	-3.338019	22852.624752
HLA A*0301	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.358931	1.020890	-3.338042	22852.377493
HLA A*6801	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.607756	1.269596	-3.338160	40528.072383
HLA B*2705	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.438689	1.100487	-3.338202	27459.293357
HLA B*0802	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.394044	1.055834	-3.338210	24776.755935
HLA A*2301	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.497901	1.159455	-3.338446	31470.314121
HLA A*2402	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.530503	1.191820	-3.338683	33923.646713
HLA A*0212	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.355976	1.017228	-3.338748	22697.380452
HLA A*0301	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.367352	1.028547	-3.338805	23299.786617
HLA B*0803	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.465243	1.126421	-3.338822	29190.614418
HLA A*0301	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.301811	0.962975	-3.338836	20035.985563
HLA B*1517	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.244267	0.905240	-3.339027	17549.596006
HLA A*1101	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.479573	1.140437	-3.339136	30169.821825
HLA A*0203	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.368212	1.028966	-3.339246	23345.966350
HLA B*4501	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.529506	1.190075	-3.339431	33845.922066
HLA B*3801	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.512115	1.172675	-3.339440	32517.373702
HLA A*6901	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-3.966645	0.627189	-3.339456	9260.723704
HLA A*0206	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.147193	0.807656	-3.339538	14034.387113
HLA B*7301	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-3.806161	0.466612	-3.339549	6399.720462
HLA B*5701	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.418949	1.079304	-3.339645	26239.102970
HLA B*1502	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.344905	1.005151	-3.339754	22126.104744
HLA A*0101	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.374269	1.034513	-3.339756	23673.846511
HLA A*0212	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.419078	1.079304	-3.339774	26246.911417
HLA B*4801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.402806	1.062990	-3.339816	25281.665004
HLA B*0803	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.431789	1.091915	-3.339874	27026.444756
HLA A*0201	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.396323	1.056396	-3.339927	24907.115992
HLA A*0301	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.368959	1.028966	-3.339993	23386.164028
HLA A*3002	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.295493	0.955413	-3.340080	19746.628009
HLA A*3101	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.373491	1.033365	-3.340126	23631.492319
HLA A*1101	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.463359	1.123169	-3.340190	29064.238545
HLA A*2603	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.589336	1.249052	-3.340284	38845.076913

HLA B*1509	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.471389	1.131046	-3.340343	29606.664960
HLA A*3002	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.345511	1.005151	-3.340361	22157.008848
HLA A*3001	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.214976	0.874608	-3.340368	16404.994680
HLA B*3801	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.550741	1.210159	-3.340582	35541.929047
HLA B*1509	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.462471	1.121826	-3.340645	29004.864705
HLA B*0803	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.505831	1.165167	-3.340664	32050.188619
HLA A*2601	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.323278	0.982586	-3.340691	21051.253184
HLA A*0216	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.481184	1.140437	-3.340748	30281.995603
HLA B*3901	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.369051	1.028301	-3.340749	23391.098694
HLA A*2501	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.418326	1.077535	-3.340791	26201.513002
HLA B*0801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.369765	1.028966	-3.340799	23429.599493
HLA B*3801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.492692	1.151838	-3.340854	31095.122323
HLA B*4403	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.148584	0.807656	-3.340929	14079.406456
HLA A*0203	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.198140	0.857166	-3.340974	15781.187665
HLA A*0101	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.384273	1.043287	-3.340986	24225.510336
HLA A*3101	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.160205	0.819048	-3.341157	14461.218881
HLA B*1509	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.441788	1.100487	-3.341301	27655.933837
HLA A*0202	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.493153	1.151838	-3.341315	31128.111158
HLA B*0802	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.467365	1.126026	-3.341339	29333.563239
HLA A*3001	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.282904	0.941565	-3.341339	19182.464550
HLA A*2902	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.254579	0.912830	-3.341749	17971.280098
HLA B*4001	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.368388	1.026553	-3.341835	23355.440704
HLA B*3901	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.457638	1.115576	-3.342062	28683.883726
HLA B*1501	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.155948	0.813884	-3.342064	14320.152162
HLA A*2301	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.465391	1.123169	-3.342222	29200.564947
HLA A*2301	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.532704	1.190433	-3.342271	34096.044500
HLA A*3301	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.574929	1.232655	-3.342274	37577.591732
HLA B*4002	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.631714	1.289436	-3.342277	42826.604881
HLA A*3201	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.580189	1.237896	-3.342294	38035.527226
HLA A*3301	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.628476	1.286148	-3.342328	42508.527021
HLA B*4002	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.481490	1.138932	-3.342558	30303.299985
HLA B*4001	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.371106	1.028547	-3.342560	23502.086520
HLA B*1502	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.524915	1.182210	-3.342706	33490.023818
HLA A*3301	1:156-164	9	ASSAGAPVA	1.425900	-0.132862	-4.635764	1.293038	-3.342726	43227.902058
HLA B*7301	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.603816	1.260962	-3.342854	40162.049007
HLA A*2902	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.422161	1.079304	-3.342857	26433.868783
HLA A*6901	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.330099	0.987241	-3.342858	21384.470910
HLA B*5401	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.093155	0.750232	-3.342924	12392.396389
HLA B*4402	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.363837	1.020890	-3.342947	23111.977931
HLA B*5701	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.387224	1.044058	-3.343166	24390.678846
HLA B*1501	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.350457	1.007289	-3.343168	22410.770958
HLA B*0802	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.406250	1.062990	-3.343260	25482.968501
HLA A*2603	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.515999	1.172675	-3.343324	32809.465914
HLA B*1501	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.270325	0.926967	-3.343359	18634.822551
HLA B*0801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.348594	1.005094	-3.343500	22314.833742
HLA B*1501	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.372089	1.028547	-3.343542	23555.292715
HLA A*3301	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.559063	1.215498	-3.343565	36229.544298
HLA A*3001	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.205714	0.862117	-3.343598	16058.849352
HLA A*0206	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.364542	1.020917	-3.343625	23149.518358
HLA B*1801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.416484	1.072837	-3.343647	26090.618472
HLA A*2402	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.534281	1.190433	-3.343848	34220.039273
HLA B*1501	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.271491	0.927581	-3.343910	18684.892611
HLA B*5701	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.406931	1.062990	-3.343941	25522.979288
HLA B*0801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.421515	1.077535	-3.343979	26394.571839
HLA A*0101	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.361213	1.017185	-3.344028	22972.736933
HLA B*3501	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.265495	0.921448	-3.344047	18428.700856
HLA A*0203	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.361293	1.017228	-3.344065	22976.962841
HLA A*0211	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.107468	0.763388	-3.344081	12807.617803
HLA B*7301	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.607234	1.263068	-3.344166	40479.427572
HLA A*2603	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.607502	1.263068	-3.344434	40504.400042
HLA B*0803	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.465260	1.120820	-3.344439	29191.719865
HLA A*6802	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.137608	0.793168	-3.344440	13728.008922
HLA B*4001	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.387804	1.043307	-3.344498	24423.292496
HLA A*2603	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.939851	0.595350	-3.344502	8706.656287
HLA A*0203	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.206631	0.862117	-3.344514	16092.766992

HLA A*6901	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.401128	1.056396	-3.344732	25184.198867
HLA B*4801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.378113	1.033365	-3.344748	23884.303712
HLA A*0101	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.401170	1.056396	-3.344774	25186.651373
HLA A*0201	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.395760	1.050933	-3.344826	24874.798240
HLA A*0301	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.362124	1.017228	-3.344897	23021.008202
HLA A*0101	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.288677	0.943730	-3.344948	19439.141852
HLA B*3501	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.120668	0.775707	-3.344961	13202.852331
HLA B*4403	1:91-99	9	GICYGFQAM	1.154925	0.134428	-4.634319	1.289353	-3.344966	43084.318281
HLA A*6802	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.422567	1.077535	-3.345032	26458.620107
HLA B*1501	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-3.778418	0.433361	-3.345057	6003.690363
HLA A*2902	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.397644	1.052564	-3.345080	24982.957769
HLA B*2705	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.382069	1.036964	-3.345105	24102.889945
HLA A*3002	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.366015	1.020890	-3.345125	23228.174862
HLA A*8001	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.307910	0.962750	-3.345160	20319.357582
HLA B*5301	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.468483	1.123169	-3.345314	29409.197651
HLA B*5801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.350548	1.005151	-3.345398	22415.499808
HLA A*3002	1:208-216	9	PANIANALI	0.995189	0.008861	-4.349468	1.004050	-3.345417	22359.787089
HLA A*2603	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.628932	1.283502	-3.345430	42553.163926
HLA B*0801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.378806	1.033365	-3.345441	23922.451517
HLA A*2402	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.510638	1.165167	-3.345471	32406.910973
HLA B*4001	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.289316	0.943730	-3.345587	19467.767408
HLA A*3201	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.518440	1.172675	-3.345765	32994.403082
HLA A*3002	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.537727	1.191820	-3.345908	34492.700553
HLA B*0702	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.389259	1.043307	-3.345952	24505.216391
HLA A*6801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.446499	1.100487	-3.346012	27957.545796
HLA A*8001	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.358840	1.012736	-3.346104	22847.556477
HLA A*0101	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.379492	1.033365	-3.346127	23960.271382
HLA B*1517	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.440207	1.094025	-3.346182	27555.425660
HLA A*0101	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.374746	1.028547	-3.346199	23699.859588
HLA A*0206	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.164660	0.818458	-3.346201	14610.313103
HLA B*1801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.498049	1.151838	-3.346211	31481.041757
HLA A*6901	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-3.878558	0.532233	-3.346325	7560.630874
HLA A*2601	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.372939	1.026553	-3.346386	23601.468126
HLA B*1801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.309421	0.962975	-3.346446	20390.162739
HLA A*2601	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.397418	1.050933	-3.346485	24969.986254
HLA B*5401	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.139656	0.793168	-3.346489	13792.922745
HLA A*2902	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.438487	1.091915	-3.346573	27446.520880
HLA A*2603	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.630628	1.284024	-3.346604	42719.699056
HLA B*5101	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.279608	0.932998	-3.346610	19037.419364
HLA B*3801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.485651	1.138932	-3.346719	30595.028568
HLA B*4001	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.380091	1.033365	-3.346726	23993.347907
HLA A*3001	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.276443	0.929716	-3.346728	18899.195629
HLA A*3002	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.309486	0.962750	-3.346736	20393.251612
HLA B*5401	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.537182	1.190433	-3.346749	34449.436118
HLA A*2403	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.375079	1.028301	-3.346778	23718.072916
HLA B*4402	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.399404	1.052564	-3.346840	25084.394260
HLA B*0802	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.419689	1.072837	-3.346852	26283.855542
HLA A*3101	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.390259	1.043307	-3.346953	24561.756552
HLA A*0219	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.462797	1.115576	-3.347221	29026.683829
HLA B*0702	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.277005	0.929716	-3.347289	18923.647404
HLA A*3002	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.128548	0.781170	-3.347378	13444.601636
HLA A*2602	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.488193	1.140721	-3.347472	30774.641739
HLA B*0802	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.441643	1.094025	-3.347618	27646.659229
HLA A*6901	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.390920	1.043287	-3.347633	24599.123210
HLA A*2601	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.391711	1.044058	-3.347654	24644.011581
HLA A*2601	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.155431	0.807776	-3.347654	14303.118805
HLA A*0201	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.254466	0.906788	-3.347679	17966.614017
HLA B*5701	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.384766	1.036964	-3.347803	24253.048014
HLA A*0101	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.365132	1.017228	-3.347904	23180.974028
HLA B*5401	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.463683	1.115576	-3.348107	29085.944981
HLA B*3501	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.381562	1.033365	-3.348197	24074.741299
HLA A*2501	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.474275	1.126026	-3.348249	29804.006996
HLA B*1801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.391559	1.043307	-3.348252	24635.347215
HLA B*7301	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.576348	1.228069	-3.348279	37700.580085
HLA B*4601	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.404676	1.056396	-3.348280	25390.769472

HLA A*1101	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.500201	1.151838	-3.348363	31637.431924
HLA B*1801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.487368	1.138932	-3.348436	30716.260109
HLA B*1502	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.121081	0.772641	-3.348440	13215.429288
HLA A*2602	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.479580	1.131046	-3.348534	30170.311475
HLA A*0203	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.149745	0.801202	-3.348543	14117.083786
HLA A*2403	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.405064	1.056396	-3.348667	25413.444197
HLA A*0202	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.101444	0.752770	-3.348675	12631.190341
HLA B*3501	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.143697	0.794851	-3.348847	13921.864993
HLA A*2602	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.496162	1.147258	-3.348904	31344.580292
HLA B*5701	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.392212	1.043287	-3.348925	24672.425400
HLA B*0702	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.428347	1.079304	-3.349043	26813.093576
HLA B*4601	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.393163	1.044058	-3.349106	24726.542074
HLA B*1801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.489631	1.140437	-3.349194	30876.700886
HLA B*4002	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.584604	1.235408	-3.349196	38424.137070
HLA A*2603	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.610239	1.260962	-3.349277	40760.486014
HLA A*8001	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.443315	1.094025	-3.349291	27753.355122
HLA A*0301	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.173921	0.824605	-3.349316	14925.235518
HLA A*2601	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.392722	1.043307	-3.349415	24701.406502
HLA A*1101	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.441147	1.091476	-3.349671	27615.118943
HLA B*5701	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.406069	1.056396	-3.349673	25472.355489
HLA B*5301	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.565193	1.215498	-3.349695	36744.528402
HLA A*2603	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.496959	1.147258	-3.349701	31402.117505
HLA A*3001	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.133844	0.783681	-3.350163	13609.547252
HLA A*2601	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.387165	1.036964	-3.350202	24387.380298
HLA A*2602	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.587212	1.236980	-3.350232	38655.567298
HLA B*5101	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.476180	1.125828	-3.350352	29935.056971
HLA B*5401	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.554211	1.203805	-3.350406	35827.061143
HLA B*1517	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.476584	1.126026	-3.350558	29962.924532
HLA A*6801	1:301-309	9	APEGKRKII	1.207147	0.122555	-4.680355	1.329702	-3.350653	47902.153122
HLA A*0101	1:208-216	9	PANIANALI	0.995189	0.008861	-4.354768	1.004050	-3.350718	22634.353900
HLA B*5801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.333313	0.982586	-3.350726	21543.318640
HLA B*1517	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.481140	1.130410	-3.350730	30278.883141
HLA B*1503	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.430090	1.079304	-3.350786	26920.941340
HLA A*0219	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.331550	0.980728	-3.350823	21456.085506
HLA B*5701	1:208-216	9	PANIANALI	0.995189	0.008861	-4.354914	1.004050	-3.350863	22641.947033
HLA B*5301	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.600085	1.249052	-3.351033	39818.498519
HLA A*1101	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.460175	1.109115	-3.351061	28851.965033
HLA A*0101	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.358400	1.007289	-3.351111	22824.454451
HLA B*4501	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.614198	1.263068	-3.351130	41133.743537
HLA A*0250	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.460443	1.109115	-3.351329	28869.764317
HLA B*1501	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.402326	1.050933	-3.351393	25253.779109
HLA A*3001	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.256665	0.905240	-3.351425	18057.821501
HLA B*4001	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.402568	1.050933	-3.351635	25267.854906
HLA B*4403	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.589585	1.237896	-3.351689	38867.358942
HLA B*0801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.402738	1.050933	-3.351804	25277.698956
HLA A*3002	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.492295	1.140437	-3.351859	31066.705939
HLA A*3301	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.452380	1.100487	-3.351893	28338.692316
HLA B*5801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.356995	1.005094	-3.351902	22750.734057
HLA B*3501	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.038196	0.686294	-3.351902	10919.333824
HLA B*3801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.517089	1.165167	-3.351923	32891.927314
HLA A*1101	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.444046	1.091915	-3.352132	27800.088766
HLA B*5301	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.474087	1.121826	-3.352260	29791.110877
HLA A*3001	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.165548	0.813260	-3.352287	14640.220858
HLA A*2301	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.482721	1.130410	-3.352311	30389.325105
HLA A*2601	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.381296	1.028966	-3.352330	24060.028486
HLA A*0202	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.279989	0.927581	-3.352408	19054.111110
HLA B*4501	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.622055	1.269596	-3.352459	41884.652229
HLA A*2403	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.312910	0.960386	-3.352524	20554.630648
HLA B*3501	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.415599	1.062990	-3.352608	26037.460147
HLA A*2902	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.130667	0.778023	-3.352644	13510.367858
HLA A*0250	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.590626	1.237896	-3.352730	38960.619420
HLA B*1517	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.258968	0.906227	-3.352741	18153.812730
HLA A*0201	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.396213	1.043287	-3.352926	24900.783795
HLA A*2501	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.396269	1.043307	-3.352963	24904.017056
HLA A*8001	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.386371	1.033365	-3.353006	24342.827681

HLA A*2902	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.279982	0.926967	-3.353015	19053.801871
HLA B*4801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.274592	0.921448	-3.353144	18818.799982
HLA B*4501	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.634484	1.281231	-3.353253	43100.637067
HLA B*1801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.475137	1.121826	-3.353311	29863.239527
HLA B*0802	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.432632	1.079304	-3.353328	27078.985175
HLA A*2602	1:113-121	9	REYGRTELK	0.904130	0.335113	-4.592621	1.239243	-3.353378	39139.976964
HLA A*2601	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.108079	0.754547	-3.353532	12825.645305
HLA B*3501	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.396974	1.043287	-3.353688	24944.468264
HLA B*0802	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.469289	1.115576	-3.353713	29463.819785
HLA A*2402	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.591641	1.237896	-3.353745	39051.779680
HLA B*0702	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.359061	1.005151	-3.353910	22859.178090
HLA B*1502	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.585791	1.231855	-3.353935	38529.255108
HLA B*3801	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.494750	1.140721	-3.354029	31242.833794
HLA A*3201	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.603109	1.249052	-3.354057	40096.703283
HLA A*0203	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.397371	1.043287	-3.354085	24967.284703
HLA A*0201	1:208-216	9	PANIANALI	0.995189	0.008861	-4.358245	1.004050	-3.354195	22816.306373
HLA B*5101	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.463350	1.109115	-3.354235	29063.609615
HLA B*5401	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.564523	1.210159	-3.354364	36687.918664
HLA A*6901	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.382915	1.028547	-3.354368	24149.877512
HLA B*4001	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.398504	1.044058	-3.354446	25032.473515
HLA B*5101	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.485573	1.131046	-3.354527	30589.567037
HLA A*3301	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.586385	1.231855	-3.354530	38582.026280
HLA B*4002	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.634766	1.280105	-3.354661	43128.626512
HLA A*0202	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.592693	1.237896	-3.354798	39146.541545
HLA A*6802	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.388175	1.033365	-3.354811	24444.177535
HLA A*6801	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.520040	1.165167	-3.354874	33116.183091
HLA A*2402	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.502217	1.147258	-3.354959	31784.624259
HLA B*4001	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.384033	1.028966	-3.355067	24212.146176
HLA B*5101	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.495563	1.140437	-3.355127	31301.369574
HLA A*0201	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.360231	1.005094	-3.355137	22920.846603
HLA B*5401	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.187045	0.831902	-3.355144	15383.155007
HLA A*2601	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.372389	1.017185	-3.355205	23571.609599
HLA B*5101	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.470880	1.115576	-3.355303	29571.928729
HLA A*3301	1:352-360	9	ANIKSHHNV	1.068822	0.166220	-4.590443	1.235042	-3.355400	38944.182623
HLA B*1503	1:494-502	9	ERISTRITN	1.065751	-0.517476	-3.903721	0.548275	-3.355446	8011.632502
HLA B*5101	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.481629	1.126026	-3.355603	30312.973841
HLA A*6801	1:174-182	9	AGVQYHPEV	1.149371	0.136777	-4.641767	1.286148	-3.355619	43829.558198
HLA A*0201	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.368365	1.012736	-3.355628	23354.177235
HLA B*1801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.411482	1.055834	-3.355648	25791.839674
HLA B*4801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.133839	0.778023	-3.355816	13609.400001
HLA A*0202	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.336656	0.980728	-3.355928	21709.804978
HLA B*4601	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.363264	1.007289	-3.355975	23081.489948
HLA B*4601	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.406913	1.050933	-3.355979	25521.874700
HLA A*0211	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.408550	1.052564	-3.355986	25618.291513
HLA A*1101	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.469468	1.113445	-3.356023	29475.936371
HLA B*3901	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.465276	1.109115	-3.356161	29192.825353
HLA A*3002	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.262426	0.906227	-3.356199	18298.955162
HLA A*2403	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.361424	1.005094	-3.356331	22983.924853
HLA A*2902	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.254076	0.897730	-3.356346	17950.486493
HLA A*3001	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.074843	0.718317	-3.356527	11880.737773
HLA B*4001	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.384893	1.028301	-3.356592	24260.134189
HLA A*1101	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.472224	1.115576	-3.356647	29663.579510
HLA A*6802	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.361800	1.005151	-3.356650	23003.827944
HLA B*0801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.258214	0.901531	-3.356683	18122.314641
HLA A*6802	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.436168	1.079304	-3.356864	27300.359086
HLA B*4403	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.620098	1.263068	-3.357030	41696.326313
HLA A*3002	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.164866	0.807776	-3.357090	14617.270294
HLA A*2902	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.146709	0.789472	-3.357238	14018.755382
HLA A*3101	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.257105	0.899837	-3.357267	18076.098926
HLA B*1502	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.547388	1.190075	-3.357313	35268.604866
HLA B*4501	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.471199	1.113845	-3.357354	29593.694132
HLA B*7301	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.522559	1.165167	-3.357392	33308.795098
HLA A*8001	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.391923	1.034513	-3.357410	24656.013426
HLA A*3201	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.498160	1.140721	-3.357438	31489.047295
HLA B*4801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.384823	1.027198	-3.357624	24256.197169

HLA A*0301	1:208-216	9	PANIANALI	0.995189	0.008861	-4.361713	1.004050	-3.357663	22999.223822
HLA B*4801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.413592	1.055834	-3.357758	25917.443356
HLA A*0216	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.386094	1.028301	-3.357792	24327.292984
HLA B*4001	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.261425	0.903619	-3.357806	18256.831714
HLA B*0802	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.445132	1.087303	-3.357829	27869.658344
HLA B*4801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.269994	0.911989	-3.358005	18620.613433
HLA B*5801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.280583	0.922498	-3.358085	19080.208365
HLA A*0301	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.363215	1.005094	-3.358121	23078.867862
HLA B*4601	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.280623	0.922498	-3.358125	19081.963216
HLA B*3901	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.384693	1.026553	-3.358140	24248.980959
HLA B*1801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.497417	1.139224	-3.358193	31435.261969
HLA A*2601	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.321178	0.962975	-3.358203	20949.685852
HLA A*0206	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.498712	1.140437	-3.358275	31529.105533
HLA B*1501	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.134055	0.775707	-3.358348	13616.175218
HLA B*1501	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.379306	1.020917	-3.358389	23950.033400
HLA A*0216	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.450359	1.091915	-3.358445	28207.152650
HLA A*6801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.467656	1.108898	-3.358758	29353.247565
HLA A*2403	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.376080	1.017228	-3.358852	23772.796925
HLA B*4601	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.387861	1.028966	-3.358895	24426.463757
HLA B*4001	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.395905	1.036964	-3.358942	24883.142974
HLA B*7301	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.574452	1.215498	-3.358954	37536.346391
HLA A*0216	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.279159	0.920085	-3.359074	19017.758370
HLA A*0250	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.221198	0.862117	-3.359081	16641.693925
HLA A*6802	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.216297	0.857166	-3.359130	16454.947631
HLA B*1517	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.482312	1.123169	-3.359143	30360.732464
HLA B*0803	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.482397	1.123169	-3.359227	30366.645975
HLA A*3201	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.541482	1.182210	-3.359272	34792.182695
HLA A*6901	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.267870	0.908582	-3.359288	18529.770898
HLA A*3001	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.032388	0.673013	-3.359375	10774.278976
HLA A*0250	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.388403	1.028966	-3.359437	24457.008209
HLA B*5801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.346695	0.987241	-3.359454	22217.504232
HLA A*2501	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.453498	1.094025	-3.359473	28411.761528
HLA B*0801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-3.736419	0.376904	-3.359515	5450.280975
HLA A*2601	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.380584	1.020890	-3.359694	24020.621680
HLA A*0201	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.376950	1.017228	-3.359722	23820.429614
HLA B*5301	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.569939	1.210159	-3.359779	37148.273771
HLA B*1502	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.490190	1.130410	-3.359780	30916.481899
HLA A*6901	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.387203	1.027198	-3.360004	24389.491317
HLA B*3501	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.410977	1.050933	-3.360044	25761.857951
HLA B*5101	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.403351	1.043287	-3.360064	25313.415798
HLA B*0802	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.386651	1.026553	-3.360098	24358.504075
HLA A*3301	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.588189	1.228069	-3.360120	38742.660154
HLA A*3301	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.609175	1.249052	-3.360123	40660.717416
HLA B*0702	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.416609	1.056396	-3.360213	26098.100354
HLA A*0219	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.377478	1.017228	-3.360250	23849.442091
HLA A*2402	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.451938	1.091476	-3.360462	28309.884842
HLA B*4501	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.644055	1.283502	-3.360553	44061.115839
HLA A*3201	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.550652	1.190075	-3.360576	35534.623238
HLA B*1801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.448106	1.087303	-3.360803	28061.190540
HLA B*4601	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.365956	1.005151	-3.360806	23225.033528
HLA A*0203	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.417217	1.056396	-3.360821	26134.693633
HLA A*0206	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.154049	0.793168	-3.360882	14257.692661
HLA A*0219	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.321283	0.960386	-3.360897	20954.786570
HLA B*3901	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.413465	1.052564	-3.360902	25909.873095
HLA A*0202	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.487507	1.126421	-3.361086	30726.065796
HLA A*3001	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.253865	0.892605	-3.361260	17941.748708
HLA A*3301	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.637164	1.275786	-3.361378	43367.506462
HLA A*2501	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.484634	1.123169	-3.361464	30523.444139
HLA A*2301	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.482291	1.120820	-3.361471	30359.254266
HLA A*3002	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.462262	1.100487	-3.361775	28990.902801
HLA A*3002	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.501045	1.139224	-3.361820	31698.936274
HLA B*1503	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.414403	1.052564	-3.361839	25965.861147
HLA B*1801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.305575	0.943730	-3.361845	20210.384922
HLA B*4402	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.395250	1.033365	-3.361885	24845.613706
HLA A*2301	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.534680	1.172675	-3.362005	34251.525274

HLA A*3001	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.006638	0.644580	-3.362057	10154.016407
HLA A*0206	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.475546	1.113445	-3.362101	29891.363647
HLA A*3101	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.383025	1.020917	-3.362108	24156.018757
HLA A*2601	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.405456	1.043287	-3.362169	25436.414385
HLA A*0101	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.295235	0.932998	-3.362237	19734.880527
HLA B*1501	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.144073	0.781791	-3.362283	13933.920730
HLA B*4403	1:428-436	9	SIVREELTA	1.468906	-0.179470	-4.651795	1.289436	-3.362358	44853.330363
HLA A*3002	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.175669	0.813260	-3.362409	14985.430016
HLA A*0206	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.115226	0.752770	-3.362457	13038.461791
HLA B*0801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.343291	0.980728	-3.362563	22044.023625
HLA B*7301	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.595231	1.232655	-3.362576	39375.931745
HLA A*2403	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.405919	1.043287	-3.362632	25463.537648
HLA B*4801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.391246	1.028547	-3.362699	24617.628082
HLA B*1502	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.488578	1.125828	-3.362750	30801.957789
HLA B*1502	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.502008	1.139224	-3.362784	31769.324278
HLA B*4002	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.599904	1.236980	-3.362924	39801.915121
HLA A*0203	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.271523	0.908582	-3.362942	18686.307829
HLA A*6802	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.413923	1.050933	-3.362990	25937.220578
HLA A*3101	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.296217	0.933159	-3.363057	19779.558173
HLA A*2601	1:208-216	9	PANIANALI	0.995189	0.008861	-4.367131	1.004050	-3.363081	23287.940998
HLA A*0211	1:208-216	9	PANIANALI	0.995189	0.008861	-4.367272	1.004050	-3.363222	23295.501336
HLA B*4001	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.406523	1.043287	-3.363236	25498.965284
HLA B*0803	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.454828	1.091476	-3.363352	28498.891592
HLA B*0803	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.441079	1.077535	-3.363543	27610.786835
HLA A*0101	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.296762	0.933159	-3.363602	19804.398969
HLA A*3301	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.511023	1.147258	-3.363765	32435.675850
HLA B*5301	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.601675	1.237896	-3.363780	39964.600955
HLA B*4801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.371365	1.007289	-3.364076	23516.076487
HLA B*4601	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.293827	0.929716	-3.364111	19671.032687
HLA B*1503	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.458148	1.094025	-3.364123	28717.576828
HLA B*0803	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.504578	1.140437	-3.364142	31957.905943
HLA A*2601	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.397557	1.033365	-3.364192	24977.957533
HLA B*5301	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.272795	0.908582	-3.364213	18741.078091
HLA A*2501	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.473351	1.109115	-3.364237	29740.708414
HLA A*3001	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.264419	0.900174	-3.364244	18383.096047
HLA A*1101	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.416809	1.052564	-3.364245	26110.104079
HLA B*4801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.368296	1.004050	-3.364246	23350.513560
HLA B*1801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.038544	0.674222	-3.364322	10928.080038
HLA B*3501	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.390943	1.026553	-3.364390	24600.454031
HLA A*3101	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.393013	1.028547	-3.364466	24717.982413
HLA A*1101	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.391312	1.026553	-3.364759	24621.357367
HLA B*5301	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.417408	1.052564	-3.364844	26146.148392
HLA B*5301	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.596821	1.231855	-3.364966	39520.410311
HLA B*5701	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.408355	1.043307	-3.365048	25606.790949
HLA A*2402	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.537786	1.172675	-3.365111	34497.365911
HLA B*3501	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-3.250484	-0.114983	-3.365468	1780.263578
HLA B*1509	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.295239	0.929716	-3.365523	19735.094055
HLA B*0803	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.481116	1.115576	-3.365540	30277.245131
HLA B*1801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.479387	1.113845	-3.365542	30156.930564
HLA B*4601	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.382793	1.017228	-3.365565	24143.084763
HLA A*2301	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.466098	1.100487	-3.365611	29248.153200
HLA B*5401	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.512966	1.147258	-3.365708	32581.117469
HLA B*3801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.486534	1.120820	-3.365714	30657.325814
HLA B*2705	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.386620	1.020890	-3.365730	24356.791036
HLA A*3301	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.629000	1.263086	-3.365914	42559.840479
HLA B*4002	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.598628	1.232655	-3.365973	39685.165780
HLA A*6801	1:204-212	9	AQWTPANIA	1.375674	-0.074527	-4.667172	1.301147	-3.366025	46469.935996
HLA B*4501	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.646309	1.280105	-3.366204	44290.302602
HLA A*3101	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.335516	0.969193	-3.366323	21652.917537
HLA B*2705	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.294057	0.927581	-3.366477	19681.464427
HLA B*0801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.395043	1.028547	-3.366496	24833.788263
HLA B*4402	1:208-216	9	PANIANALI	0.995189	0.008861	-4.370592	1.004050	-3.366542	23474.258542
HLA A*6802	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.272844	0.906227	-3.366617	18743.207342
HLA A*3201	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.574172	1.207422	-3.366750	37512.189139
HLA A*0206	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.079030	0.712255	-3.366776	11995.826967

HLA A*6801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.296585	0.929716	-3.366870	19796.365129
HLA B*4402	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.429886	1.062990	-3.366896	26908.273701
HLA A*0211	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.458987	1.091915	-3.367072	28773.093552
HLA A*3201	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-3.924646	0.557541	-3.367104	8407.086836
HLA B*5301	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.400506	1.033365	-3.367141	25148.120148
HLA B*5101	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.476065	1.108898	-3.367167	29927.122701
HLA A*3002	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.454720	1.087303	-3.367417	28491.800385
HLA B*0801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.395757	1.028301	-3.367456	24874.663671
HLA A*2602	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.602867	1.235408	-3.367459	40074.366879
HLA B*4402	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.394127	1.026553	-3.367574	24781.447762
HLA B*3801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.494048	1.126421	-3.367627	31192.337586
HLA B*4801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.418627	1.050933	-3.367694	26219.662938
HLA B*0702	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.411753	1.044058	-3.367695	25807.890731
HLA A*2403	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.411776	1.044058	-3.367718	25809.286947
HLA B*0702	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.423780	1.055834	-3.367945	26532.582604
HLA B*0803	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.477181	1.109115	-3.368066	30004.125243
HLA A*0201	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.396671	1.028547	-3.368124	24927.066199
HLA B*7301	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.603557	1.235408	-3.368149	40138.156171
HLA A*2602	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.571997	1.203805	-3.368192	37324.739588
HLA B*0801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.372333	1.004050	-3.368283	23568.549323
HLA A*3301	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.419252	1.050933	-3.368319	26257.420994
HLA A*3001	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.143674	0.775312	-3.368362	13921.111856
HLA A*0212	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.424790	1.056396	-3.368394	26594.375932
HLA A*0219	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.411729	1.043287	-3.368442	25806.494591
HLA A*0201	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.395666	1.027198	-3.368467	24869.416027
HLA A*3201	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.629491	1.260962	-3.368529	42607.988694
HLA B*4002	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.631655	1.263086	-3.368569	42820.813093
HLA B*3801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.559014	1.190433	-3.368581	36225.428577
HLA B*5701	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.397266	1.028547	-3.368719	24961.207282
HLA A*2601	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.324133	0.955413	-3.368721	21092.748147
HLA A*2402	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.576172	1.207422	-3.368750	37685.286491
HLA A*0216	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.484636	1.115576	-3.369060	30523.609268
HLA A*0216	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.296705	0.927581	-3.369125	19801.827785
HLA A*0212	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.144867	0.775707	-3.369161	13959.422805
HLA B*1509	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.478281	1.109115	-3.369166	30080.186777
HLA B*3801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.551451	1.182210	-3.369241	35600.044433
HLA A*2601	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.397790	1.028547	-3.369243	24991.338786
HLA A*3001	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.291764	0.922498	-3.369266	19577.819142
HLA A*2301	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.510076	1.140721	-3.369355	32365.037096
HLA B*3801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.499976	1.130410	-3.369565	31621.005310
HLA A*2501	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.485179	1.115576	-3.369602	30561.777991
HLA B*1501	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.299428	0.929716	-3.369713	19926.376520
HLA B*4001	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.382499	1.012736	-3.369763	24126.763856
HLA A*2501	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.483769	1.113845	-3.369924	30462.737319
HLA B*4801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.413230	1.043287	-3.369944	25895.859932
HLA B*1517	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.269787	0.899837	-3.369950	18611.750823
HLA A*6801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.420998	1.050933	-3.370064	26363.176350
HLA A*0101	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.177897	0.807776	-3.370120	15062.481329
HLA B*1501	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.391382	1.020890	-3.370493	24625.353655
HLA B*4402	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.421470	1.050933	-3.370537	26391.858936
HLA A*2601	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.391521	1.020917	-3.370604	24633.214916
HLA B*5701	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.405125	1.034513	-3.370611	25417.019030
HLA A*3002	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.462605	1.091915	-3.370690	29013.810131
HLA A*3001	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.178470	0.807776	-3.370693	15082.377128
HLA B*4403	1:514-522	9	ITSKPPATI	1.110493	0.169612	-4.650846	1.280105	-3.370741	44755.406190
HLA B*4403	1:492-500	9	VLERISTRI	1.151890	0.131612	-4.654386	1.283502	-3.370884	45121.775140
HLA A*0201	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.351667	0.980728	-3.370939	22473.296509
HLA A*3301	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.536233	1.165167	-3.371066	34374.225815
HLA B*0801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.263688	0.892605	-3.371083	18352.192942
HLA B*5301	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.574959	1.203805	-3.371155	37580.234603
HLA A*2902	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.152376	0.781170	-3.371207	14202.879927
HLA A*0216	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.422151	1.050933	-3.371218	26433.296772
HLA B*4002	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.609123	1.237896	-3.371228	40655.878364
HLA A*3101	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.388493	1.017228	-3.371265	24462.036495
HLA A*8001	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.408266	1.036964	-3.371302	25601.527354

HLA B*2705	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.415437	1.044058	-3.371379	26027.742636
HLA B*1502	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.531050	1.159455	-3.371595	33966.434573
HLA A*6801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.384365	1.012736	-3.371628	24230.622111
HLA B*4001	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.398880	1.027198	-3.371681	25054.150561
HLA B*4601	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.384480	1.012736	-3.371743	24237.046126
HLA B*4402	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.400757	1.028966	-3.371791	25162.681556
HLA B*1501	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.277080	0.905240	-3.371840	18926.923682
HLA A*0216	1:208-216	9	PANIANALI	0.995189	0.008861	-4.376003	1.004050	-3.371952	23768.553233
HLA B*0702	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.409267	1.036964	-3.372303	25660.597001
HLA A*8001	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.084636	0.712255	-3.372382	12151.672712
HLA A*3101	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.377485	1.005094	-3.372392	23849.829163
HLA B*7301	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.600935	1.228391	-3.372544	39896.554671
HLA A*2603	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.576691	1.203805	-3.372886	37730.369418
HLA B*1501	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.279796	0.906788	-3.373008	19045.660373
HLA B*4402	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.378190	1.005151	-3.373040	23888.568070
HLA A*6801	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.563529	1.190433	-3.373096	36604.058639
HLA A*6901	1:9-17	9	VPETPARPV	0.601332	-0.092772	-3.881669	0.508560	-3.373109	7614.979763
HLA B*3901	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.428993	1.055834	-3.373159	26853.013626
HLA B*1517	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.275341	0.902116	-3.373225	18851.304653
HLA B*5301	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.601772	1.228391	-3.373381	39973.466304
HLA A*0203	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.424409	1.050933	-3.373476	26571.078777
HLA B*0702	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.406861	1.033365	-3.373496	25518.837330
HLA B*1502	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.482550	1.108898	-3.373651	30377.326064
HLA B*4501	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.589266	1.215498	-3.373767	38838.772997
HLA B*5101	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.391018	1.017185	-3.373834	24604.713143
HLA B*4601	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.394876	1.020890	-3.373986	24824.251384
HLA B*0702	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.356685	0.982586	-3.374099	22734.493435
HLA A*2601	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.386926	1.012736	-3.374189	24373.926841
HLA B*4801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.426766	1.052564	-3.374202	26715.648479
HLA A*1101	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.447105	1.072837	-3.374268	27996.594825
HLA A*0211	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.395222	1.020917	-3.374304	24844.000814
HLA B*0801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.357047	0.982586	-3.374461	22753.441955
HLA A*8001	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.417835	1.043287	-3.374549	26171.904562
HLA A*0203	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.297201	0.922498	-3.374703	19824.444212
HLA A*0212	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.427428	1.052564	-3.374865	26756.436677
HLA B*4002	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.564967	1.190075	-3.374892	36725.450110
HLA B*4501	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.607606	1.232655	-3.374950	40514.042660
HLA B*1501	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.055427	0.680376	-3.375051	11361.280083
HLA A*8001	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.427851	1.052564	-3.375287	26782.504251
HLA A*6801	1:375-383	9	LRLLFKDEV	1.112372	0.171652	-4.659355	1.284024	-3.375331	45641.019591
HLA B*4403	1:313-321	9	FIRAFEGAV	1.145484	0.149816	-4.670699	1.295300	-3.375399	46848.819427
HLA A*3201	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.607272	1.231855	-3.375417	40482.931551
HLA A*3002	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.583091	1.207422	-3.375669	38290.501509
HLA A*2902	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.402223	1.026553	-3.375670	25247.768538
HLA A*0211	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.516255	1.140437	-3.375819	32828.818637
HLA B*0802	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.489697	1.113845	-3.375852	30881.378347
HLA B*4001	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.393133	1.017228	-3.375905	24724.803153
HLA A*2603	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.608122	1.231855	-3.376267	40562.290191
HLA B*7301	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.276472	0.900174	-3.376297	18900.422580
HLA B*0802	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.485475	1.109115	-3.376360	30582.617407
HLA B*1801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.404880	1.028301	-3.376579	25402.722713
HLA A*2601	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.403818	1.027198	-3.376620	25340.682084
HLA A*0203	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.126885	0.750232	-3.376653	13393.204596
HLA A*0219	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.456045	1.079304	-3.376741	28578.866685
HLA A*0216	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.381923	1.005094	-3.376830	24094.806875
HLA A*3301	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.528867	1.151838	-3.377029	33796.154760
HLA A*6801	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.640144	1.263086	-3.377057	43666.018944
HLA A*2301	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.220591	0.843518	-3.377073	16618.482460
HLA B*3501	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.486194	1.109115	-3.377079	30633.286598
HLA A*2902	1:208-216	9	PANIANALI	0.995189	0.008861	-4.381174	1.004050	-3.377124	24053.261010
HLA B*0803	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.502955	1.125828	-3.377127	31838.662850
HLA A*1101	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.398046	1.020917	-3.377128	25006.079973
HLA A*8001	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.406165	1.028966	-3.377200	25478.006023
HLA A*6901	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.289288	0.911989	-3.377299	19466.503627
HLA B*5101	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.454990	1.077535	-3.377455	28509.531711

HLA A*6801	1:378-386	9	LFKDEVRAV	1.032886	0.230182	-4.640538	1.263068	-3.377470	43705.723342
HLA B*3901	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.500704	1.123169	-3.377535	31674.080304
HLA A*0202	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.283922	0.906227	-3.377694	19227.451798
HLA B*0803	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.508774	1.131046	-3.377728	32268.181750
HLA A*8001	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.398673	1.020890	-3.377783	25042.225864
HLA A*2603	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.610526	1.232655	-3.377871	40787.397079
HLA B*4402	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.406234	1.028301	-3.377932	25482.003499
HLA B*1502	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.414934	1.036964	-3.377970	25997.627331
HLA A*3001	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.286654	0.908582	-3.378072	19348.806541
HLA B*5701	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.395261	1.017185	-3.378077	24846.285775
HLA A*2403	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.358866	0.980728	-3.378138	22848.916148
HLA B*4601	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.406882	1.028547	-3.378335	25520.079847
HLA B*1801	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.504569	1.126026	-3.378543	31957.214396
HLA B*1502	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.585983	1.207422	-3.378561	38546.350898
HLA A*0250	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.586051	1.207422	-3.378629	38552.398785
HLA A*1101	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.192656	0.813920	-3.378736	15583.176382
HLA A*2602	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.276500	0.897730	-3.378770	18901.649610
HLA A*2602	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.405341	1.026553	-3.378788	25429.672478
HLA A*0301	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.300293	0.921448	-3.378845	19966.086246
HLA B*0801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.422302	1.043287	-3.379015	26442.450433
HLA A*0202	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.431615	1.052564	-3.379051	27015.627376
HLA B*3901	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.488101	1.108898	-3.379203	30768.149415
HLA B*4801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.407528	1.028301	-3.379227	25558.074824
HLA A*1101	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.396413	1.017185	-3.379228	24912.236819
HLA A*0202	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.172446	0.793168	-3.379278	14874.614407
HLA B*4501	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.569861	1.190433	-3.379428	37141.642418
HLA A*0101	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.384581	1.005151	-3.379430	24242.684931
HLA A*0219	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.312900	0.933159	-3.379741	20554.185860
HLA B*1517	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.416719	1.036964	-3.379756	26104.737026
HLA A*3001	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.154087	0.774258	-3.379829	14258.926835
HLA B*4501	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.608294	1.228391	-3.379903	40578.312292
HLA B*1503	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.409067	1.028966	-3.380101	25648.799930
HLA B*5401	1:208-216	9	PANIANALI	0.995189	0.008861	-4.384240	1.004050	-3.380190	24223.675603
HLA B*0702	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.431166	1.050933	-3.380233	26987.726847
HLA B*1801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.431190	1.050933	-3.380256	26989.186893
HLA A*2902	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.242378	0.862117	-3.380262	17473.428912
HLA A*0203	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.066587	0.686294	-3.380293	11657.014055
HLA A*8001	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.407505	1.027198	-3.380306	25556.692198
HLA B*1501	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-3.475809	0.095477	-3.380332	2990.951125
HLA B*5101	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.393147	1.012736	-3.380411	24725.605716
HLA B*1501	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.367794	0.987241	-3.380553	23323.495933
HLA B*1801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.423874	1.043287	-3.380587	26538.324759
HLA B*2705	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.415131	1.034513	-3.380618	26009.444135
HLA B*5301	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.501449	1.120820	-3.380628	31728.445891
HLA B*0802	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.433264	1.052564	-3.380701	27118.420831
HLA B*5701	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.401626	1.020890	-3.380736	25213.099106
HLA B*3901	1:494-502	9	ERISTRITN	1.065751	-0.517476	-3.929072	0.548275	-3.380797	8493.211966
HLA A*0250	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.503982	1.123169	-3.380812	31914.022364
HLA B*5401	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.398020	1.017185	-3.380835	25004.591936
HLA A*6901	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.936116	0.555251	-3.380865	8632.085215
HLA B*5301	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.588380	1.207422	-3.380958	38759.640948
HLA A*6801	1:477-485	9	SEDAMTADW	0.981632	0.294154	-4.656816	1.275786	-3.381029	45374.885739
HLA A*6901	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.361810	0.980728	-3.381082	23004.325742
HLA B*0802	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.425203	1.044058	-3.381146	26619.709573
HLA A*2501	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.433741	1.052564	-3.381178	27148.218844
HLA A*0206	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.200254	0.819048	-3.381206	15858.212053
HLA B*0801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.279030	0.897730	-3.381300	19012.100594
HLA A*0211	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.182567	0.801202	-3.381365	15225.350449
HLA B*0803	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.495213	1.113845	-3.381368	31276.148536
HLA A*0216	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.316206	0.934761	-3.381445	20711.235395
HLA A*0203	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.206076	0.824605	-3.381471	16072.233922
HLA A*0211	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.494969	1.113445	-3.381524	31258.556634
HLA B*3501	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.425589	1.044058	-3.381531	26643.337640
HLA B*1509	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.522033	1.140437	-3.381596	33268.455442
HLA B*4601	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.402521	1.020917	-3.381604	25265.121128

HLA A*3201	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.573432	1.191820	-3.381613	37448.318489
HLA A*2601	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.386768	1.005094	-3.381674	24365.093806
HLA A*3301	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.572150	1.190433	-3.381717	37337.866871
HLA B*5701	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.386902	1.005151	-3.381751	24372.608275
HLA B*4002	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.597493	1.215498	-3.381995	39581.604737
HLA A*3301	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.512672	1.130410	-3.382262	32559.092388
HLA A*0212	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.425551	1.043287	-3.382264	26641.031540
HLA A*0101	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.369741	0.987241	-3.382500	23428.332012
HLA A*0211	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.302758	0.920085	-3.382673	20079.715377
HLA A*3301	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.618101	1.235408	-3.382693	41505.029852
HLA A*6901	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.282832	0.900138	-3.382694	19179.247794
HLA A*2601	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.399979	1.017228	-3.382751	25117.663732
HLA B*4801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.417391	1.034513	-3.382878	26145.158276
HLA A*0203	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.363612	0.980728	-3.382884	23099.977857
HLA B*1501	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.410094	1.027198	-3.382895	25709.508544
HLA A*3201	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.289154	0.906227	-3.382927	19460.501790
HLA B*4002	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.643940	1.260962	-3.382978	44049.437466
HLA A*6802	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.426399	1.043287	-3.383112	26693.111514
HLA A*1101	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.416567	1.033365	-3.383202	26095.559097
HLA A*8001	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.426721	1.043307	-3.383414	26712.902575
HLA B*3801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.492612	1.109115	-3.383498	31089.403330
HLA A*3101	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.316547	0.932998	-3.383549	20727.488364
HLA B*5701	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.388645	1.005094	-3.383552	24470.639906
HLA B*1503	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.434505	1.050933	-3.383572	27195.993208
HLA B*5701	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.416950	1.033365	-3.383585	26118.580621
HLA A*0301	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.364321	0.980728	-3.383594	23137.749136
HLA A*0202	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.132035	0.748391	-3.383644	13552.973038
HLA B*4801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.426984	1.043307	-3.383678	26729.093030
HLA B*4403	1:509-517	9	RVVLDITSK	0.817327	0.463904	-4.665144	1.281231	-3.383914	46253.485878
HLA A*2301	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.497379	1.113445	-3.383935	31432.541106
HLA A*2403	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.396674	1.012736	-3.383937	24927.201052
HLA B*1502	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.410700	1.026553	-3.384147	25745.417681
HLA A*3101	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.246346	0.862117	-3.384230	17633.820580
HLA B*5801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.353450	0.969193	-3.384257	22565.763954
HLA B*4002	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.588185	1.203805	-3.384380	38742.240970
HLA A*3002	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.493519	1.109115	-3.384405	31154.392589
HLA A*2403	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.405376	1.020917	-3.384459	25431.736137
HLA A*8001	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.412796	1.028301	-3.384494	25869.955556
HLA A*2602	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.591927	1.207422	-3.384506	39077.562615
HLA B*4501	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.566741	1.182210	-3.384531	36875.760733
HLA A*0211	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.137401	0.752770	-3.384631	13721.474981
HLA A*0101	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.389799	1.005094	-3.384705	24535.726585
HLA A*3201	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.137650	0.752770	-3.384880	13729.345794
HLA A*2602	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.616754	1.231855	-3.384899	41376.569010
HLA A*2403	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.413667	1.028547	-3.385120	25921.930480
HLA A*0203	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.413735	1.028547	-3.385189	25925.997608
HLA B*1503	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.508368	1.123169	-3.385199	32237.995738
HLA A*0202	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.406116	1.020917	-3.385199	25475.111690
HLA A*6802	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.307715	0.922498	-3.385217	20310.235816
HLA A*6901	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.312872	0.927581	-3.385291	20552.851553
HLA B*3501	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.412516	1.027198	-3.385318	25853.306439
HLA A*2301	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.511852	1.126421	-3.385431	32497.677146
HLA B*2705	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.418832	1.033365	-3.385467	26232.006398
HLA A*2902	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.428793	1.043307	-3.385487	26840.668359
HLA B*4001	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.392893	1.007289	-3.385604	24711.163555
HLA A*0250	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.305779	0.920085	-3.385694	20219.899388
HLA B*4403	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.622703	1.236980	-3.385723	41947.238148
HLA B*1503	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.286095	0.900174	-3.385921	19323.909946
HLA A*0219	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.391171	1.005094	-3.386077	24613.366735
HLA B*1509	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.348869	0.962750	-3.386118	22328.962544
HLA A*8001	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.403572	1.017228	-3.386344	25326.291692
HLA A*0201	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.248581	0.862117	-3.386464	17724.776917
HLA B*5701	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.415448	1.028966	-3.386482	26028.446682
HLA A*0212	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.313617	0.926967	-3.386650	20588.128595
HLA B*0802	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.415697	1.028966	-3.386731	26043.376930

HLA B*1509	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.415347	1.028301	-3.387046	26022.392513
HLA B*4001	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.407993	1.020917	-3.387076	25585.466229
HLA B*1509	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.442958	1.055834	-3.387124	27730.542832
HLA A*2301	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.496376	1.109115	-3.387262	31360.015025
HLA B*4601	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.414476	1.027198	-3.387277	25970.216157
HLA B*4501	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.650369	1.263086	-3.387282	44706.282446
HLA B*3801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.481340	1.094025	-3.387315	30292.809802
HLA B*5301	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.569643	1.182210	-3.387433	37122.960426
HLA A*2501	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.404634	1.017185	-3.387449	25388.297090
HLA B*1509	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.481485	1.094025	-3.387460	30302.972112
HLA A*2601	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.356709	0.969193	-3.387515	22735.723379
HLA B*3501	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.443980	1.056396	-3.387584	27795.878014
HLA B*1509	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.510847	1.123169	-3.387677	32422.518013
HLA A*6802	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.444119	1.056396	-3.387723	27804.751415
HLA B*1503	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.219661	0.831902	-3.387759	16582.918525
HLA B*3801	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.496816	1.108898	-3.387917	31391.756414
HLA B*0803	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.400705	1.012736	-3.387969	25159.686933
HLA B*1509	1:208-216	9	PANIANALI	0.995189	0.008861	-4.392057	1.004050	-3.388006	24663.617617
HLA A*3101	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.163349	0.775312	-3.388037	14566.275188
HLA A*0212	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.370662	0.982586	-3.388076	23478.068645
HLA A*0101	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.368816	0.980728	-3.388088	23378.447791
HLA B*5801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.350847	0.962750	-3.388096	22430.905802
HLA B*5301	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.460977	1.072837	-3.388139	28905.239460
HLA A*0101	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.357338	0.969193	-3.388145	22768.710682
HLA A*0212	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.416726	1.028547	-3.388179	26105.160701
HLA A*2301	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.514209	1.126026	-3.388183	32674.492681
HLA B*4601	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.369072	0.980728	-3.388344	23392.237611
HLA A*0250	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.421719	1.033365	-3.388354	26406.997641
HLA A*0212	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.369138	0.980728	-3.388410	23395.781263
HLA A*6802	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.316006	0.927581	-3.388426	20701.713718
HLA A*3001	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.269959	0.881518	-3.388441	18619.102463
HLA B*1801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.511615	1.123169	-3.388446	32479.925305
HLA B*4403	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.561168	1.172675	-3.388493	36405.584655
HLA B*1517	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.432602	1.044058	-3.388544	27077.080816
HLA A*0219	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.315555	0.926967	-3.388589	20680.222038
HLA A*0212	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.161248	0.772641	-3.388607	14495.996346
HLA B*5801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.351657	0.962975	-3.388683	22472.810202
HLA A*2602	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.578775	1.190075	-3.388700	37911.856391
HLA B*4801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.417760	1.028966	-3.388794	26167.374167
HLA A*0203	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.154773	0.765882	-3.388891	14281.469285
HLA B*4501	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.161563	0.772641	-3.388922	14506.508668
HLA B*4801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.425894	1.036964	-3.388930	26662.082106
HLA B*1503	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.061959	0.673013	-3.388946	11533.439310
HLA B*5801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.344388	0.955413	-3.388976	22099.786459
HLA B*4501	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.540941	1.151838	-3.389103	34748.918591
HLA B*1501	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.207655	0.818458	-3.389197	16130.769991
HLA A*2402	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.528496	1.139224	-3.389272	33767.279418
HLA A*0101	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.344689	0.955413	-3.389276	22115.095105
HLA B*0802	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.423827	1.034513	-3.389313	26535.453526
HLA B*0702	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.344802	0.955413	-3.389389	22120.838581
HLA B*3501	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.468819	1.079304	-3.389515	29431.957825
HLA A*0250	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.295756	0.906227	-3.389529	19758.596266
HLA A*0212	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.402301	1.012736	-3.389564	25252.276333
HLA B*3501	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.394766	1.005151	-3.389615	24817.940253
HLA A*0202	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.406967	1.017228	-3.389739	25525.050520
HLA B*4403	1:300-308	9	SAPEGKRKI	0.972348	0.290738	-4.652901	1.263086	-3.389815	44967.764972
HLA B*5801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.292089	0.902116	-3.389973	19592.440708
HLA A*2402	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.520426	1.130410	-3.390015	33145.577529
HLA A*0216	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.446600	1.056396	-3.390204	27964.050183
HLA A*3001	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.291753	0.901531	-3.390222	19577.289580
HLA B*5401	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.434357	1.044058	-3.390299	27186.725767
HLA B*2705	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.397630	1.007289	-3.390341	24982.146852
HLA B*7301	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.521290	1.130410	-3.390880	33211.630773
HLA B*4403	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.640040	1.249052	-3.390989	43655.626135
HLA A*6901	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.154566	0.763388	-3.391178	14274.671921

HLA A*3101	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.215822	0.824605	-3.391217	16436.975525
HLA B*5101	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.424639	1.033365	-3.391275	26585.169678
HLA B*5101	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.412283	1.020917	-3.391366	25839.463657
HLA A*3001	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-3.922254	0.530534	-3.391720	8360.914022
HLA A*0206	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.298552	0.906788	-3.391764	19886.207852
HLA B*4501	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.628751	1.236980	-3.391770	42535.441609
HLA B*1517	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.471155	1.079304	-3.391851	29590.652414
HLA B*1501	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.352318	0.960386	-3.391932	22506.998872
HLA B*4001	1:208-216	9	PANIANALI	0.995189	0.008861	-4.396112	1.004050	-3.392062	24894.991918
HLA B*5701	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.372807	0.980728	-3.392080	23594.319055
HLA A*2301	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.531353	1.139224	-3.392129	33990.147195
HLA B*5401	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.027370	0.635184	-3.392186	10650.493127
HLA A*3001	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.206109	0.813920	-3.392189	16073.451255
HLA A*0211	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.397310	1.005094	-3.392217	24963.773124
HLA B*1501	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.397446	1.005094	-3.392353	24971.607325
HLA B*5101	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.373127	0.980728	-3.392399	23611.684843
HLA A*6801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-3.987753	0.595350	-3.392403	9721.934715
HLA B*5801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.327232	0.934761	-3.392471	21243.796757
HLA B*5401	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.501416	1.108898	-3.392518	31726.042919
HLA B*4403	1:62-70	9	VLSGGPASV	1.079564	0.190032	-4.662304	1.269596	-3.392708	45951.949547
HLA A*0206	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.397919	1.005094	-3.392825	24998.775913
HLA B*3501	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.410019	1.017185	-3.392834	25705.058190
HLA A*2603	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.582910	1.190075	-3.392835	38274.554483
HLA A*2301	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.472179	1.079304	-3.392875	29660.530610
HLA B*5101	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.436946	1.044058	-3.392888	27349.288906
HLA A*1101	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.449325	1.056396	-3.392929	28140.089568
HLA B*7301	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.603109	1.210159	-3.392949	40096.703283
HLA A*2902	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.420182	1.027198	-3.392984	26313.732987
HLA B*4402	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.421790	1.028547	-3.393243	26411.283757
HLA A*3201	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.485207	1.091915	-3.393292	30563.762085
HLA A*0206	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.296933	0.903619	-3.393314	19812.221705
HLA A*0211	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.045188	0.651841	-3.393347	11096.556039
HLA A*0212	1:208-216	9	PANIANALI	0.995189	0.008861	-4.397569	1.004050	-3.393518	24978.633182
HLA B*4501	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.654485	1.260962	-3.393523	45132.028665
HLA B*4402	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.414485	1.020917	-3.393568	25970.778147
HLA A*0250	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.421973	1.028301	-3.393671	26422.430914
HLA A*3101	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.305694	0.911989	-3.393705	20215.961824
HLA B*4402	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.305732	0.911989	-3.393743	20217.711758
HLA A*2601	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.401194	1.007289	-3.393905	25188.013980
HLA A*6801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.481269	1.087303	-3.393966	30287.893778
HLA B*4601	1:208-216	9	PANIANALI	0.995189	0.008861	-4.398125	1.004050	-3.394075	25010.679920
HLA A*2403	1:208-216	9	PANIANALI	0.995189	0.008861	-4.398156	1.004050	-3.394106	25012.438947
HLA B*2705	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.399373	1.005151	-3.394223	25082.630172
HLA B*5701	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.421425	1.027198	-3.394227	26389.146312
HLA B*5401	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.363440	0.969193	-3.394247	23090.856970
HLA A*2603	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.631326	1.236980	-3.394346	42788.393553
HLA B*1501	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.226324	0.831902	-3.394422	16839.302803
HLA A*0219	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.349839	0.955413	-3.394426	22378.907567
HLA B*4402	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.431413	1.036964	-3.394449	27003.061266
HLA B*5801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.354984	0.960386	-3.394598	22645.622044
HLA A*8001	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.399834	1.005151	-3.394683	25109.240350
HLA A*2301	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.535129	1.140437	-3.394692	34286.935284
HLA A*2602	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.508152	1.113445	-3.394707	32221.954564
HLA B*4601	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.399904	1.005094	-3.394810	25113.315827
HLA B*4601	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.315703	0.920891	-3.394812	20687.271535
HLA B*0702	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.297044	0.902116	-3.394928	19817.259895
HLA A*3001	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.297163	0.902116	-3.395047	19822.728318
HLA A*3301	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.633121	1.237896	-3.395225	42965.610609
HLA B*5701	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.377960	0.982586	-3.395373	23875.906445
HLA A*3002	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.378070	0.982586	-3.395484	23881.978019
HLA B*7301	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.402951	1.007289	-3.395662	25290.146229
HLA A*0301	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.322667	0.926967	-3.395700	21021.663913
HLA A*2902	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.209121	0.813260	-3.395861	16185.315789
HLA A*6802	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.424806	1.028547	-3.396259	26595.383060
HLA A*1101	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.439876	1.043307	-3.396569	27534.414551

HLA A*3101	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.359592	0.962975	-3.396617	22887.143613
HLA B*1801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.474178	1.077535	-3.396643	29797.397038
HLA A*2403	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.180363	0.783681	-3.396683	15148.285471
HLA A*3002	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.452535	1.055834	-3.396700	28348.812529
HLA A*0250	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.417645	1.020917	-3.396728	26160.438520
HLA B*4001	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.352141	0.955413	-3.396729	22497.868697
HLA B*5301	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.556274	1.159455	-3.396819	35997.640274
HLA B*4002	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.562291	1.165167	-3.397124	36499.848667
HLA A*2402	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.423787	1.026553	-3.397234	26533.013223
HLA B*1517	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.952506	0.555251	-3.397255	8964.080054
HLA A*0250	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.378037	0.980728	-3.397310	23880.169304
HLA A*2301	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.489262	1.091915	-3.397347	30850.486814
HLA A*0202	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.491452	1.094025	-3.397427	31006.428283
HLA B*1801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.506599	1.109115	-3.397484	32106.936664
HLA A*0206	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.414880	1.017228	-3.397652	25994.392714
HLA A*2403	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.402857	1.005151	-3.397707	25284.674145
HLA A*6802	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.290345	0.892605	-3.397740	19513.951591
HLA B*3801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.519803	1.121826	-3.397977	33098.093390
HLA A*0219	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.179156	0.781170	-3.397986	15106.221401
HLA A*3001	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.192900	0.794851	-3.398049	15591.946388
HLA A*6801	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.608409	1.210159	-3.398250	40589.070402
HLA B*4801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.442357	1.044058	-3.398299	27692.164508
HLA A*0250	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.498853	1.100487	-3.398365	31539.341332
HLA A*2603	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.613921	1.215498	-3.398423	41107.493495
HLA A*3301	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.454330	1.055834	-3.398496	28466.225049
HLA B*1801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.405862	1.007289	-3.398573	25460.231744
HLA B*4402	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.403696	1.005094	-3.398602	25333.554392
HLA A*0219	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.419567	1.020917	-3.398650	26276.462559
HLA A*3301	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.635757	1.236980	-3.398777	43227.200489
HLA A*3002	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.435901	1.036964	-3.398937	27283.527398
HLA B*7301	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.051818	0.652880	-3.398939	11267.263666
HLA A*0202	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.153561	0.754590	-3.398971	14241.658116
HLA A*8001	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.425598	1.026553	-3.399045	26643.914196
HLA A*3101	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.359439	0.960386	-3.399053	22879.096928
HLA B*5401	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.538042	1.138932	-3.399110	34517.714245
HLA B*1501	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.428084	1.028966	-3.399118	26796.852240
HLA B*0801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.307788	0.908582	-3.399206	20313.642261
HLA A*6802	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.381811	0.982586	-3.399224	24088.550876
HLA A*0206	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.525294	1.126026	-3.399268	33519.206073
HLA B*0702	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.406668	1.007289	-3.399379	25507.519406
HLA B*4801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.343321	0.943730	-3.399592	22045.574004
HLA A*8001	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.406913	1.007289	-3.399623	25521.874700
HLA A*0219	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.382332	0.982586	-3.399746	24117.498494
HLA A*0212	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.427048	1.027198	-3.399849	26732.997553
HLA B*2705	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.428232	1.028301	-3.399931	26805.986781
HLA A*0216	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.443292	1.043287	-3.400005	27751.853737
HLA A*6802	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.209525	0.809432	-3.400093	16200.383249
HLA B*4601	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.369302	0.969193	-3.400109	23404.642741
HLA B*4501	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.628222	1.228069	-3.400153	42483.697902
HLA B*0702	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.313051	0.912830	-3.400221	20561.303628
HLA B*0801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.305509	0.905240	-3.400268	20207.323747
HLA B*5101	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.479627	1.079304	-3.400323	30173.576012
HLA B*3801	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.526386	1.125828	-3.400558	33603.633083
HLA A*0101	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.383166	0.982586	-3.400580	24163.860912
HLA B*3901	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.312590	0.911989	-3.400601	20539.513245
HLA B*4001	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.383204	0.982586	-3.400617	24165.952584
HLA B*0702	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.429282	1.028547	-3.400735	26870.888007
HLA A*0202	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.514188	1.113445	-3.400743	32672.901831
HLA B*1502	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.501273	1.100487	-3.400785	31715.574950
HLA A*0212	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.421740	1.020917	-3.400823	26408.283403
HLA B*7301	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.526743	1.125828	-3.400915	33631.276821
HLA B*1503	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.091929	0.690895	-3.401034	12357.450098
HLA A*2403	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.363821	0.962750	-3.401070	23111.102715
HLA B*5701	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.418409	1.017228	-3.401181	26206.474627
HLA A*2602	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.583458	1.182210	-3.401248	38322.830138

HLA A*0301	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.364063	0.962750	-3.401312	23123.984239
HLA B*0702	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.307797	0.906227	-3.401570	20314.081844
HLA A*0301	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.362157	0.960386	-3.401771	23022.751843
HLA A*2402	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.527714	1.125828	-3.401886	33706.502658
HLA B*5401	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.511103	1.109115	-3.401988	32441.642494
HLA A*2501	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.446212	1.044058	-3.402155	27939.099723
HLA A*2403	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.192468	0.790294	-3.402174	15576.433581
HLA A*2402	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.523163	1.120820	-3.402342	33355.137908
HLA A*2603	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.515825	1.113445	-3.402381	32796.333871
HLA B*3801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.445792	1.043307	-3.402485	27912.057428
HLA A*2301	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.533651	1.131046	-3.402605	34170.461288
HLA A*0101	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.365822	0.962975	-3.402848	23217.872875
HLA B*4002	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.631253	1.228391	-3.402862	42781.218260
HLA A*0216	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.415784	1.012736	-3.403048	26048.590447
HLA B*2705	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.415928	1.012736	-3.403191	26057.187985
HLA B*4001	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.324885	0.921448	-3.403437	21129.294789
HLA A*2301	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.529335	1.125828	-3.403507	33832.558209
HLA A*0206	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.151982	0.748391	-3.403591	14189.977343
HLA B*4403	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.639009	1.235408	-3.403601	43552.069603
HLA A*0301	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.347374	0.943730	-3.403645	22252.267534
HLA B*5101	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.440630	1.036964	-3.403666	27582.271652
HLA B*4501	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.576343	1.172675	-3.403668	37700.172175
HLA A*2601	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.336886	0.933159	-3.403727	21721.317898
HLA A*0219	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.460241	1.056396	-3.403845	28856.335770
HLA B*7301	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.551164	1.147258	-3.403906	35576.555925
HLA B*0803	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.261127	0.857166	-3.403961	18244.292558
HLA B*5401	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.555806	1.151838	-3.403968	35958.907222
HLA B*7301	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.555870	1.151838	-3.404032	35964.160016
HLA A*3001	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.306486	0.902388	-3.404098	20252.851822
HLA B*4001	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.391368	0.987241	-3.404127	24624.554346
HLA A*3001	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.304318	0.900138	-3.404180	20151.974762
HLA A*3301	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.594256	1.190075	-3.404181	39287.627847
HLA B*4001	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.364598	0.960386	-3.404212	23152.524225
HLA B*1502	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.437599	1.033365	-3.404234	27390.451792
HLA A*0250	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.498312	1.094025	-3.404287	31500.122139
HLA A*1101	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.438828	1.034513	-3.404315	27468.059308
HLA B*3901	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.483734	1.079304	-3.404430	30460.265419
HLA A*0211	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.421686	1.017228	-3.404458	26404.997692
HLA B*5301	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.594895	1.190433	-3.404462	39345.481747
HLA A*3001	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.140554	0.736037	-3.404517	13821.456364
HLA A*2402	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.448602	1.044058	-3.404544	28093.240302
HLA A*6802	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.431789	1.027198	-3.404591	27026.444756
HLA A*2501	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.441661	1.036964	-3.404698	27647.855778
HLA B*4801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.417509	1.012736	-3.404773	26152.231353
HLA B*1502	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.518635	1.113845	-3.404790	33009.221582
HLA A*1101	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.505473	1.100487	-3.404986	32023.844481
HLA B*0702	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.448294	1.043287	-3.405007	28073.337803
HLA A*3002	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.449119	1.044058	-3.405061	28126.696097
HLA B*5401	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.526905	1.121826	-3.405079	33643.833126
HLA A*3002	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.531583	1.126421	-3.405162	34008.172500
HLA A*6801	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.535582	1.130410	-3.405172	34322.753264
HLA B*5801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.318041	0.912830	-3.405211	20798.928046
HLA B*0803	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.422459	1.017185	-3.405274	26452.036569
HLA B*3501	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.418075	1.012736	-3.405339	26186.350432
HLA B*0801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.360783	0.955413	-3.405370	22950.004955
HLA B*4403	1:402-410	9	FPGPGLGIR	0.923788	0.337174	-4.666498	1.260962	-3.405536	46397.840982
HLA A*0301	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.360975	0.955413	-3.405563	22960.188086
HLA A*6802	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.392924	0.987241	-3.405683	24712.901517
HLA A*0219	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.267877	0.862117	-3.405761	18530.071633
HLA B*4001	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.410982	1.005151	-3.405831	25762.136690
HLA B*1509	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.434484	1.028547	-3.405937	27194.669094
HLA B*3801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.521666	1.115576	-3.406090	33240.390616
HLA B*5401	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.529314	1.123169	-3.406144	33830.910976
HLA B*3801	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.506634	1.100487	-3.406147	32109.542194
HLA A*0206	1:208-216	9	PANIANALI	0.995189	0.008861	-4.410207	1.004050	-3.406156	25716.185519

HLA A*8001	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.434719	1.028547	-3.406172	27209.385089
HLA B*1517	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.366600	0.960386	-3.406214	23259.485747
HLA A*2501	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.449518	1.043287	-3.406231	28152.575588
HLA B*0702	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.440759	1.034513	-3.406246	27590.479810
HLA A*2402	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.519747	1.113445	-3.406302	33093.796301
HLA A*6901	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.133496	0.727191	-3.406305	13598.654944
HLA A*0201	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.393572	0.987241	-3.406331	24749.828638
HLA B*5101	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.413728	1.007289	-3.406439	25925.576841
HLA A*0203	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-3.634136	0.227657	-3.406479	4306.618599
HLA B*1517	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.441168	1.034513	-3.406655	27616.463528
HLA B*4601	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.369434	0.962750	-3.406683	23411.734341
HLA B*0803	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.450084	1.043287	-3.406798	28189.304383
HLA B*4402	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.450895	1.044058	-3.406837	28241.966362
HLA A*3101	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.336574	0.929716	-3.406858	21705.694700
HLA A*1101	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.443846	1.036964	-3.406883	27787.308096
HLA A*2403	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.336851	0.929716	-3.407135	21719.555321
HLA B*1801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.419875	1.012736	-3.407138	26295.091170
HLA A*0219	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.458246	1.050933	-3.407313	28724.102644
HLA B*0702	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.428413	1.020890	-3.407523	26817.155448
HLA B*1502	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.320369	0.912830	-3.407540	20910.734703
HLA B*0702	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.424903	1.017228	-3.407675	26601.282715
HLA B*3801	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.463549	1.055834	-3.407715	29076.977315
HLA B*5101	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.470746	1.062990	-3.407756	29562.811226
HLA B*0802	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.441133	1.033365	-3.407768	27614.222589
HLA B*7301	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.598226	1.190433	-3.407794	39648.470365
HLA B*3501	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.341073	0.933159	-3.407914	21931.733196
HLA A*0201	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.390612	0.982586	-3.408025	24581.696099
HLA A*2902	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.425290	1.017185	-3.408106	26625.038464
HLA B*4403	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.623606	1.215498	-3.408107	42034.469809
HLA A*0101	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.308114	0.899837	-3.408277	20328.923349
HLA B*3801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.531555	1.123169	-3.408386	34005.964806
HLA B*7301	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.524236	1.115576	-3.408660	33437.704484
HLA A*6801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.445677	1.036964	-3.408713	27904.659353
HLA A*1101	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.429754	1.020890	-3.408864	26900.122973
HLA A*2603	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.518060	1.108898	-3.409161	32965.499388
HLA B*2705	1:208-216	9	PANIANALI	0.995189	0.008861	-4.413270	1.004050	-3.409220	25898.241635
HLA A*1101	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.422006	1.012736	-3.409269	26424.432184
HLA B*4002	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.591599	1.182210	-3.409389	39047.977081
HLA A*2501	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.438485	1.028966	-3.409519	27446.372397
HLA A*3002	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.462100	1.052564	-3.409536	28980.083028
HLA A*6801	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.599662	1.190075	-3.409587	39779.742932
HLA B*7301	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.548565	1.138932	-3.409633	35364.324946
HLA B*2705	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-3.631890	0.222188	-3.409702	4284.402894
HLA B*4501	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.489123	1.079304	-3.409819	30840.641420
HLA A*2402	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.307727	0.897730	-3.409997	20310.785204
HLA A*2902	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.353885	0.943730	-3.410155	22588.359741
HLA B*5101	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.462793	1.052564	-3.410229	29026.369769
HLA A*0211	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.536327	1.126026	-3.410301	34381.665050
HLA B*7301	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.519258	1.108898	-3.410360	33056.578221
HLA B*4801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.397651	0.987241	-3.410410	24983.363237
HLA B*3901	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.443985	1.033365	-3.410620	27796.178761
HLA B*5401	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.551413	1.140437	-3.410976	35596.963089
HLA B*4402	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.428211	1.017228	-3.410983	26804.681656
HLA A*2601	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.398306	0.987241	-3.411065	25021.100575
HLA B*5101	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.439620	1.028301	-3.411318	27518.182901
HLA B*5801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.352903	0.941565	-3.411337	22537.337634
HLA B*1517	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.467750	1.056396	-3.411354	29359.600164
HLA B*1503	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.428688	1.017228	-3.411460	26834.134928
HLA A*0212	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.416689	1.005094	-3.411595	26102.901182
HLA A*3002	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.123868	0.712255	-3.411613	13300.493782
HLA A*0206	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.166285	0.754590	-3.411696	14665.111412
HLA A*3101	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.338728	0.926967	-3.411762	21813.641327
HLA A*8001	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.399051	0.987241	-3.411810	25064.046948
HLA B*1801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.338827	0.926967	-3.411860	21818.598284
HLA B*3801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.455209	1.043287	-3.411922	28523.879026

HLA A*0206	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.527575	1.115576	-3.411999	33695.745817
HLA B*1801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.438595	1.026553	-3.412042	27453.351931
HLA A*0301	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.345081	0.932998	-3.412083	22135.084049
HLA A*1101	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.429362	1.017228	-3.412134	26875.830991
HLA B*5401	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.538169	1.126026	-3.412143	34527.799516
HLA B*0802	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.399535	0.987241	-3.412294	25091.994823
HLA A*1101	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.342046	0.929716	-3.412330	21980.908618
HLA B*7301	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.130719	0.718317	-3.412402	13511.975924
HLA A*0211	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.425257	1.012736	-3.412521	26623.022002
HLA B*0702	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.287150	0.874608	-3.412542	19370.905555
HLA A*2902	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.433469	1.020917	-3.412552	27131.187401
HLA A*2501	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.433518	1.020890	-3.412628	27134.269887
HLA A*0101	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.375455	0.962750	-3.412705	23738.611747
HLA B*1801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.475771	1.062990	-3.412781	29906.891740
HLA B*3801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.553318	1.140437	-3.412882	35753.485033
HLA B*2705	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.456181	1.043287	-3.412895	28587.835385
HLA B*5101	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.325820	0.912830	-3.412990	21174.838045
HLA A*2603	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.544085	1.131046	-3.413039	35001.358797
HLA B*4002	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.334501	0.921448	-3.413054	21602.372194
HLA A*2601	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.270339	0.857166	-3.413173	18635.427435
HLA A*2501	1:208-216	9	PANIANALI	0.995189	0.008861	-4.417260	1.004050	-3.413209	26137.238701
HLA A*2601	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.319580	0.906227	-3.413353	20872.759310
HLA B*0702	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.426291	1.012736	-3.413555	26686.469628
HLA B*4001	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.418651	1.005094	-3.413557	26221.081431
HLA A*3101	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.311319	0.897730	-3.413589	20479.487108
HLA B*4801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.434552	1.020890	-3.413662	27198.935913
HLA A*2402	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.539792	1.126026	-3.413767	34657.114043
HLA B*4402	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.426538	1.012736	-3.413802	26701.632873
HLA B*0801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.316067	0.902116	-3.413951	20704.625766
HLA B*0803	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.508011	1.094025	-3.413986	32211.497229
HLA A*8001	1:208-216	9	PANIANALI	0.995189	0.008861	-4.418176	1.004050	-3.414126	26192.442747
HLA B*4801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.435203	1.020917	-3.414285	27239.725142
HLA B*5801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.314155	0.899837	-3.414318	20613.650305
HLA B*1509	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.435250	1.020890	-3.414360	27242.672579
HLA A*0101	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.335836	0.921448	-3.414388	21668.854423
HLA A*6801	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.649800	1.235408	-3.414392	44647.791582
HLA B*4501	1:123-131	9	LGGKLHSDL	0.983281	0.252127	-4.649805	1.235408	-3.414397	44648.274664
HLA A*0101	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.316570	0.902116	-3.414454	20728.609729
HLA A*2403	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.335935	0.921448	-3.414487	21673.778479
HLA A*2301	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.528449	1.113845	-3.414604	33763.626071
HLA B*4801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.431866	1.017228	-3.414639	27031.270119
HLA A*2603	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.555409	1.140721	-3.414688	35926.046051
HLA B*5101	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.419875	1.005094	-3.414781	26295.091170
HLA B*5801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.334922	0.920085	-3.414837	21623.301419
HLA B*4402	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.442237	1.027198	-3.415039	27684.525173
HLA B*4601	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.317205	0.902116	-3.415089	20758.909512
HLA B*4801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.321365	0.906227	-3.415138	20958.754653
HLA B*2705	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.466110	1.050933	-3.415177	29248.944357
HLA A*3201	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.538373	1.123169	-3.415204	34544.054208
HLA B*4601	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.375594	0.960386	-3.415208	23746.189929
HLA A*2403	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.350196	0.934761	-3.415435	22397.317382
HLA A*6801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.436439	1.020917	-3.415521	27317.348941
HLA B*4001	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.345281	0.929716	-3.415565	22145.264999
HLA B*4601	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.402942	0.987241	-3.415701	25289.598967
HLA B*5401	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.468274	1.052564	-3.415710	29395.041115
HLA A*3301	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.619541	1.203805	-3.415736	41642.899888
HLA A*2403	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.317860	0.902116	-3.415744	20790.265819
HLA B*5101	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.376153	0.960386	-3.415767	23776.784113
HLA B*4001	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.378608	0.962750	-3.415858	23911.582891
HLA A*3001	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.206203	0.790294	-3.415909	16076.929855
HLA B*4801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.421270	1.005151	-3.416120	26379.725678
HLA B*2705	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.459527	1.043307	-3.416220	28808.917461
HLA B*1517	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.437148	1.020890	-3.416258	27362.016135
HLA B*4801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.421367	1.005094	-3.416273	26385.577494
HLA B*3801	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.503587	1.087303	-3.416284	31885.030118

HLA A*0101	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.316425	0.900138	-3.416287	20721.658247
HLA A*3301	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.555534	1.139224	-3.416310	35936.348392
HLA B*1509	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.297831	0.881518	-3.416313	19853.207535
HLA A*3201	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.225798	0.809432	-3.416365	16818.909039
HLA A*2403	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.331597	0.915104	-3.416493	21458.407132
HLA A*3201	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.543204	1.126421	-3.416783	34930.423224
HLA A*3301	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.379792	0.962975	-3.416818	23976.868797
HLA B*4001	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.397552	0.980728	-3.416825	24977.687279
HLA B*1503	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.230711	0.813884	-3.416827	17010.246023
HLA A*2403	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.360621	0.943730	-3.416891	22941.439722
HLA B*1503	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.291614	0.874608	-3.417006	19571.041830
HLA A*2603	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.557465	1.140437	-3.417029	36096.510628
HLA B*0802	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.454191	1.036964	-3.417228	28457.140550
HLA A*2603	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.543286	1.125828	-3.417458	34937.037790
HLA B*1801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.338926	0.921448	-3.417478	21823.556368
HLA B*1503	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.315245	0.897730	-3.417515	20665.459452
HLA B*0802	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.400144	0.982586	-3.417557	25127.177397
HLA B*1517	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.446187	1.028547	-3.417640	27937.437151
HLA A*0101	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.378056	0.960386	-3.417670	23881.202839
HLA B*1801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.422823	1.005151	-3.417673	26474.226772
HLA A*0202	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.543772	1.126026	-3.417747	34976.183843
HLA A*2403	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.445007	1.027198	-3.417809	27861.668586
HLA B*1509	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.468845	1.050933	-3.417912	29433.709337
HLA B*4601	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.350953	0.932998	-3.417955	22436.367159
HLA B*0702	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.219158	0.801202	-3.417956	16563.731320
HLA B*3901	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.468937	1.050933	-3.418003	29439.920083
HLA A*0206	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.474474	1.056396	-3.418078	29817.715239
HLA B*0802	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.461397	1.043287	-3.418110	28933.243988
HLA A*0216	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.317973	0.899837	-3.418136	20795.665225
HLA B*4002	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.430948	1.012736	-3.418212	26974.152205
HLA A*6801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.495946	1.077535	-3.418411	31328.983668
HLA B*4403	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.646539	1.228069	-3.418470	44313.790179
HLA B*1517	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.461848	1.043287	-3.418561	28963.312525
HLA A*0201	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.373980	0.955413	-3.418567	23658.098787
HLA A*3002	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.532582	1.113845	-3.418737	34086.454147
HLA B*3501	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.447305	1.028547	-3.418758	28009.471756
HLA B*1801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.471333	1.052564	-3.418769	29602.821159
HLA B*0802	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.447192	1.028301	-3.418891	28002.199349
HLA A*2601	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.379351	0.960386	-3.418965	23952.495300
HLA A*0101	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.348685	0.929716	-3.418969	22319.542349
HLA A*0219	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.431725	1.012736	-3.418989	27022.497372
HLA A*0301	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.346728	0.927581	-3.419147	22219.187015
HLA B*1509	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.533038	1.113845	-3.419193	34122.247290
HLA B*7301	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-3.758495	0.339229	-3.419266	5734.488060
HLA A*3002	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.534854	1.115576	-3.419278	34265.239994
HLA B*0803	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.453855	1.034513	-3.419342	28435.134217
HLA B*0802	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.470283	1.050933	-3.419350	29531.321498
HLA B*5401	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.462687	1.043307	-3.419380	29019.304304
HLA B*0802	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.475950	1.056396	-3.419554	29919.190534
HLA B*4501	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.558600	1.138932	-3.419668	36190.953295
HLA A*0202	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.560653	1.140437	-3.420217	36362.478107
HLA A*2501	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.301775	0.881518	-3.420258	20034.359742
HLA A*6901	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.383009	0.962750	-3.420259	24155.104004
HLA B*0802	1:208-216	9	PANIANALI	0.995189	0.008861	-4.424395	1.004050	-3.420345	26570.216312
HLA A*0216	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.407622	0.987241	-3.420381	25563.606076
HLA B*2705	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.332420	0.911989	-3.420430	21499.076284
HLA A*2902	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.383321	0.962750	-3.420571	24172.490224
HLA A*6801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.121875	0.701295	-3.420581	13239.616370
HLA B*4403	1:320-328	9	AVRDVLDGK	0.895050	0.333341	-4.649090	1.228391	-3.420699	44574.906178
HLA B*5801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.325978	0.905240	-3.420737	21182.514522
HLA B*5801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.348406	0.927581	-3.420825	22305.178169
HLA B*0801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.362498	0.941565	-3.420933	23040.818756
HLA B*1502	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.541860	1.120820	-3.421040	34822.499614
HLA A*2902	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.321279	0.900138	-3.421141	20954.559845
HLA B*4501	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.586310	1.165167	-3.421143	38575.347675

HLA B*5301	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.573235	1.151838	-3.421397	37431.304689
HLA B*7301	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.625206	1.203805	-3.421401	42189.616064
HLA B*0702	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.326645	0.905240	-3.421404	21215.084532
HLA A*0212	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.354496	0.932998	-3.421498	22620.154232
HLA B*4403	1:499-507	9	RITNEVAEV	0.947033	0.285622	-4.654360	1.232655	-3.421705	45119.090078
HLA A*6801	1:45-53	9	PHTASIEEI	1.223034	0.013946	-4.658730	1.236980	-3.421750	45575.388006
HLA A*3002	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.356610	0.934761	-3.421849	22730.558061
HLA A*6901	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.356643	0.934761	-3.421882	22732.279703
HLA B*0803	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.484937	1.062990	-3.421946	30544.753144
HLA A*0201	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.344501	0.922498	-3.422003	22105.525959
HLA B*1517	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.439187	1.017185	-3.422003	27490.804391
HLA B*0803	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.443142	1.020890	-3.422252	27742.246796
HLA B*2705	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.391491	0.969193	-3.422297	24631.482558
HLA B*5101	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.451358	1.028966	-3.422392	28272.081230
HLA B*7301	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.595142	1.172675	-3.422466	39367.837839
HLA A*0203	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.326297	0.903619	-3.422678	21198.105184
HLA B*5801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.349721	0.926967	-3.422755	22372.855015
HLA B*7301	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.553899	1.131046	-3.422853	35801.292298
HLA B*5801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.344308	0.921448	-3.422861	22095.721881
HLA B*1502	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.067490	0.644580	-3.422909	11681.255477
HLA B*3801	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.500464	1.077535	-3.422929	31656.607092
HLA B*5401	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.554044	1.131046	-3.422998	35813.302535
HLA A*0211	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.357982	0.934761	-3.423221	22802.485987
HLA B*1501	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.345723	0.922498	-3.423224	22167.799501
HLA B*1502	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.575065	1.151838	-3.423227	37589.384437
HLA B*5801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.297857	0.874608	-3.423249	19854.389010
HLA B*5301	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.553871	1.130410	-3.423460	35798.968201
HLA B*1501	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.207209	0.783681	-3.423528	16114.198031
HLA B*2705	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.367293	0.943730	-3.423564	23296.635598
HLA A*2601	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.404330	0.980728	-3.423603	25370.585395
HLA B*4501	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.532923	1.109115	-3.423808	34113.203208
HLA B*7301	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.545671	1.121826	-3.423844	35129.406041
HLA B*1501	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.344750	0.920891	-3.423859	22118.205969
HLA A*2601	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.367589	0.943730	-3.423860	23312.521071
HLA B*4002	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.518083	1.094025	-3.424058	32967.282833
HLA B*5801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.243111	0.819048	-3.424063	

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17502.946963
HLA A*1101	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.367899	0.943730	-3.424170	23329.174613
HLA B*3801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.555353	1.131046	-3.424307	35921.381811
HLA A*2501	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.475332	1.050933	-3.424399	29876.651753
HLA A*2601	1:51-59 9	EEIRARQPV	0.859860	0.021658	-4.306059	0.881518	-3.424541	20232.920681
HLA A*3201	1:20-28 9	VDFGAQYAQ	0.984953	-0.084779	-4.324753	0.900174	-3.424579	21122.894559
HLA A*2403	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.431869	1.007289	-3.424580	27031.416355
HLA B*1517	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.467893	1.043307	-3.424587	29369.290526
HLA A*3301	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.407180	0.982586	-3.424594	25537.619594
HLA B*2705	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.451938	1.027198	-3.424740	28309.884842
HLA B*2705	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.326957	0.902116	-3.424841	21230.354602
HLA A*0211	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.243363	0.818458	-3.424904	17513.081619
HLA B*0802	1:29-37 9	LIARRVREA	1.156929	-0.187736	-4.394256	0.969193	-3.425063	24788.822428
HLA A*6801	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.616945	1.191820	-3.425125	41394.704238
HLA A*0211	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.468434	1.043287	-3.425147	29405.856730
HLA A*2403	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.358325	0.933159	-3.425166	22820.503505
HLA B*5301	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.407829	0.982586	-3.425242	25575.779046
HLA A*2603	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.632703	1.207422	-3.425281	42924.256348
HLA A*2301	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.534330	1.108898	-3.425432	34223.927153
HLA A*0201	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.334053	0.908582	-3.425471	21580.062233
HLA B*7301	1:11-19 9	ETPARPVLV	1.191696	-0.032241	-4.585001	1.159455	-3.425546	38459.283218
HLA A*0301	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.330888	0.905240	-3.425648	21423.377299
HLA B*0802	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.468958	1.043307	-3.425651	29441.353518
HLA A*6901	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.199949	0.774258	-3.425691	15847.063122
HLA B*5701	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.412937	0.987241	-3.425696	25878.354135
HLA A*0219	1:37-45 9	ARVFSEVIP	0.871286	0.157261	-4.454339	1.028547	-3.425792	28466.841052
HLA B*7301	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.539640	1.113845	-3.425795	34644.929261
HLA B*1509	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.482195	1.056396	-3.425799	30352.521164
HLA B*3901	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.454882	1.028966	-3.425916	28502.437857
HLA A*2902	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.443156	1.017228	-3.425928	27743.147305
HLA B*7301	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.566682	1.140721	-3.425961	36870.773726
HLA B*4001	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.388948	0.962975	-3.425974	24487.723331
HLA A*2301	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.541707	1.115576	-3.426131	34810.256685
HLA B*5701	1:29-37 9	LIARRVREA	1.156929	-0.187736	-4.395325	0.969193	-3.426132	24849.915263
HLA B*3801	1:35-43 9	REARVFSEV	0.807139	0.210046	-4.443360	1.017185	-3.426175	27756.207978
HLA B*1517	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.353774	0.927581	-3.426194	22582.617047
HLA B*1509	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.505511	1.079304	-3.426207	32026.616528
HLA A*0203	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.453432	1.027198	-3.426234	28407.458128
HLA B*4002	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.552064	1.125828	-3.426236	35650.346526
HLA A*0101	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.367864	0.941565	-3.426299	23327.281566
HLA A*2501	1:54-62 9	RARQPVALV	0.737262	0.289291	-4.452871	1.026553	-3.426318	28370.752057
HLA B*4403	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.176586	0.750232	-3.426354	15017.080504
HLA B*5701	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.389407	0.962975	-3.426432	24513.569756
HLA A*0301	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.368057	0.941565	-3.426492	23337.632098
HLA B*3501	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.389277	0.962750	-3.426527	24506.276978
HLA A*3201	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.455542	1.028966	-3.426576	28545.799610
HLA A*3101	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.328708	0.902116	-3.426592	21316.093394
HLA B*4402	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.433962	1.007289	-3.426673	27162.028027
HLA A*2402	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.557724	1.131046	-3.426678	36117.997614
HLA B*4402	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.389522	0.962750	-3.426771	24520.068787
HLA B*4501	1:12-20 9	TPARPVLVV	1.197961	-0.071540	-4.553323	1.126421	-3.426902	35753.871880
HLA B*0702	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.454158	1.027198	-3.426960	28454.985332
HLA A*3101	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.347055	0.920085	-3.426970	22235.901563
HLA A*0301	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.356702	0.929716	-3.426986	22735.354389
HLA A*1101	1:37-45 9	ARVFSEVIP	0.871286	0.157261	-4.455554	1.028547	-3.427007	28546.571769
HLA A*2902	1:37-45 9	ARVFSEVIP	0.871286	0.157261	-4.455704	1.028547	-3.427157	28556.457242
HLA A*0101	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.340063	0.912830	-3.427233	21880.773745
HLA B*3901	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.332502	0.905240	-3.427262	21503.147436
HLA A*1101	1:90-98 9	LGICYGFQA	1.194766	-0.294929	-4.327112	0.899837	-3.427275	21237.936310
HLA B*4002	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.574581	1.147258	-3.427323	37547.516764
HLA B*5101	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.470851	1.043307	-3.427545	29570.009021
HLA B*1501	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.193474	0.765882	-3.427592	15612.541549
HLA A*6802	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.408346	0.980728	-3.427618	25606.236836
HLA B*1501	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.362439	0.934761	-3.427678	23037.702760
HLA B*1509	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.371445	0.943730	-3.427715	23520.402344
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HLA B*4402	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.410338	0.982586	-3.427752	25723.977515
HLA B*7301	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.355407	0.927581	-3.427826	22667.684639
HLA A*3201	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.480473	1.052564	-3.427909	30232.398126
HLA A*2603	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.551201	1.123169	-3.428032	35579.635502
HLA A*2501	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.461456	1.033365	-3.428091	28937.157394
HLA B*5701	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.388483	0.960386	-3.428097	24461.507153
HLA A*0219	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.362869	0.934761	-3.428108	23060.521603
HLA A*0101	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.302795	0.874608	-3.428188	20081.453517
HLA B*0801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.349099	0.920891	-3.428208	22340.803809
HLA B*5301	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.371990	0.943730	-3.428260	23549.941199
HLA A*0212	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.310069	0.881518	-3.428551	20420.630631
HLA B*0702	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.449506	1.020917	-3.428589	28151.814087
HLA A*0219	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.073180	0.644580	-3.428600	11835.319190
HLA A*3101	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.409375	0.980728	-3.428647	25666.983561
HLA A*0202	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.434035	1.005094	-3.428941	27166.583659
HLA A*0211	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.411713	0.982586	-3.429126	25805.517337
HLA B*4601	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.384541	0.955413	-3.429128	24240.455479
HLA B*4501	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.520642	1.091476	-3.429166	33162.078513
HLA A*2301	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.506742	1.077535	-3.429207	32117.533806
HLA B*0702	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.434315	1.005094	-3.429221	27184.078507
HLA B*7301	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.611475	1.182210	-3.429265	40876.639307
HLA A*2501	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.485773	1.056396	-3.429377	30603.636595
HLA A*0202	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.521304	1.091915	-3.429390	33212.708818
HLA B*0802	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.434568	1.005151	-3.429418	27199.965935
HLA A*2902	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.434552	1.005094	-3.429458	27198.935913
HLA B*1509	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.456019	1.026553	-3.429466	28577.166042
HLA A*8001	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.450385	1.020917	-3.429468	28208.831273
HLA B*3801	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.521137	1.091476	-3.429661	33199.954195
HLA A*0219	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.456964	1.027198	-3.429765	28639.382589
HLA B*0702	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.458754	1.028966	-3.429788	28757.687412
HLA B*3801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.543775	1.113845	-3.429930	34976.373061
HLA A*6801	1:417-425	9	AKRLDTLRH	1.360069	-0.122173	-4.667837	1.237896	-3.429941	46541.135894
HLA A*6801	1:449-457	9	VLLADVRSV	1.028902	0.199167	-4.658171	1.228069	-3.430102	45516.745011
HLA A*0301	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.364965	0.934761	-3.430204	23172.071876
HLA B*3901	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.435412	1.005151	-3.430261	27252.843686
HLA A*1101	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.473577	1.043287	-3.430290	29756.158243
HLA A*2601	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.351775	0.921448	-3.430327	22478.889794
HLA B*4402	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.417692	0.987241	-3.430451	26163.269174
HLA A*0216	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.339118	0.908582	-3.430536	21833.239683
HLA B*1509	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.464101	1.033365	-3.430737	29113.967081
HLA B*4402	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.391277	0.960386	-3.430891	24619.359466
HLA B*4403	1:232-240	9	LSGGVDSAV	1.094342	0.070825	-4.596173	1.165167	-3.431006	39461.445257
HLA B*5701	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.365820	0.934761	-3.431059	23217.747269
HLA A*0301	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.364432	0.933159	-3.431272	23143.632999
HLA B*4001	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.366041	0.934761	-3.431280	23229.557183
HLA B*7301	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.557796	1.126421	-3.431376	36124.055347
HLA A*6802	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.250618	0.819048	-3.431570	17808.108022
HLA B*4001	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.209779	0.778023	-3.431756	16209.851381
HLA A*2501	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.157893	0.726094	-3.431799	14384.441564
HLA B*0802	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.375629	0.943730	-3.431900	23748.116971
HLA B*4001	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.401123	0.969193	-3.431930	25183.926381
HLA B*4002	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.642131	1.210159	-3.431972	43866.326134
HLA B*0803	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.338272	0.906227	-3.432045	21790.759516
HLA B*0801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.347231	0.915104	-3.432127	22244.925426
HLA A*3001	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-3.399460	-0.032788	-3.432249	2508.767712
HLA B*4002	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.541397	1.109115	-3.432282	34785.407368
HLA B*4501	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.445089	1.012736	-3.432353	27866.944584
HLA B*0803	1:208-216	9	PANIANALI	0.995189	0.008861	-4.436483	1.004050	-3.432433	27320.156978
HLA B*1501	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.395226	0.962750	-3.432476	24844.269622
HLA B*4001	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.330303	0.897730	-3.432573	21394.538102
HLA B*0802	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.445435	1.012736	-3.432698	27889.114690
HLA A*0216	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.208445	0.775707	-3.432738	16160.117924
HLA B*4002	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.251299	0.818458	-3.432841	17836.068517
HLA A*3001	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.242510	0.809432	-3.433077	17478.723356
HLA B*0801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.362813	0.929716	-3.433097	23057.527681

HLA B*4002	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.476478	1.043307	-3.433172	29955.631096
HLA A*6801	1:31-39	9	ARRVREARV	0.936445	0.312607	-4.682270	1.249052	-3.433218	48113.822862
HLA A*3301	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.524744	1.091476	-3.433268	33476.800485
HLA A*0201	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.396020	0.962750	-3.433270	24889.739985
HLA A*3101	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.396027	0.962750	-3.433277	24890.143941
HLA A*0250	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.573733	1.140437	-3.433296	37474.259149
HLA B*1801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.368130	0.934761	-3.433368	23341.546301
HLA A*0203	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.314893	0.881518	-3.433375	20648.696578
HLA B*5801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.145662	0.712255	-3.433407	13984.971555
HLA A*8001	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.438619	1.005094	-3.433525	27454.837167
HLA A*0211	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.549127	1.115576	-3.433551	35410.079300
HLA B*3501	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.315109	0.881518	-3.433591	20658.976194
HLA A*0201	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.361387	0.927581	-3.433806	22981.935492
HLA B*1517	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.414659	0.980728	-3.433931	25981.177157
HLA B*0802	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.454859	1.020917	-3.433941	28500.895948
HLA B*3501	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.421193	0.987241	-3.433952	26375.016623
HLA A*8001	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.349080	0.915104	-3.433976	22339.836940
HLA B*0803	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.470945	1.036964	-3.433982	29576.408532
HLA B*3901	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.340291	0.906227	-3.434063	21892.258897
HLA A*0201	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.340370	0.906227	-3.434143	21896.286047
HLA B*1517	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.451433	1.017228	-3.434205	28276.976016
HLA B*4402	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.354322	0.920085	-3.434237	22611.100478
HLA A*2601	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.397056	0.962750	-3.434306	24949.191850
HLA B*5801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.355308	0.920891	-3.434417	22662.534779
HLA A*3301	1:502-510	9	NEVAEVNRV	1.061309	0.130511	-4.626246	1.191820	-3.434427	42290.848148
HLA B*4801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.415164	0.980728	-3.434436	26011.414125
HLA A*3001	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.212495	0.778023	-3.434472	16311.542715
HLA A*8001	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.367639	0.933159	-3.434479	23315.169703
HLA B*1503	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.224134	0.789472	-3.434663	16754.612442
HLA B*1509	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.487288	1.052564	-3.434725	30710.610795
HLA B*5801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.346742	0.911989	-3.434753	22219.908247
HLA B*0803	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.491198	1.056396	-3.434802	30988.317509
HLA A*8001	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.417542	0.982586	-3.434955	26154.212157
HLA A*0216	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.224529	0.789472	-3.435057	16769.846984
HLA A*8001	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.347137	0.911989	-3.435148	22240.112243
HLA A*2601	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.364927	0.929716	-3.435211	23170.066230
HLA B*3501	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-3.621064	0.185815	-3.435249	4178.918267
HLA B*0801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.462487	1.027198	-3.435289	29005.963118
HLA B*0801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.362301	0.926967	-3.435334	23030.350680
HLA A*0203	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.376926	0.941565	-3.435361	23819.140990
HLA A*2601	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.340657	0.905240	-3.435417	21910.742508
HLA A*2603	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.574367	1.138932	-3.435435	37529.036674
HLA B*0803	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.478769	1.043307	-3.435463	30114.053767
HLA B*4501	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.645801	1.210159	-3.435642	44238.578013
HLA B*3901	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.243323	0.807656	-3.435667	17511.471048
HLA B*1517	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.486727	1.050933	-3.435794	30670.928755
HLA B*1801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.492431	1.056396	-3.436035	31076.455379
HLA A*6802	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.151643	0.715584	-3.436060	14178.927314
HLA A*2402	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.576522	1.140437	-3.436085	37715.675847
HLA A*0301	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.356185	0.920085	-3.436100	22708.311421
HLA B*4601	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.348986	0.912830	-3.436156	22335.003221
HLA A*0212	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.333891	0.897730	-3.436161	21572.008280
HLA B*0803	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.487157	1.050933	-3.436224	30701.308308
HLA B*3501	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.457262	1.020890	-3.436372	28659.066208
HLA A*2902	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.391789	0.955413	-3.436376	24648.411579
HLA B*3801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.457297	1.020890	-3.436407	28661.391938
HLA B*1517	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.268417	0.831902	-3.436516	18553.142479
HLA B*0801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.340192	0.903619	-3.436573	21887.285205
HLA B*3801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.463157	1.026553	-3.436604	29050.719540
HLA A*6801	1:250-258	9	GDRLTCVFV	1.283110	-0.051255	-4.668478	1.231855	-3.436623	46609.923269
HLA B*3501	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.217795	0.781170	-3.436626	16511.840161
HLA A*0219	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.336545	0.899837	-3.436708	21704.285641
HLA B*4002	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.471270	1.034513	-3.436756	29598.497479
HLA A*1101	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.442037	1.005151	-3.436887	27671.797632
HLA B*0702	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.417645	0.980728	-3.436917	26160.438520

HLA B*0702	1:208-216	9	PANIANALI	0.995189	0.008861	-4.441128	1.004050	-3.437078	27613.923811
HLA A*0212	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.392534	0.955413	-3.437121	24690.718265
HLA A*2501	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.343397	0.906227	-3.437169	22049.390786
HLA B*1517	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.370409	0.933159	-3.437249	23464.355167
HLA A*2902	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.370514	0.933159	-3.437355	23470.068142
HLA A*0212	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.372154	0.934761	-3.437393	23558.861068
HLA A*2902	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.129854	0.692424	-3.437430	13485.102512
HLA A*3301	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.644878	1.207422	-3.437456	44144.622886
HLA B*1517	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.407021	0.969193	-3.437827	25528.226734
HLA A*0301	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.350732	0.912830	-3.437902	22424.960503
HLA A*3002	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.494302	1.056396	-3.437906	31210.567596
HLA B*2705	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.425173	0.987241	-3.437932	26617.837513
HLA B*4001	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.371097	0.933159	-3.437938	23501.577951
HLA B*1502	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.564053	1.126026	-3.438027	36648.244617
HLA A*0212	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.346644	0.908582	-3.438062	22214.860116
HLA B*4002	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.610754	1.172675	-3.438079	40808.806259
HLA B*3901	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.339654	0.901531	-3.438123	21860.186611
HLA B*0801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.239561	0.801202	-3.438359	17360.455062
HLA B*1503	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.295594	0.857166	-3.438428	19751.222107
HLA B*0801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.186862	0.748391	-3.438471	15376.665125
HLA A*2602	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.559303	1.120820	-3.438482	36249.541592
HLA B*5301	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.577509	1.138932	-3.438576	37801.469081
HLA B*0802	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.443691	1.005094	-3.438598	27777.388334
HLA A*6901	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.361105	0.922498	-3.438606	22967.020766
HLA A*2902	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.282183	0.843518	-3.438665	19150.632064
HLA A*0202	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.338970	0.900174	-3.438796	21825.799680
HLA B*1502	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.530272	1.091476	-3.438796	33905.666209
HLA A*6901	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.331440	0.892605	-3.438835	21450.630672
HLA B*5801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-3.996418	0.557541	-3.438876	9917.851494
HLA B*0803	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.467851	1.028966	-3.438885	29366.430743
HLA A*2403	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.257953	0.819048	-3.438905	18111.435499
HLA B*5701	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.354077	0.915104	-3.438973	22598.382407
HLA B*5801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.345241	0.906227	-3.439014	22143.228435
HLA B*5701	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.351895	0.912830	-3.439065	22485.092674
HLA A*0101	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.217114	0.778023	-3.439091	16485.955576
HLA B*5101	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.351105	0.911989	-3.439116	22444.258133
HLA B*5701	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.372295	0.933159	-3.439136	23566.509359
HLA B*1501	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.380963	0.941565	-3.439397	24041.552567
HLA A*2403	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.395092	0.955413	-3.439680	24836.609733
HLA A*0101	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.341259	0.901531	-3.439728	21941.108410
HLA A*0212	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.346545	0.906788	-3.439757	22209.813133
HLA B*1502	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.580196	1.140437	-3.439760	38036.144535
HLA A*0202	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.126147	0.686294	-3.439853	13370.472803
HLA B*5301	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.345138	0.905240	-3.439897	22137.958196
HLA B*0801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.400299	0.960386	-3.439913	25136.150725
HLA A*8001	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.361361	0.921448	-3.439913	22980.567905
HLA A*2501	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.345196	0.905240	-3.439956	22140.952496
HLA A*3201	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.534034	1.094025	-3.440009	34200.606497
HLA A*2403	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.403290	0.962975	-3.440315	25309.855536
HLA B*1509	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.477493	1.036964	-3.440530	30025.721437
HLA A*0216	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.395985	0.955413	-3.440573	24887.720306
HLA B*5101	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.363163	0.922498	-3.440665	23076.121235
HLA A*0203	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.427973	0.987241	-3.440732	26790.039610
HLA B*5301	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.588023	1.147258	-3.440765	38727.781874
HLA A*0101	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.375528	0.934761	-3.440767	23742.593202
HLA A*0206	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.484135	1.043287	-3.440849	30488.456975
HLA B*1801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.248687	0.807776	-3.440910	17729.092450
HLA B*3501	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.410209	0.969193	-3.441016	25716.324641
HLA B*4001	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.343157	0.902116	-3.441041	22037.227097
HLA A*0101	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.353095	0.911989	-3.441106	22547.337660
HLA A*0216	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.468375	1.027198	-3.441177	29401.879939
HLA A*2501	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.458430	1.017228	-3.441202	28736.225950
HLA A*6901	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.343380	0.902116	-3.441264	22048.555808
HLA A*2402	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.484824	1.043287	-3.441537	30536.822475
HLA B*4501	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.462499	1.020917	-3.441582	29006.747724

HLA A*2403	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.354439	0.912830	-3.441609	22617.217482
HLA B*1503	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.190053	0.748391	-3.441662	15490.047766
HLA B*4402	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.410874	0.969193	-3.441680	25755.726453
HLA B*7301	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.353699	0.911989	-3.441710	22578.707963
HLA A*1101	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.492652	1.050933	-3.441719	31092.262695
HLA A*0203	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.424341	0.982586	-3.441755	26566.910453
HLA B*1501	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-3.585074	0.143276	-3.441798	3846.577313
HLA A*3301	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.470264	1.028301	-3.441963	29530.043436
HLA A*2501	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.449368	1.007289	-3.442079	28142.829927
HLA A*0203	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.344477	0.902388	-3.442089	22104.330107
HLA A*0101	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.364779	0.922498	-3.442281	23162.170683
HLA B*1503	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.463277	1.020917	-3.442359	29058.735865
HLA A*3201	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.475745	1.033365	-3.442381	29905.112070
HLA B*5101	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.463321	1.020890	-3.442432	29061.722905
HLA B*4403	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.075868	0.633434	-3.442433	11908.794083
HLA B*7301	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.582929	1.140437	-3.442492	38276.211008
HLA A*1101	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.471599	1.028966	-3.442633	29620.923413
HLA A*2603	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.522089	1.079304	-3.442785	33272.775211
HLA B*3901	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.479782	1.036964	-3.442818	30184.351492
HLA B*1509	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.460126	1.017228	-3.442898	28848.687414
HLA B*4402	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.271345	0.828408	-3.442937	18678.626503
HLA A*0203	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.078170	0.635184	-3.442986	11972.098496
HLA B*5101	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.406048	0.962975	-3.443073	25471.115295
HLA B*1517	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.197646	0.754547	-3.443099	15763.269206
HLA A*0212	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.345509	0.902388	-3.443121	22156.888981
HLA B*1503	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.464123	1.020890	-3.443233	29115.384645
HLA B*4601	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.317938	0.874608	-3.443330	20793.977760
HLA B*4403	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.134337	0.690895	-3.443442	13625.017528
HLA A*0301	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.366104	0.922498	-3.443606	23232.950503
HLA A*6802	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-3.998885	0.555251	-3.443634	9974.349007
HLA B*1509	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.506632	1.062990	-3.443642	32109.368486
HLA A*0101	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.370728	0.926967	-3.443762	23481.625299
HLA B*5801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.343951	0.900138	-3.443814	22077.559968
HLA A*2603	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.219548	0.775634	-3.443914	16578.612920
HLA B*4402	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.385481	0.941565	-3.443915	24292.967546
HLA B*0802	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.451217	1.007289	-3.443928	28262.905790
HLA B*5701	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.406833	0.962750	-3.444082	25517.180735
HLA A*3002	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.318769	0.874608	-3.444162	20833.838479
HLA B*5801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.351084	0.906788	-3.444297	22443.165371
HLA B*5401	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.544863	1.100487	-3.444375	35064.090945
HLA A*2402	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.477742	1.033365	-3.444378	30042.944572
HLA A*3001	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.225624	0.781170	-3.444454	16812.177243
HLA B*5801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.353072	0.908582	-3.444490	22546.117907
HLA B*0802	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.471695	1.027198	-3.444497	29627.494225
HLA A*6802	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.194850	0.750232	-3.444619	15662.114888
HLA B*5101	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.501019	1.056396	-3.444623	31697.049966
HLA B*2705	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.263716	0.819048	-3.444668	18353.384380
HLA A*6901	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.359803	0.915104	-3.444699	22898.289848
HLA A*1101	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.425560	0.980728	-3.444833	26641.608046
HLA A*1101	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.360040	0.915104	-3.444936	22910.804865
HLA A*2603	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.584186	1.139224	-3.444962	38387.153962
HLA B*4403	1:409-417	9	IRIVGEVTA	1.305072	-0.114997	-4.635134	1.190075	-3.445059	43165.273483
HLA A*0201	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.386716	0.941565	-3.445151	24362.194105
HLA A*0212	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.351392	0.906227	-3.445165	22459.076378
HLA B*1509	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.432454	0.987241	-3.445213	27067.853896
HLA A*0301	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.366114	0.920891	-3.445223	23233.453259
HLA A*3301	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.576322	1.131046	-3.445276	37698.336636
HLA A*0250	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.558877	1.113445	-3.445433	36214.063778
HLA A*6801	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.592693	1.147258	-3.445435	39146.541545
HLA A*2902	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.357494	0.911989	-3.445504	22776.841763
HLA A*8001	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.375324	0.929716	-3.445608	23731.421134
HLA A*2403	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.414856	0.969193	-3.445663	25992.986484
HLA B*0802	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.375390	0.929716	-3.445674	23735.016168
HLA B*4801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.345903	0.900174	-3.445729	22177.035676
HLA A*2501	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.458470	1.012736	-3.445733	28738.868888

HLA A*2601	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.347280	0.901531	-3.445749	22247.452763
HLA A*0301	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.357782	0.911989	-3.445793	22792.002890
HLA A*3002	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.240658	0.794851	-3.445807	17404.370283
HLA A*0216	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.428464	0.982586	-3.445878	26820.347350
HLA B*1501	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.346110	0.900174	-3.445936	22187.596016
HLA B*5101	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.496917	1.050933	-3.445983	31399.059778
HLA B*1509	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.480513	1.034513	-3.445999	30235.178670
HLA A*3301	1:238-246	9	SAVAAALVQ	1.200798	-0.028123	-4.618679	1.172675	-3.446003	41560.302876
HLA B*0801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.433330	0.987241	-3.446089	27122.528957
HLA A*2902	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.415324	0.969193	-3.446130	26020.984768
HLA A*6901	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.367133	0.920891	-3.446242	23288.066984
HLA B*4403	1:84-92	9	DLGVPVLGI	1.157263	0.052896	-4.656402	1.210159	-3.446243	45331.703035
HLA B*3901	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.346484	0.900174	-3.446310	22206.689384
HLA B*3901	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.467243	1.020890	-3.446353	29325.312450
HLA B*4403	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.374013	0.927581	-3.446432	23659.890682
HLA B*0802	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.475135	1.028547	-3.446588	29863.077970
HLA A*2301	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.489967	1.043287	-3.446680	30900.596781
HLA B*0801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.374304	0.927581	-3.446723	23675.767683
HLA A*6901	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.366974	0.920085	-3.446889	23279.501521
HLA A*0211	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.526229	1.079304	-3.446925	33591.455231
HLA A*6801	1:137-145	9	VWMSHGDAV	0.981503	0.233995	-4.662450	1.215498	-3.446951	45967.365019
HLA A*2403	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.347097	0.900138	-3.446959	22238.066956
HLA A*3301	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.568827	1.121826	-3.447001	37053.337404
HLA B*5701	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.321673	0.874608	-3.447066	20973.613292
HLA A*0212	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.374882	0.927581	-3.447301	23707.297145
HLA B*5301	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.490604	1.043287	-3.447317	30945.932751
HLA B*5301	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.573226	1.125828	-3.447397	37430.494701
HLA A*0201	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.382180	0.934761	-3.447418	24109.019240
HLA A*6802	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.389045	0.941565	-3.447480	24493.155444
HLA B*1509	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.454812	1.007289	-3.447522	28497.812381
HLA B*0702	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.375131	0.927581	-3.447550	23720.895951
HLA A*0201	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.345281	0.897730	-3.447551	22145.264999
HLA B*4002	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.556504	1.108898	-3.447606	36016.730172
HLA B*7301	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.548124	1.100487	-3.447636	35328.375619
HLA A*2902	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.434888	0.987241	-3.447647	27219.985536
HLA A*2402	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.539586	1.091915	-3.447671	34640.618749
HLA B*5701	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.223430	0.775707	-3.447723	16727.442317
HLA B*4601	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.374692	0.926967	-3.447725	23696.910859
HLA A*8001	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.428455	0.980728	-3.447727	26819.766976
HLA A*3001	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.138693	0.690895	-3.447798	13762.363193
HLA A*0211	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.403555	0.955413	-3.448143	25325.332623
HLA A*6901	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.389712	0.941565	-3.448147	24530.815860
HLA A*2403	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.376097	0.927581	-3.448516	23773.697199
HLA B*4801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.376130	0.927581	-3.448549	23775.497850
HLA A*0212	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.435835	0.987241	-3.448594	27279.394887
HLA A*2402	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.557559	1.108898	-3.448661	36104.322598
HLA A*2603	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.630929	1.182210	-3.448719	42749.291232
HLA A*2902	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.409145	0.960386	-3.448759	25653.379325
HLA B*5801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.346531	0.897730	-3.448801	22209.092228
HLA A*3002	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.572006	1.123169	-3.448837	37325.547287
HLA A*2603	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.575312	1.126421	-3.448891	37610.742715
HLA A*3001	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.201669	0.752770	-3.448899	15909.942528
HLA B*0702	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.330484	0.881518	-3.448966	21403.452098
HLA A*3301	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.589813	1.140721	-3.449091	38887.760300
HLA B*4002	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.639554	1.190433	-3.449121	43606.765874
HLA A*0202	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.526755	1.077535	-3.449220	33632.186540
HLA B*5801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.350800	0.901531	-3.449269	22428.478959
HLA A*2402	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.477637	1.028301	-3.449335	30035.631657
HLA A*3101	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.222020	0.772641	-3.449379	16673.234177
HLA B*3501	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.263282	0.813884	-3.449398	18335.024961
HLA A*6801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.456719	1.007289	-3.449430	28623.273789
HLA A*3301	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.631641	1.182210	-3.449431	42819.423181
HLA B*3801	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.528752	1.079304	-3.449448	33787.197109
HLA A*8001	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.418740	0.969193	-3.449546	26226.472404
HLA A*0216	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.257363	0.807776	-3.449587	18086.858994

HLA A*0203	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.351291	0.901531	-3.449760	22453.852438
HLA A*3002	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.225746	0.775707	-3.450039	16816.907413
HLA B*0801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.362056	0.911989	-3.450067	23017.396793
HLA A*2902	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.353716	0.903619	-3.450096	22579.563017
HLA A*2902	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.370263	0.920085	-3.450178	23456.486234
HLA A*6801	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.589503	1.139224	-3.450278	38860.000255
HLA B*1801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.356526	0.906227	-3.450298	22726.131579
HLA B*4402	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.383390	0.932998	-3.450392	24176.282866
HLA B*5701	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.373038	0.922498	-3.450539	23606.831351
HLA B*4801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.353018	0.902388	-3.450630	22543.312726
HLA B*1801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.494696	1.044058	-3.450639	31238.946570
HLA A*2301	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.544740	1.094025	-3.450716	35054.228305
HLA A*2301	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.507123	1.056396	-3.450727	32145.694016
HLA A*0211	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.354390	0.903619	-3.450770	22614.648139
HLA B*4001	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.357075	0.906227	-3.450848	22754.919126
HLA A*0202	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.252199	0.801202	-3.450997	17873.062942
HLA B*0802	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.357244	0.906227	-3.451017	22763.784167
HLA A*0219	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.258827	0.807776	-3.451050	18147.921080
HLA B*2705	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.472188	1.020917	-3.451271	29661.172458
HLA B*4002	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.504085	1.052564	-3.451521	31921.619926
HLA A*0250	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.577579	1.126026	-3.451553	37807.604631
HLA B*3901	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.472501	1.020917	-3.451584	29682.521804
HLA B*0803	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.485073	1.033365	-3.451708	30554.338784
HLA B*5301	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.577793	1.126026	-3.451767	37826.221894
HLA A*2403	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.393417	0.941565	-3.451852	24740.993223
HLA A*2902	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.414842	0.962975	-3.451868	25992.142783
HLA A*2601	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.384997	0.932998	-3.451999	24265.909640
HLA A*8001	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.414983	0.962975	-3.452009	26000.581029
HLA A*2601	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-3.293936	-0.158117	-3.452053	1967.594873
HLA A*0101	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.358866	0.906788	-3.452078	22848.916148
HLA B*3501	1:294-302	9	EALSGVSAP	0.479426	0.006871	-3.938399	0.486297	-3.452103	8677.595829
HLA B*4601	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.358353	0.906227	-3.452126	22821.985029
HLA A*2902	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.432870	0.980728	-3.452142	27093.785143
HLA B*0702	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.309346	0.857166	-3.452179	20386.633172
HLA A*3101	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.379771	0.927581	-3.452191	23975.701415
HLA B*5401	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.486734	1.034513	-3.452221	30671.426538
HLA A*0219	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.230405	0.778023	-3.452382	16998.287168
HLA A*3201	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.561549	1.109115	-3.452434	36437.504569
HLA B*0702	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.228072	0.775634	-3.452438	16907.216865
HLA A*3301	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.233683	0.781170	-3.452513	17127.055043
HLA A*1101	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.413040	0.960386	-3.452654	25884.514825
HLA A*3002	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.495975	1.043287	-3.452688	31331.017570
HLA B*4501	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.525583	1.072837	-3.452745	33541.517723
HLA B*0803	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.481107	1.028301	-3.452806	30276.589952
HLA B*5701	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.857197	0.404390	-3.452807	7197.746015
HLA B*3501	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.345420	0.892605	-3.452814	22152.334530
HLA B*5801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.356450	0.903619	-3.452831	22722.197652
HLA B*3901	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.496893	1.044058	-3.452836	31397.361170
HLA B*4001	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.379957	0.926967	-3.452990	23985.950370
HLA B*4402	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.382750	0.929716	-3.453035	24140.733872
HLA A*0202	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.568905	1.115576	-3.453329	37059.952991
HLA A*8001	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.359570	0.906227	-3.453343	22886.029288
HLA A*2403	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.357024	0.903619	-3.453404	22752.211052
HLA A*0301	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.353617	0.900174	-3.453443	22574.433176
HLA B*0803	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.458620	1.005151	-3.453469	28748.820953
HLA A*0219	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.440825	0.987241	-3.453584	27594.659447
HLA B*1517	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.373745	0.920085	-3.453660	23645.303479
HLA B*1502	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.547713	1.094025	-3.453688	35294.944993
HLA A*2301	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.366729	0.912830	-3.453900	23266.407494
HLA A*1101	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.461298	1.007289	-3.454009	28926.670658
HLA A*0101	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.374941	0.920891	-3.454050	23710.503708
HLA B*4001	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.359415	0.905240	-3.454175	22877.859228
HLA A*0216	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.355745	0.901531	-3.454215	22685.350190
HLA B*0702	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.417020	0.962750	-3.454270	26122.819924
HLA B*4801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.417058	0.962750	-3.454307	26125.081167

HLA A*2403	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.441659	0.987241	-3.454418	27647.706206
HLA A*3001	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.240792	0.786323	-3.454470	17409.737986
HLA A*2501	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.238227	0.783681	-3.454546	17307.191436
HLA A*0101	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.360987	0.906227	-3.454760	22960.809155
HLA B*3901	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.472005	1.017228	-3.454777	29648.658933
HLA A*0101	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.370040	0.915104	-3.454936	23444.434117
HLA B*4403	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-3.533433	0.078424	-3.455009	3415.330885
HLA A*0101	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.382692	0.927581	-3.455111	24137.469126
HLA B*4801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-3.689791	0.234640	-3.455151	4895.431887
HLA A*2501	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.482350	1.027198	-3.455152	30363.360549
HLA B*1502	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.578362	1.123169	-3.455192	37875.776157
HLA B*4801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.390048	0.934761	-3.455287	24549.800589
HLA B*0803	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.483022	1.027198	-3.455824	30410.375961
HLA B*4402	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.436563	0.980728	-3.455835	27325.182606
HLA A*8001	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.357437	0.901531	-3.455906	22773.884670
HLA B*5801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.356138	0.900174	-3.455964	22705.854565
HLA B*2705	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.461118	1.005094	-3.456024	28914.623431
HLA B*5801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.318248	0.862117	-3.456131	20808.832154
HLA B*5301	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.596622	1.140437	-3.456185	39502.241401
HLA A*0301	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.358377	0.902116	-3.456261	22823.219707
HLA A*6802	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.183540	0.727191	-3.456349	15259.488792
HLA A*3101	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.411790	0.955413	-3.456378	25810.124713
HLA A*0201	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.232109	0.775707	-3.456402	17065.088250
HLA A*3002	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.569910	1.113445	-3.456466	37145.862233
HLA B*5301	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.570369	1.113845	-3.456524	37185.069134
HLA A*0219	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.363355	0.906788	-3.456568	23086.360325
HLA A*2601	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.379203	0.922498	-3.456704	23944.333129
HLA B*1517	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.484030	1.027198	-3.456831	30481.035616
HLA B*4501	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.597573	1.140721	-3.456852	39588.885898
HLA B*1801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.331560	0.874608	-3.456952	21456.549811
HLA B*1501	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.377192	0.920085	-3.457107	23833.706498
HLA A*0101	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.349773	0.892605	-3.457168	22375.517936
HLA B*3501	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.380046	0.922498	-3.457548	23990.881808
HLA B*0702	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.444838	0.987241	-3.457597	27850.818245
HLA B*2705	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.474834	1.017228	-3.457606	29842.405968
HLA A*8001	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.401354	0.943730	-3.457624	25197.281661
HLA B*0802	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.475026	1.017228	-3.457799	29855.647322
HLA A*2301	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.494783	1.036964	-3.457820	31245.200168
HLA A*2902	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.359420	0.901531	-3.457889	22878.106763
HLA A*2602	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.247432	0.789472	-3.457960	17677.949125
HLA A*0212	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.420760	0.962750	-3.458010	26348.775477
HLA A*0301	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.358318	0.900138	-3.458181	22820.133138
HLA A*0216	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.486767	1.028547	-3.458220	30673.749633
HLA B*4501	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.521227	1.062990	-3.458237	33206.780003
HLA A*2601	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.379276	0.920891	-3.458384	23948.349087
HLA B*5101	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.485627	1.027198	-3.458429	30593.373455
HLA B*1801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.495411	1.036964	-3.458447	31290.364608
HLA A*2601	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.400127	0.941565	-3.458562	25126.225869
HLA B*3901	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.367296	0.908582	-3.458714	23296.761631
HLA B*5401	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.479798	1.020917	-3.458881	30185.494572
HLA A*0216	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.213604	0.754590	-3.459014	16353.246934
HLA B*0803	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.421994	0.962975	-3.459019	26423.717427
HLA B*0702	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.374130	0.915104	-3.459026	23666.291417
HLA B*5801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.361450	0.902388	-3.459062	22985.292639
HLA B*4001	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.371976	0.912830	-3.459146	23549.176796
HLA A*3002	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.553250	1.094025	-3.459225	35747.876224
HLA A*0203	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.240459	0.781170	-3.459289	17396.368887
HLA A*6801	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.590403	1.131046	-3.459357	38940.601165
HLA B*4402	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.414802	0.955413	-3.459390	25989.752444
HLA A*0201	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.363111	0.903619	-3.459492	23073.374935
HLA B*4601	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.401069	0.941565	-3.459504	25180.793004
HLA A*0301	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.368087	0.908582	-3.459505	23339.273458
HLA A*3201	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.494076	1.034513	-3.459563	31194.362616
HLA B*1801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.191115	0.731526	-3.459589	15527.971462
HLA B*7301	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.503039	1.043307	-3.459733	31844.864225

HLA B*4801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.422887	0.962975	-3.459912	26478.094066
HLA A*0216	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.278981	0.819048	-3.459933	19009.940796
HLA A*2603	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.134191	0.674222	-3.459970	13620.448284
HLA B*7301	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.210211	0.750232	-3.459980	16225.995018
HLA A*2601	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.387736	0.927581	-3.460155	24419.461105
HLA A*0206	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.380377	0.920085	-3.460292	24009.188899
HLA B*0801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.367098	0.906788	-3.460311	23286.177273
HLA B*5101	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.381787	0.921448	-3.460340	24087.247747
HLA B*4001	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.382894	0.922498	-3.460395	24148.701707
HLA A*2501	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.317562	0.857166	-3.460396	20775.986649
HLA A*1101	1:208-216	9	PANIANALI	0.995189	0.008861	-4.464461	1.004050	-3.460411	29138.075067
HLA A*6901	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.322528	0.862117	-3.460412	21014.955216
HLA A*3201	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.504635	1.044058	-3.460577	31962.055542
HLA B*1509	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.416052	0.955413	-3.460640	26064.660281
HLA A*0301	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.360513	0.899837	-3.460675	22935.731343
HLA B*3901	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.465842	1.005094	-3.460749	29230.911294
HLA A*3101	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.360990	0.900174	-3.460815	22960.933371
HLA A*2501	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.481831	1.020917	-3.460913	30327.080247
HLA B*1509	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.466228	1.005151	-3.461077	29256.857104
HLA A*0203	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.423843	0.962750	-3.461093	26536.458422
HLA A*6801	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.587536	1.126421	-3.461115	38684.436956
HLA A*3002	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.388084	0.926967	-3.461117	24439.020707
HLA A*2301	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.489610	1.028301	-3.461308	30875.197567
HLA B*3801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.494786	1.033365	-3.461421	31245.369201
HLA B*4801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.421815	0.960386	-3.461429	26412.855507
HLA B*5401	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.538989	1.077535	-3.461453	34593.051353
HLA A*2301	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.505572	1.044058	-3.461515	32031.121616
HLA A*3201	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.512498	1.050933	-3.461565	32546.060556
HLA B*3501	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.057133	0.595350	-3.461783	11405.990157
HLA A*1101	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.394808	0.932998	-3.461810	24820.357093
HLA A*0212	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.324091	0.862117	-3.461974	21090.694277
HLA B*4601	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.382118	0.920085	-3.462033	24105.628374
HLA A*0101	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.382274	0.920085	-3.462188	24114.236890
HLA B*1503	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.467301	1.005094	-3.462208	29329.278886
HLA A*3101	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.276246	0.813920	-3.462326	18890.609206
HLA A*2601	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.397092	0.934761	-3.462331	24951.216517
HLA B*4402	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.406194	0.943730	-3.462464	25479.660075
HLA A*0301	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.360219	0.897730	-3.462489	22920.226615
HLA A*2603	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.425546	0.962975	-3.462572	26640.743291
HLA B*5401	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.505948	1.043287	-3.462661	32058.859190
HLA B*5701	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.418082	0.955413	-3.462670	26186.775431
HLA B*1517	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.276112	0.813260	-3.462852	18884.784926
HLA B*4501	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.395983	0.932998	-3.462985	24887.585667
HLA A*2301	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.483943	1.020890	-3.463053	30474.934963
HLA A*6801	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.614929	1.151838	-3.463091	41203.008305
HLA A*0219	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.390699	0.927581	-3.463118	24586.617008
HLA B*4403	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.363471	0.900174	-3.463296	23092.480974
HLA B*4402	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.384188	0.920891	-3.463297	24220.792732
HLA A*0216	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.287979	0.824605	-3.463374	19407.933341
HLA A*2402	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.578956	1.115576	-3.463380	37927.652299
HLA A*3101	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.367084	0.903619	-3.463465	23285.421431
HLA B*1801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-3.460359	-0.003120	-3.463479	2886.417194
HLA A*3201	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.550969	1.087303	-3.463666	35560.584897
HLA A*8001	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.419118	0.955413	-3.463706	26249.325407
HLA A*0203	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.282164	0.818458	-3.463706	19149.803260
HLA A*0206	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.019038	0.555251	-3.463788	10448.126993
HLA A*6802	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.282350	0.818458	-3.463892	19157.989276
HLA A*6801	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.604403	1.140437	-3.463967	40216.403813
HLA A*2301	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.375975	0.911989	-3.463985	23767.010260
HLA B*0803	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.516554	1.052564	-3.463990	32851.381621
HLA A*2402	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.541557	1.077535	-3.464021	34798.206315
HLA A*3101	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.376853	0.912830	-3.464024	23815.146698
HLA A*0101	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.361779	0.897730	-3.464049	23002.707937
HLA B*5801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.356674	0.892605	-3.464068	22733.878488
HLA A*0211	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.520473	1.056396	-3.464076	33149.164001

HLA A*6801	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.646309	1.182210	-3.464099	44290.302602
HLA B*4402	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.397291	0.933159	-3.464132	24962.692737
HLA B*0801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.426935	0.962750	-3.464184	26726.056572
HLA A*0101	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.372866	0.908582	-3.464284	23597.510337
HLA B*5701	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.391996	0.927581	-3.464415	24660.148748
HLA A*0301	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.368104	0.903619	-3.464484	23340.157315
HLA A*0250	1:208-216	9	PANIANALI	0.995189	0.008861	-4.468535	1.004050	-3.464485	29412.698070
HLA B*0801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.386987	0.922498	-3.464488	24377.355449
HLA A*3301	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.326654	0.862117	-3.464538	21215.543622
HLA A*3101	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.373223	0.908582	-3.464641	23616.922624
HLA A*3101	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.399411	0.934761	-3.464650	25084.801374
HLA B*5301	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.491301	1.026553	-3.464748	30995.694695
HLA B*3501	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.399519	0.934761	-3.464758	25091.044627
HLA B*4403	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.590588	1.125828	-3.464760	38957.247204
HLA B*4601	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.237510	0.772641	-3.464869	17278.657837
HLA B*4001	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.364775	0.899837	-3.464937	23161.920075
HLA A*2601	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.377777	0.912830	-3.464947	23865.833622
HLA B*3901	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.492248	1.027198	-3.465050	31063.344772
HLA A*0301	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.367479	0.902388	-3.465091	23306.594271
HLA A*2402	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.574243	1.109115	-3.465128	37518.277736
HLA B*0801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.371400	0.906227	-3.465173	23517.984855
HLA A*0212	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.357832	0.892605	-3.465227	22794.592383
HLA B*4001	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.365367	0.900138	-3.465229	23193.518071
HLA A*2501	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.452478	0.987241	-3.465238	28345.132033
HLA A*3101	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.406953	0.941565	-3.465387	25524.222007
HLA A*3201	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.605912	1.140437	-3.465475	40356.324211
HLA A*3201	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.591582	1.126026	-3.465556	39046.498392
HLA B*5301	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.581320	1.115576	-3.465743	38134.630512
HLA A*2403	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.377791	0.911989	-3.465801	23866.608303
HLA A*0301	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.367401	0.901531	-3.465870	23302.433802
HLA B*4001	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.374541	0.908582	-3.465960	23688.707629
HLA B*5101	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.494548	1.028547	-3.466001	31228.301432
HLA A*6901	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.218801	0.752770	-3.466031	16550.116510
HLA A*3001	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.255559	0.789472	-3.466087	18011.867700
HLA B*7301	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.557576	1.091476	-3.466100	36105.689867
HLA A*3301	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.575016	1.108898	-3.466118	37585.114237
HLA B*2705	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.399286	0.933159	-3.466127	25077.609988
HLA B*4402	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.284612	0.818458	-3.466154	19258.057535
HLA A*0219	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.363926	0.897730	-3.466196	23116.729683
HLA B*2705	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.400975	0.934761	-3.466214	25175.344582
HLA A*0206	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.494840	1.028547	-3.466293	31249.257225
HLA A*6801	1:316-324	9	AFEGAVRDV	0.937984	0.265821	-4.670168	1.203805	-3.466363	46791.575425
HLA B*5401	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.449006	0.982586	-3.466419	28119.393254
HLA A*0201	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.386510	0.920085	-3.466425	24350.598749
HLA B*7301	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.471584	1.005094	-3.466491	29619.961954
HLA B*0803	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.510598	1.044058	-3.466540	32403.930707
HLA B*4501	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.280430	0.813884	-3.466547	19073.500126
HLA A*0206	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.368170	0.901531	-3.466639	23343.693077
HLA A*0202	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.217044	0.750232	-3.466812	16483.280178
HLA A*2602	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.582433	1.115576	-3.466857	38232.544153
HLA A*3001	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.221559	0.754547	-3.467012	16655.564279
HLA A*6901	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.242326	0.775312	-3.467015	17471.349391
HLA A*3002	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.539924	1.072837	-3.467087	34667.615138
HLA B*0803	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.474397	1.007289	-3.467108	29812.392467
HLA A*0212	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.245151	0.778023	-3.467128	17585.330293
HLA B*4002	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.593624	1.126421	-3.467203	39230.495707
HLA B*4801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.422732	0.955413	-3.467319	26468.641679
HLA A*3101	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.388258	0.920891	-3.467366	24448.806383
HLA A*2603	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.544917	1.077535	-3.467381	35068.454152
HLA A*3201	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.248623	0.781170	-3.467454	17726.503004
HLA A*2501	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.411212	0.943730	-3.467483	25775.798601
HLA A*6901	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.374377	0.906788	-3.467589	23679.738597
HLA B*5801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.349125	0.881518	-3.467607	22342.133323
HLA B*4403	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.589449	1.121826	-3.467622	38855.165305
HLA B*4501	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.627179	1.159455	-3.467724	42381.774910

HLA B*4402	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.389197	0.921448	-3.467750	24501.769800
HLA B*7301	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.524197	1.056396	-3.467800	33434.629422
HLA A*6901	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.286278	0.818458	-3.467820	19332.065803
HLA B*1501	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.113793	0.645964	-3.467829	12995.505363
HLA B*5101	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.485061	1.017228	-3.467833	30553.512317
HLA A*1101	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.380843	0.912830	-3.468013	24034.920314
HLA B*4403	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.380182	0.911989	-3.468193	23998.410694
HLA B*1509	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.450956	0.982586	-3.468370	28245.939075
HLA A*6901	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.368569	0.900174	-3.468395	23365.171707
HLA B*5701	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.410002	0.941565	-3.468437	25704.084778
HLA B*3501	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.258770	0.790294	-3.468477	18145.564955
HLA B*3501	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.396098	0.927581	-3.468517	24894.183856
HLA A*3201	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.589357	1.120820	-3.468537	38846.968287
HLA A*0203	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.389576	0.920891	-3.468685	24523.119946
HLA A*0203	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.023944	0.555251	-3.468693	10566.816541
HLA B*4801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.383850	0.915104	-3.468746	24201.931500
HLA B*1501	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.330921	0.862117	-3.468804	21424.999934
HLA B*4601	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.374215	0.905240	-3.468974	23670.901018
HLA A*2601	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.384099	0.915104	-3.468995	24215.814035
HLA B*1502	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.398741	0.929716	-3.469025	25046.154966
HLA B*2705	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.374370	0.905240	-3.469130	23679.354286
HLA A*0216	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.350708	0.881518	-3.469190	22423.747371
HLA B*0702	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.390215	0.920891	-3.469324	24559.232031
HLA A*6802	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.369523	0.900174	-3.469349	23416.547721
HLA B*7301	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.513483	1.044058	-3.469425	32619.917805
HLA B*4601	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.369373	0.899837	-3.469535	23408.441545
HLA A*0212	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.259020	0.789472	-3.469548	18155.973481
HLA A*0219	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.222391	0.752770	-3.469621	16687.491925
HLA B*5701	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.391117	0.921448	-3.469669	24610.304347
HLA B*4801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.438884	0.969193	-3.469691	27471.625920
HLA B*4403	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.621562	1.151838	-3.469723	41837.095070
HLA A*3301	1:157-165	9	SSAGAPVAA	1.242787	-0.116959	-4.595555	1.125828	-3.469727	39405.339402
HLA B*4601	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.397341	0.927581	-3.469760	24965.528852
HLA A*0212	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.283760	0.813884	-3.469876	19220.275869
HLA A*2501	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.371456	0.901531	-3.469926	23521.038566
HLA A*2902	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.403024	0.932998	-3.470026	25294.387908
HLA B*1503	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.392567	0.922498	-3.470068	24692.588373
HLA A*6901	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.373764	0.903619	-3.470144	23646.326849
HLA B*7301	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.543063	1.072837	-3.470226	34919.086880
HLA A*3002	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.025683	0.555251	-3.470432	10609.203655
HLA B*5401	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.400167	0.929716	-3.470451	25128.536787
HLA A*0211	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.521441	1.050933	-3.470507	33223.131723
HLA A*0202	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.245846	0.775312	-3.470534	17613.512719
HLA A*2601	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.368334	0.897730	-3.470604	23352.534827
HLA A*2403	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.403649	0.932998	-3.470651	25330.813506
HLA A*0211	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.379360	0.908582	-3.470778	23953.013626
HLA B*3901	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.385894	0.915104	-3.470790	24316.108879
HLA A*2601	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.372923	0.902116	-3.470807	23600.574374
HLA A*0301	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.363452	0.892605	-3.470847	23091.481574
HLA B*4601	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.382861	0.911989	-3.470871	24146.872792
HLA A*0250	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.488111	1.017228	-3.470883	30768.815232
HLA B*0803	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.458124	0.987241	-3.470883	28716.023281
HLA A*0211	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.393553	0.922498	-3.471055	24748.757511
HLA A*8001	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.412622	0.941565	-3.471057	25859.601063
HLA A*8001	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.371348	0.900138	-3.471211	23515.185969
HLA A*2602	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.483966	1.012736	-3.471230	30476.583667
HLA A*2603	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.586890	1.115576	-3.471314	38626.928153
HLA B*4001	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.386444	0.915104	-3.471340	24346.910475
HLA B*4403	1:335-343	9	QGTLYPDVV	1.152597	0.029613	-4.653749	1.182210	-3.471540	45055.671479
HLA A*0201	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-3.905027	0.433361	-3.471666	8035.766957
HLA B*4402	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.406593	0.934761	-3.471832	25503.104017
HLA A*2501	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.500403	1.028547	-3.471856	31652.154678
HLA B*0802	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.393363	0.921448	-3.471916	24737.914956
HLA A*0202	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.551251	1.079304	-3.471947	35583.677851
HLA B*7301	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.611207	1.139224	-3.471983	40851.437337

HLA B*3801	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.500323	1.028301	-3.472022	31646.333236
HLA B*5301	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.603137	1.131046	-3.472091	40099.306392
HLA A*8001	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.405273	0.932998	-3.472275	25425.683211
HLA A*0203	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.316053	0.843518	-3.472535	20703.953718
HLA A*3101	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.372692	0.900138	-3.472555	23588.065394
HLA B*4403	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.588234	1.115576	-3.472658	38746.642635
HLA B*1502	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.489913	1.017185	-3.472728	30896.752137
HLA B*3801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.535768	1.062990	-3.472778	34337.425300
HLA B*1501	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.373172	0.900138	-3.473034	23614.111963
HLA A*2501	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.442284	0.969193	-3.473091	27687.520740
HLA B*2705	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.406093	0.932998	-3.473095	25473.733552
HLA B*4801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.406281	0.933159	-3.473121	25484.760744
HLA A*0202	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.524072	1.050933	-3.473139	33425.044282
HLA B*0702	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.407902	0.934761	-3.473141	25580.068631
HLA B*5101	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.414786	0.941565	-3.473221	25988.768251
HLA A*6802	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.436039	0.962750	-3.473289	27292.237239
HLA B*1801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.490580	1.017228	-3.473352	30944.258656
HLA B*3801	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.455939	0.982586	-3.473353	28571.910149
HLA B*0801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.268293	0.794851	-3.473442	18547.823608
HLA B*1801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.375695	0.902116	-3.473579	23751.714534
HLA A*6801	1:322-330	9	RDVLDGKTA	1.412297	-0.204875	-4.681013	1.207422	-3.473591	47974.768800
HLA A*0216	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.371341	0.897730	-3.473611	23514.804328
HLA A*0201	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.375157	0.901531	-3.473626	23722.307595
HLA A*0211	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.401255	0.927581	-3.473674	25191.557103
HLA B*4501	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.490991	1.017228	-3.473763	30973.568404
HLA A*3301	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.612716	1.138932	-3.473783	40993.567135
HLA B*1517	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.502830	1.028966	-3.473864	31829.535246
HLA B*4501	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.604920	1.131046	-3.473874	40264.296891
HLA A*2602	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.551537	1.077535	-3.474002	35607.171061
HLA A*0211	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.293261	0.819048	-3.474213	19645.402635
HLA A*3201	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.588077	1.113845	-3.474232	38732.600973
HLA A*2601	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.394503	0.920085	-3.474418	24802.907430
HLA A*3101	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.192863	0.718317	-3.474546	15590.596835
HLA B*4403	1:389-397	9	ELGLPEEIV	1.148424	0.042009	-4.665041	1.190433	-3.474608	46242.477234
HLA B*3901	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.401777	0.926967	-3.474810	25221.830222
HLA B*5401	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.537821	1.062990	-3.474831	34500.165428
HLA B*2705	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.437841	0.962975	-3.474867	27405.718514
HLA A*0101	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.377302	0.902388	-3.474914	23839.767341
HLA A*2603	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.508307	1.033365	-3.474942	32233.461553
HLA A*0201	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.395842	0.920891	-3.474951	24879.508633
HLA A*8001	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.387865	0.912830	-3.475036	24426.728047
HLA B*4002	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-3.736320	0.261282	-3.475038	5449.042728
HLA B*1509	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.375427	0.900174	-3.475253	23737.070718
HLA B*4002	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.634756	1.159455	-3.475301	43127.693237
HLA B*4403	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.552844	1.077535	-3.475308	35714.435051
HLA A*2501	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.396798	0.921448	-3.475350	24934.349307
HLA A*0219	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.395515	0.920085	-3.475430	24860.806907
HLA B*2705	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.456273	0.980728	-3.475545	28593.867645
HLA A*8001	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.402526	0.926967	-3.475559	25265.394492
HLA A*2601	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.387558	0.911989	-3.475568	24409.423068
HLA B*4402	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.438565	0.962975	-3.475590	27451.421244
HLA B*1509	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.502807	1.027198	-3.475609	31827.813350
HLA B*4002	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.567758	1.091915	-3.475844	36962.242791
HLA A*0206	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.431335	0.955413	-3.475923	26998.240939
HLA A*2403	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.398422	0.922498	-3.475923	25027.734162
HLA B*4501	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.623194	1.147258	-3.475936	41994.693322
HLA A*0206	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.226193	0.750232	-3.475961	16834.202045
HLA A*3002	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.397714	0.921448	-3.476267	24987.012749
HLA B*0801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.389233	0.912830	-3.476403	24503.758159
HLA B*4001	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.304834	0.828408	-3.476427	20175.973429
HLA A*6802	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.388474	0.911989	-3.476484	24460.977822
HLA A*0201	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.290420	0.813884	-3.476537	19517.330069
HLA A*2902	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.411409	0.934761	-3.476648	25787.514576
HLA B*0803	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.505271	1.028547	-3.476725	32008.948838
HLA B*4002	1:114-122	9	EYGRTELKV	1.003669	0.148169	-4.628582	1.151838	-3.476744	42518.876770

HLA A*0219	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.380387	0.903619	-3.476768	24009.708453
HLA A*2601	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.385401	0.908582	-3.476819	24288.499600
HLA B*1801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.404488	0.927581	-3.476907	25379.782950
HLA A*3002	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.397033	0.920085	-3.476948	24947.842163
HLA A*0301	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.334229	0.857166	-3.477063	21588.819940
HLA A*1101	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.440099	0.962975	-3.477125	27548.569210
HLA A*2403	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.383498	0.906227	-3.477270	24182.300001
HLA B*0801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.351918	0.874608	-3.477311	22486.309125
HLA A*3001	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.305875	0.828408	-3.477467	20224.384769
HLA B*2705	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.130489	0.652880	-3.477609	13504.814191
HLA A*8001	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.398579	0.920891	-3.477688	25036.807423
HLA B*5401	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.557021	1.079304	-3.477717	36059.621925
HLA B*4002	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.608162	1.130410	-3.477752	40566.020800
HLA A*0212	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.272607	0.794851	-3.477756	18732.968874
HLA A*3101	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.400266	0.922498	-3.477768	25134.247024
HLA B*0702	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.438156	0.960386	-3.477770	27425.592811
HLA B*3901	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.485132	1.007289	-3.477842	30558.471453
HLA B*5101	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.377697	0.899837	-3.477860	23861.444234
HLA B*4002	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.534360	1.056396	-3.477964	34226.334157
HLA B*1801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.498883	1.020890	-3.477993	31541.559526
HLA B*4403	1:11-19	9	ETPARPVLV	1.191696	-0.032241	-4.637460	1.159455	-3.478006	43397.077828
HLA A*0216	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.271242	0.793168	-3.478074	18674.180863
HLA A*0101	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.381811	0.903619	-3.478191	24088.550876
HLA A*3001	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.285874	0.807656	-3.478218	19314.085664
HLA B*1502	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.287888	0.809432	-3.478455	19403.838977
HLA B*0802	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.360050	0.881518	-3.478532	22911.300650
HLA A*6801	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.592482	1.113845	-3.478637	39127.486124
HLA B*2705	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.378792	0.900138	-3.478654	23921.675023
HLA B*1503	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.286314	0.807656	-3.478658	19333.634632
HLA A*0201	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.381054	0.902388	-3.478666	24046.625526
HLA B*7301	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.601896	1.123169	-3.478727	39984.929305
HLA A*2602	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.587959	1.109115	-3.478845	38722.125436
HLA A*3001	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.159256	0.680376	-3.478880	14429.647024
HLA B*2705	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.439272	0.960386	-3.478886	27496.158912
HLA A*1101	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.448087	0.969193	-3.478894	28059.976103
HLA B*4001	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.379092	0.900174	-3.478918	23938.245702
HLA B*4001	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.420495	0.941565	-3.478930	26332.672932
HLA A*3301	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.556511	1.077535	-3.478976	36017.314717
HLA A*0212	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.401488	0.922498	-3.478989	25205.052786
HLA A*1101	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.484220	1.005094	-3.479126	30494.395364
HLA B*4403	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.551984	1.072837	-3.479147	35643.789739
HLA B*3901	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.260427	0.781170	-3.479257	18214.903773
HLA A*0219	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.387877	0.908582	-3.479295	24427.388786
HLA B*4403	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.535335	1.055834	-3.479501	34303.262160
HLA A*0101	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.207740	0.728232	-3.479508	16133.911861
HLA A*2601	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.386312	0.906788	-3.479525	24339.535604
HLA A*0219	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.442345	0.962750	-3.479595	27691.415460
HLA A*2301	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.542631	1.062990	-3.479640	34884.345031
HLA A*2603	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.605728	1.126026	-3.479703	40339.298590
HLA A*0202	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.274597	0.794851	-3.479746	18819.003599
HLA A*2501	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.460518	0.980728	-3.479791	28874.762581
HLA A*3201	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.593349	1.113445	-3.479904	39205.672346
HLA B*5101	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.449260	0.969193	-3.480066	28135.827317
HLA B*3801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.485258	1.005151	-3.480108	30567.399926
HLA B*1503	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-3.933433	0.452913	-3.480520	8578.919785
HLA B*3801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.537046	1.056396	-3.480650	34438.628491
HLA B*0802	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.413848	0.933159	-3.480689	25932.730807
HLA B*4601	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.380864	0.900174	-3.480690	24036.090578
HLA B*4002	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.594690	1.113845	-3.480846	39326.967746
HLA B*4601	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.415707	0.934761	-3.480946	26043.940503
HLA B*1502	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.270452	0.789472	-3.480980	18640.267212
HLA A*0202	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.415812	0.934761	-3.481051	26050.281542
HLA B*1801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.486147	1.005094	-3.481053	30629.972323
HLA A*0201	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.373773	0.892605	-3.481168	23646.838550
HLA A*0203	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.212819	0.731526	-3.481293	16323.724883

HLA B*1503	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.441692	0.960386	-3.481306	27649.800280
HLA B*0801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.212847	0.731526	-3.481322	16324.784632
HLA B*3901	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.289109	0.807776	-3.481333	19458.501589
HLA A*0250	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.597033	1.115576	-3.481457	39539.657090
HLA B*1517	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.468786	0.987241	-3.481545	29429.728779
HLA B*4501	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.510123	1.028547	-3.481576	32368.539111
HLA B*1503	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.508836	1.027198	-3.481637	32272.720819
HLA B*1509	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.450878	0.969193	-3.481685	28240.896881
HLA A*3301	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.508251	1.026553	-3.481698	32229.276718
HLA B*1501	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.390325	0.908582	-3.481743	24565.477373
HLA A*2301	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.469174	0.987241	-3.481933	29456.010416
HLA A*0212	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.383507	0.901531	-3.481976	24182.823301
HLA A*0206	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.423643	0.941565	-3.482078	26524.258687
HLA B*3901	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.469477	0.987241	-3.482236	29476.574224
HLA B*4501	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.503155	1.020890	-3.482265	31853.306926
HLA B*3501	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.402613	0.920085	-3.482528	25270.452269
HLA B*4402	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.382527	0.899837	-3.482690	24128.330184
HLA A*2402	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.412455	0.929716	-3.482739	25849.670243
HLA B*3801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.511288	1.028547	-3.482742	32455.510407
HLA A*2402	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.596601	1.113845	-3.482756	39500.318123
HLA A*0202	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.539158	1.056396	-3.482762	34606.528387
HLA B*5401	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.538604	1.055834	-3.482769	34562.373255
HLA A*2603	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.380666	0.897730	-3.482936	24025.170323
HLA B*4001	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.389747	0.906788	-3.482960	24532.806576
HLA A*2603	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.574560	1.091476	-3.483084	37545.688657
HLA A*0219	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.384703	0.901531	-3.483172	24249.505702
HLA A*2403	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.410277	0.926967	-3.483310	25720.359509
HLA B*4001	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.384940	0.901531	-3.483409	24262.759224
HLA A*0212	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.302478	0.819048	-3.483430	20066.792682
HLA B*4501	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.404911	0.921448	-3.483463	25404.509313
HLA B*1502	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.446372	0.962750	-3.483622	27949.379639
HLA A*2603	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.571064	1.087303	-3.483761	37244.662297
HLA B*4801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.376651	0.892605	-3.484046	23804.069267
HLA B*0702	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.404164	0.920085	-3.484079	25360.842371
HLA B*5101	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.489408	1.005151	-3.484257	30860.836208
HLA B*4002	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.575770	1.091476	-3.484294	37650.440290
HLA B*1502	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.491593	1.007289	-3.484303	31016.494397
HLA B*1801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.511549	1.027198	-3.484351	32475.005719
HLA A*0206	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.471674	0.987241	-3.484433	29626.051727
HLA A*3002	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.563893	1.079304	-3.484589	36634.765216
HLA B*4501	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.540495	1.055834	-3.484661	34713.219260
HLA B*3901	1:208-216	9	PANIANALI	0.995189	0.008861	-4.488719	1.004050	-3.484669	30811.957522
HLA A*6901	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.298702	0.813920	-3.484782	19893.094304
HLA A*6802	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.391608	0.906788	-3.484820	24638.146139
HLA A*0301	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.274390	0.789472	-3.484918	18810.046563
HLA B*4001	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.417927	0.932998	-3.484929	26177.427042
HLA A*0203	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.237731	0.752770	-3.484961	17287.446780
HLA B*1801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.406180	0.920891	-3.485288	25478.833035
HLA B*5701	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.405437	0.920085	-3.485352	25435.313544
HLA B*0803	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.454572	0.969193	-3.485378	28482.091378
HLA B*4001	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.405465	0.920085	-3.485380	25436.964824
HLA A*3002	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.512837	1.027198	-3.485638	32571.424598
HLA A*0216	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.378249	0.892605	-3.485644	23891.799151
HLA B*5801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.293491	0.807776	-3.485715	19655.820783
HLA B*5301	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.594655	1.108898	-3.485757	39323.776558
HLA A*6801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.441215	0.955413	-3.485803	27619.451730
HLA B*4801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.427386	0.941565	-3.485821	26753.831315
HLA B*4501	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.542367	1.056396	-3.485971	34863.214744
HLA A*0219	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.427682	0.941565	-3.486117	26772.074175
HLA A*2501	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.491250	1.005094	-3.486156	30992.005883
HLA B*5701	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.392430	0.906227	-3.486203	24684.841707
HLA A*3001	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.001140	0.514746	-3.486394	10026.285473
HLA B*3901	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.499184	1.012736	-3.486448	31563.408542
HLA A*0212	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.428044	0.941565	-3.486479	26794.387897
HLA B*1503	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.294297	0.807776	-3.486521	19692.327827

HLA A*0216	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.428086	0.941565	-3.486521	26796.997208
HLA B*5701	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.413658	0.926967	-3.486691	25921.369547
HLA A*2902	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.407643	0.920891	-3.486752	25564.850773
HLA A*2403	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.393577	0.906788	-3.486789	24750.096427
HLA A*0301	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.368334	0.881518	-3.486816	23352.534827
HLA B*5101	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.469428	0.982586	-3.486841	29473.225650
HLA A*0101	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.368501	0.881518	-3.486983	23361.506308
HLA B*1501	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.390635	0.903619	-3.487016	24583.025977
HLA B*0702	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.420321	0.933159	-3.487162	26322.133236
HLA B*5301	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.543582	1.056396	-3.487186	34960.860601
HLA A*2301	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.539757	1.052564	-3.487193	34654.301790
HLA A*8001	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.414800	0.927581	-3.487219	25989.611843
HLA B*0803	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.508199	1.020917	-3.487282	32225.441096
HLA B*1801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.468067	0.980728	-3.487340	29381.050341
HLA A*2602	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.626580	1.139224	-3.487356	42323.348640
HLA B*0802	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.450152	0.962750	-3.487402	28193.727260
HLA A*0250	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.530730	1.043287	-3.487444	33941.453132
HLA B*1509	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.380131	0.892605	-3.487526	23995.554631
HLA A*2602	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.531680	1.044058	-3.487622	34015.716535
HLA B*1502	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.540218	1.052564	-3.487654	34691.066560
HLA B*3801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.522218	1.034513	-3.487705	33282.676795
HLA A*3101	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.392975	0.905240	-3.487735	24715.842961
HLA A*0202	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.083104	0.595350	-3.487754	12108.886256
HLA A*3002	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.508786	1.020917	-3.487869	32269.054599
HLA B*4403	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.628793	1.140721	-3.488072	42539.583828
HLA A*6802	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-3.414154	-0.073933	-3.488087	2595.100199
HLA B*3801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.400990	0.912830	-3.488160	25176.161770
HLA B*0801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.302093	0.813884	-3.488209	20048.996881
HLA B*0801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.306686	0.818458	-3.488228	20262.167046
HLA B*3901	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.415817	0.927581	-3.488236	26050.563402
HLA A*2602	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.540831	1.052564	-3.488267	34740.084287
HLA B*4403	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.588798	1.100487	-3.488311	38796.982918
HLA B*4402	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.121852	0.633434	-3.488417	13238.900140
HLA B*3501	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.251811	0.763388	-3.488424	17857.115997
HLA A*2601	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.388636	0.900138	-3.488498	24470.110378
HLA B*1801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.492556	1.004050	-3.488506	31085.367026
HLA B*5701	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.409464	0.920891	-3.488573	25672.260614
HLA A*6802	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.423368	0.934761	-3.488607	26507.475283
HLA B*1509	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.509550	1.020917	-3.488633	32325.840408
HLA B*0801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.408771	0.920085	-3.488686	25631.322485
HLA B*0801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.388845	0.900138	-3.488707	24481.895087
HLA B*5401	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.545112	1.056396	-3.488716	35084.204153
HLA B*4601	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.397376	0.908582	-3.488794	24967.554845
HLA B*7301	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.582837	1.094025	-3.488812	38268.136127
HLA B*4601	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.395623	0.906788	-3.488836	24866.994410
HLA B*1509	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.501599	1.012736	-3.488863	31739.433225
HLA B*4801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.416047	0.926967	-3.489081	26064.378268
HLA A*0212	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.307567	0.818458	-3.489109	20303.314800
HLA B*5301	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.598283	1.109115	-3.489168	39653.618551
HLA A*3301	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.615201	1.126026	-3.489176	41228.873250
HLA B*0802	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.402009	0.912830	-3.489179	25235.342123
HLA A*2601	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.392813	0.903619	-3.489194	24706.618695
HLA B*5401	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.518189	1.028966	-3.489223	32975.309530
HLA A*1101	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.416191	0.926967	-3.489224	26072.981017
HLA A*6801	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.610221	1.120820	-3.489400	40758.721975
HLA A*8001	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.449849	0.960386	-3.489464	28174.058407
HLA A*2301	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.516723	1.027198	-3.489525	32864.180122
HLA A*0201	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.389792	0.900174	-3.489618	24535.328381
HLA A*6802	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.145671	0.656026	-3.489645	13985.274186
HLA A*0250	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.581827	1.091915	-3.489912	38179.218249
HLA B*1517	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.424686	0.934761	-3.489925	26588.046290
HLA A*0101	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.390182	0.900174	-3.490008	24557.372023
HLA B*7301	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.577328	1.087303	-3.490025	37785.725725
HLA B*1801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.523459	1.033365	-3.490094	33377.882056
HLA A*3301	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.527065	1.036964	-3.490102	33656.212043

HLA B*1801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.398689	0.908582	-3.490108	25043.174211
HLA B*5701	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.390067	0.899837	-3.490230	24550.863106
HLA B*5101	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.395748	0.905240	-3.490507	24874.125400
HLA B*1502	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.511411	1.020890	-3.490521	32464.641889
HLA B*1503	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.334046	0.843518	-3.490528	21579.711998
HLA A*2602	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.582125	1.091476	-3.490649	38205.458520
HLA A*0301	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.352931	0.862117	-3.490814	22538.800775
HLA A*8001	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.425596	0.934761	-3.490835	26643.770056
HLA B*2705	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.446248	0.955413	-3.490835	27941.367026
HLA A*3301	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.611734	1.120820	-3.490913	40900.971735
HLA A*3101	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.392503	0.901531	-3.490972	24688.981864
HLA B*2705	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-3.725682	0.234640	-3.491041	5317.184686
HLA A*2301	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.534494	1.043307	-3.491188	34236.889942
HLA B*4402	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.388977	0.897730	-3.491247	24489.313093
HLA A*2402	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.554268	1.062990	-3.491277	35831.713135
HLA A*3101	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.372852	0.881518	-3.491334	23596.744390
HLA B*1503	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.418517	0.926967	-3.491550	26212.997048
HLA A*0201	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.284730	0.793168	-3.491562	19263.267438
HLA A*3201	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.512508	1.020890	-3.491618	32546.764846
HLA B*3801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.454410	0.962750	-3.491659	28471.461500
HLA A*3301	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.605127	1.113445	-3.491682	40283.470089
HLA A*3101	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.384397	0.892605	-3.491792	24232.457370
HLA A*6801	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.535089	1.043287	-3.491802	34283.782124
HLA B*4002	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.403816	0.911989	-3.491826	25340.544994
HLA A*0216	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.394242	0.902388	-3.491854	24788.017812
HLA A*3301	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.618282	1.126421	-3.491861	41522.322850
HLA A*6802	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.335432	0.843518	-3.491914	21648.700912
HLA A*2403	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.397205	0.905240	-3.491964	24957.696558
HLA B*2705	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.391911	0.899837	-3.492074	24655.346503
HLA B*4601	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.384762	0.892605	-3.492156	24252.785603
HLA A*0206	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.543091	1.050933	-3.492158	34921.353855
HLA A*3301	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.536219	1.044058	-3.492161	34373.110069
HLA B*0801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.426925	0.934761	-3.492164	26725.478238
HLA B*4002	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.396328	0.903619	-3.492709	24907.385483
HLA A*3101	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.349898	0.857166	-3.492731	22381.934457
HLA B*7301	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.066225	0.573435	-3.492791	11647.306374
HLA B*5401	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.543824	1.050933	-3.492891	34980.346871
HLA A*0211	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.390741	0.897730	-3.493011	24589.011321
HLA B*4601	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.395456	0.902388	-3.493068	24857.444779
HLA B*3501	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.390920	0.897730	-3.493190	24599.123210
HLA A*0202	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.475830	0.982586	-3.493244	29910.936838
HLA A*0250	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.549782	1.056396	-3.493386	35463.566180
HLA B*4801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.426399	0.932998	-3.493401	26693.111514
HLA B*3901	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.456186	0.962750	-3.493436	28588.144700
HLA A*2601	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.395877	0.902388	-3.493489	24881.527645
HLA B*0802	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.448966	0.955413	-3.493554	28116.807286
HLA B*4403	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.602690	1.109115	-3.493576	40058.110336
HLA A*0202	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.449015	0.955413	-3.493603	28120.001752
HLA B*0803	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.510952	1.017228	-3.493725	32430.412075
HLA B*4403	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.581066	1.087303	-3.493763	38112.356175
HLA A*2301	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.520318	1.026553	-3.493765	33137.330115
HLA A*2501	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.393941	0.900174	-3.493767	24770.858899
HLA B*1801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.514690	1.020917	-3.493773	32710.749686
HLA B*4601	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.397411	0.903619	-3.493792	24969.581003
HLA B*4402	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-3.680487	0.186500	-3.493987	4791.671666
HLA A*6802	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.246772	0.752770	-3.494002	17651.095896
HLA B*4801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.423883	0.929716	-3.494167	26538.899043
HLA B*1503	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.414558	0.920085	-3.494473	25975.133982
HLA B*4002	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.633753	1.139224	-3.494529	43028.182269
HLA A*8001	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.376101	0.881518	-3.494584	23773.954427
HLA A*0211	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.351784	0.857166	-3.494618	22479.376233
HLA B*1503	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.415512	0.920891	-3.494620	26032.248857
HLA B*4402	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.403205	0.908582	-3.494623	25304.926770
HLA B*5801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.308542	0.813884	-3.494658	20348.949060
HLA B*1502	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.603811	1.109115	-3.494696	40161.614465

HLA B*1801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.450329	0.955413	-3.494916	28205.168951
HLA A*3002	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.538249	1.043307	-3.494942	34534.151014
HLA A*2601	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.394994	0.899837	-3.495156	24830.967115
HLA B*1502	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.551023	1.055834	-3.495189	35565.009886
HLA A*0201	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.210822	0.715584	-3.495239	16248.834094
HLA B*0702	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.402336	0.906788	-3.495548	25254.325596
HLA B*4501	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.634777	1.139224	-3.495553	43129.793133
HLA B*5701	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.397686	0.902116	-3.495570	24985.390678
HLA B*7301	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.377128	0.881518	-3.495610	23830.225434
HLA B*4002	1:276-284	9	VAATGANLV	0.993882	0.146839	-4.636420	1.140721	-3.495698	43293.197749
HLA B*5701	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.404396	0.908582	-3.495814	25374.428744
HLA B*4601	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.410940	0.915104	-3.495836	25759.628146
HLA A*8001	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.393631	0.897730	-3.495901	24753.176210
HLA A*2602	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.619090	1.123169	-3.495921	41599.667917
HLA A*6901	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.398323	0.902388	-3.495935	25022.048123
HLA A*0211	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.261905	0.765882	-3.496023	18276.991393
HLA B*1501	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.277200	0.781170	-3.496030	18932.146423
HLA B*0802	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.397902	0.901531	-3.496371	24997.829247
HLA B*4001	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.237334	0.740887	-3.496447	17271.648587
HLA B*4402	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.398029	0.901531	-3.496498	25005.133030
HLA A*3301	1:452-460	9	ADVRSVGVQ	1.203811	-0.063374	-4.636951	1.140437	-3.496514	43346.161897
HLA B*5401	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.417537	0.920891	-3.496646	26153.929176
HLA B*4403	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.610524	1.113845	-3.496679	40787.176424
HLA B*5701	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.389284	0.892605	-3.496679	24506.674710
HLA A*2501	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.429851	0.933159	-3.496691	26906.090228
HLA A*0250	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.574269	1.077535	-3.496733	37520.510470
HLA A*2602	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.590811	1.094025	-3.496787	38977.274017
HLA B*3901	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.477517	0.980728	-3.496789	30027.345839
HLA A*1101	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.459602	0.962750	-3.496852	28813.905190
HLA B*4801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.409737	0.912830	-3.496907	25688.376224
HLA B*4001	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.371553	0.874608	-3.496945	23526.256240
HLA A*6801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.132161	0.635184	-3.496978	13556.932901
HLA B*3501	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.286516	0.789472	-3.497044	19342.631707
HLA B*7301	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.509900	1.012736	-3.497164	32351.907915
HLA B*3801	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.534179	1.036964	-3.497216	34212.079754
HLA A*0212	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.278445	0.781170	-3.497276	18986.507350
HLA B*3801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.526269	1.028966	-3.497303	33594.544716
HLA B*0801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.397540	0.900174	-3.497366	24977.011655
HLA A*2403	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.417476	0.920085	-3.497391	26150.250699
HLA B*1503	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.279225	0.781791	-3.497435	19020.639340
HLA B*4002	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.618336	1.120820	-3.497515	41527.489688
HLA B*7301	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.589510	1.091915	-3.497595	38860.630945
HLA A*3001	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.239397	0.741770	-3.497627	17353.882037
HLA B*7301	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.611116	1.113445	-3.497671	40842.819178
HLA A*3201	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.441509	0.943730	-3.497779	27638.135318
HLA B*1509	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.406363	0.908582	-3.497781	25489.586642
HLA A*8001	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.401497	0.903619	-3.497878	25205.598218
HLA B*2705	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.312019	0.813920	-3.498099	20512.529678
HLA B*4002	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.570970	1.072837	-3.498133	37236.603590
HLA A*0219	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.355508	0.857166	-3.498342	22672.958328
HLA B*5401	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.503653	1.005094	-3.498559	31889.860330
HLA B*0803	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.420063	0.921448	-3.498615	26306.473915
HLA A*6901	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.330552	0.831902	-3.498650	21406.810281
HLA A*8001	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.373313	0.874608	-3.498705	23621.778191
HLA A*2402	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.592783	1.094025	-3.498758	39154.589954
HLA A*2501	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.428478	0.929716	-3.498763	26821.217935
HLA A*6901	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.308288	0.809432	-3.498856	20337.063293
HLA B*2705	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.373517	0.874608	-3.498909	23632.898642
HLA A*3201	1:208-216	9	PANIANALI	0.995189	0.008861	-4.503187	1.004050	-3.499137	31855.719537
HLA A*2403	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.317667	0.818458	-3.499209	20781.045075
HLA B*3801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.503350	1.004050	-3.499299	31867.612935
HLA B*4402	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.426460	0.926967	-3.499494	26696.866354
HLA B*1501	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.275193	0.775634	-3.499559	18844.880789
HLA A*0201	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.381103	0.881518	-3.499586	24049.357562
HLA B*4801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.422125	0.922498	-3.499627	26431.723805

HLA A*1101	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.432797	0.933159	-3.499637	27089.241718
HLA A*2501	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.462461	0.962750	-3.499711	29004.237060
HLA B*4402	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.403377	0.903619	-3.499757	25314.922213
HLA A*2602	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.613634	1.113845	-3.499789	41080.371235
HLA A*0201	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.318842	0.819048	-3.499794	20837.332743
HLA A*2301	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.507144	1.007289	-3.499855	32147.259196
HLA B*7301	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.555743	1.055834	-3.499909	35953.655196
HLA B*0702	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.426984	0.926967	-3.500018	26729.093030
HLA A*0203	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.294875	0.794851	-3.500024	19718.552467
HLA B*1509	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-3.239855	-0.260222	-3.500078	1737.221664
HLA B*1509	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.505192	1.005094	-3.500098	32003.061774
HLA A*0211	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.487455	0.987241	-3.500214	30722.409072
HLA B*4403	1:422-430	9	TLRHADSIV	1.051790	0.095468	-4.647516	1.147258	-3.500258	44413.631284
HLA B*1509	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.281549	0.781170	-3.500379	19122.679729
HLA A*0203	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.420641	0.920085	-3.500556	26341.506738
HLA A*2403	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.409177	0.908582	-3.500596	25655.322346
HLA A*2902	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.253533	0.752770	-3.500764	17928.068061
HLA B*5701	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.412791	0.911989	-3.500802	25869.675651
HLA A*2301	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.434063	0.933159	-3.500904	27168.347335
HLA A*2601	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.401140	0.900174	-3.500966	25184.880095
HLA B*4801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.421094	0.920085	-3.501009	26369.024495
HLA A*0250	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.264398	0.763388	-3.501010	18382.201014
HLA B*1801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.136386	0.635184	-3.501202	13689.444348
HLA B*7301	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.530188	1.028966	-3.501222	33899.063520
HLA A*0203	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.435999	0.934761	-3.501238	27289.727338
HLA A*2601	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.393892	0.892605	-3.501286	24768.044899
HLA A*1101	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.436081	0.934761	-3.501320	27294.895032
HLA B*7301	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.627365	1.126026	-3.501339	42399.891957
HLA B*4001	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.403891	0.902388	-3.501503	25344.932239
HLA B*3801	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.552524	1.050933	-3.501591	35688.168001
HLA B*3801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.545661	1.044058	-3.501604	35128.645864
HLA A*2603	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.623502	1.121826	-3.501676	42024.465319
HLA B*4801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.383277	0.881518	-3.501759	24170.005712
HLA A*3201	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.277569	0.775707	-3.501862	18948.233322
HLA A*3101	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.279930	0.778023	-3.501907	19051.534269
HLA A*0250	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.581249	1.079304	-3.501945	38128.441891
HLA A*0212	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.422140	0.920085	-3.502055	26432.581775
HLA B*4501	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.528614	1.026553	-3.502061	33776.414515
HLA A*8001	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.424625	0.922498	-3.502127	26584.306755
HLA B*4002	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.617772	1.115576	-3.502196	41473.606488
HLA A*0211	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.233812	0.731526	-3.502286	17132.151852
HLA B*0802	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.400019	0.897730	-3.502289	25119.973862
HLA A*2603	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.623270	1.120820	-3.502449	42001.963923
HLA B*0802	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.483245	0.980728	-3.502517	30426.009071
HLA A*6901	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.346094	0.843518	-3.502576	22186.755805
HLA B*1502	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.244352	0.741770	-3.502582	17553.014229
HLA B*4501	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.623420	1.120820	-3.502600	42016.508903
HLA B*1501	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.316077	0.813260	-3.502816	20705.073810
HLA A*2501	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.404970	0.902116	-3.502854	25407.945435
HLA B*3801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.490169	0.987241	-3.502928	30914.976643
HLA A*0219	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.395534	0.892605	-3.502929	24861.882884
HLA A*3002	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.465974	0.962975	-3.502999	29239.768251
HLA B*5301	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.580622	1.077535	-3.503086	38073.407386
HLA B*4801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.424313	0.920891	-3.503422	26565.185820
HLA B*5301	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.436446	0.932998	-3.503448	27317.792296
HLA B*4402	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.416308	0.912830	-3.503478	26080.034568
HLA A*6802	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.278812	0.775312	-3.503500	19002.537638
HLA B*5701	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.410329	0.906788	-3.503541	25723.420866
HLA A*2602	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.590912	1.087303	-3.503610	38986.342169
HLA A*2301	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.532161	1.028547	-3.503614	34053.461819
HLA B*3901	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.464031	0.960386	-3.503645	29109.242364
HLA B*1517	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.328329	0.824605	-3.503724	21297.535327
HLA B*0803	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.416599	0.912830	-3.503770	26097.535609
HLA A*0301	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.317113	0.813260	-3.503852	20754.530142
HLA B*5801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.347494	0.843518	-3.503976	22258.407879

HLA A*6801	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.619633	1.115576	-3.504056	41651.686870
HLA A*2602	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.630111	1.126026	-3.504085	42668.885357
HLA A*2402	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.366379	0.862117	-3.504263	23247.660617
HLA A*6901	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.297633	0.793168	-3.504466	19844.187678
HLA A*0250	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.386145	0.881518	-3.504628	24330.188532
HLA B*2705	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.397237	0.892605	-3.504632	24959.586886
HLA A*2602	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.473875	0.969193	-3.504682	29776.609413
HLA B*4601	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.386225	0.881518	-3.504707	24334.664146
HLA B*4601	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.404869	0.900138	-3.504731	25402.035593
HLA B*3501	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.246671	0.741770	-3.504901	17646.990284
HLA A*2402	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.561412	1.056396	-3.505016	36426.073237
HLA A*6901	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.324295	0.819048	-3.505247	21100.623167
HLA B*0702	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.446837	0.941565	-3.505272	27979.333882
HLA B*4403	1:289-297	9	AETFLEALS	0.785461	-0.921388	-3.369401	-0.135927	-3.505328	2340.998528
HLA A*2602	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.556450	1.050933	-3.505517	36012.248981
HLA B*1801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.534168	1.028547	-3.505621	34211.154349
HLA A*3101	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.408012	0.902388	-3.505624	25586.573569
HLA A*6901	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.287627	0.781791	-3.505836	19392.190514
HLA A*0219	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.387426	0.881518	-3.505908	24402.029261
HLA A*8001	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.414492	0.908582	-3.505910	25971.199648
HLA B*3901	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.221503	0.715584	-3.505919	16653.401905
HLA B*0803	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.468671	0.962750	-3.505921	29421.928446
HLA A*0206	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.533150	1.027198	-3.505952	34131.109124
HLA A*6801	1:480-488	9	AMTADWTRV	0.947260	0.174566	-4.627835	1.121826	-3.506008	42445.792527
HLA A*2403	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.380662	0.874608	-3.506054	24024.910377
HLA A*3201	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.621644	1.115576	-3.506067	41845.017512
HLA A*2403	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.320036	0.813920	-3.506116	20894.677156
HLA A*6801	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.511279	1.005151	-3.506128	32454.808092
HLA A*0212	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.406306	0.900174	-3.506132	25486.277356
HLA B*3801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.558706	1.052564	-3.506142	36199.764875
HLA A*2403	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.406032	0.899837	-3.506194	25470.150742
HLA A*3002	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.439192	0.932998	-3.506194	27491.101837
HLA B*1502	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.281845	0.775634	-3.506211	19135.719071
HLA B*3501	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.313904	0.807656	-3.506248	20601.721378
HLA A*3201	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.433983	0.927581	-3.506403	27163.350551
HLA B*3901	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.014993	0.508560	-3.506433	10351.245992
HLA A*3201	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.461900	0.955413	-3.506487	28966.759873
HLA B*4403	1:12-20	9	TPARPVLVV	1.197961	-0.071540	-4.632973	1.126421	-3.506552	42950.969435
HLA B*0802	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.469545	0.962975	-3.506571	29481.199072
HLA B*5701	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.408207	0.901531	-3.506676	25598.065053
HLA B*0702	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.325912	0.819048	-3.506864	21179.306103
HLA B*4601	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.408491	0.901531	-3.506960	25614.826944
HLA B*0702	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.407274	0.900174	-3.507100	25543.146419
HLA B*3501	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.428041	0.920891	-3.507150	26794.242943
HLA A*0203	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.407328	0.900174	-3.507154	25546.324886
HLA B*4402	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.422457	0.915104	-3.507353	26451.893467
HLA B*4601	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.405141	0.897730	-3.507411	25417.981571
HLA A*3001	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.234728	0.727191	-3.507537	17168.336398
HLA B*4002	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.585095	1.077535	-3.507560	38467.606537
HLA B*5701	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.413047	0.905240	-3.507807	25884.934926
HLA B*1801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.477259	0.969193	-3.508065	30009.482247
HLA A*3301	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.623873	1.115576	-3.508297	42060.401612
HLA A*0216	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.365470	0.857166	-3.508304	23199.039600
HLA B*1501	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.301595	0.793168	-3.508427	20026.015938
HLA A*6802	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.429364	0.920891	-3.508473	26875.976387
HLA B*1509	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.552557	1.044058	-3.508500	35690.871070
HLA A*3001	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.224116	0.715584	-3.508532	16753.887333
HLA B*4002	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.609039	1.100487	-3.508552	40647.961158
HLA B*5701	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.408823	0.900138	-3.508685	25634.373244
HLA B*4501	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.634754	1.126026	-3.508728	43127.459922
HLA B*5701	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.409048	0.900174	-3.508874	25647.689897
HLA B*5701	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.412629	0.903619	-3.509009	25860.020760
HLA B*5301	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.546042	1.036964	-3.509078	35159.446176
HLA B*7301	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.560033	1.050933	-3.509100	36310.581893
HLA B*3901	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.383836	0.874608	-3.509228	24201.145934

HLA B*4403	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.648188	1.138932	-3.509256	44482.402499
HLA B*4002	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.596626	1.087303	-3.509324	39502.668808
HLA A*6802	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.285024	0.775634	-3.509389	19276.298361
HLA A*0219	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.415674	0.906227	-3.509447	26041.968050
HLA A*0250	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.514742	1.005094	-3.509648	32714.643071
HLA B*3501	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.310887	0.801202	-3.509685	20459.111568
HLA B*4801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.334403	0.824605	-3.509798	21597.464361
HLA A*0301	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.202228	0.692424	-3.509804	15930.440626
HLA A*3201	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.582800	1.072837	-3.509962	38264.823849
HLA A*2902	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.432468	0.922498	-3.509970	27068.732515
HLA B*0802	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.470459	0.960386	-3.510073	29543.306017
HLA A*2301	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.409922	0.899837	-3.510085	25699.357300
HLA B*5801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.367335	0.857166	-3.510169	23298.904289
HLA B*4001	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.431117	0.920891	-3.510226	26984.661008
HLA A*6801	1:126-134	9	KLHSDLPEV	0.948868	0.190064	-4.649290	1.138932	-3.510358	44595.408242
HLA A*2501	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.423239	0.912830	-3.510409	26499.589319
HLA A*2402	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.517712	1.007289	-3.510423	32939.115676
HLA B*5401	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.527824	1.017228	-3.510596	33715.074125
HLA A*6802	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.372934	0.862117	-3.510818	23601.212765
HLA B*5401	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.411022	0.900174	-3.510848	25764.506094
HLA A*8001	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.411153	0.900174	-3.510979	25772.312731
HLA B*0802	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.413143	0.902116	-3.511027	25890.676982
HLA B*3501	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.304231	0.793168	-3.511063	20147.941427
HLA A*0216	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.411332	0.900174	-3.511158	25782.911237
HLA B*3901	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.466681	0.955413	-3.511269	29287.420393
HLA B*1501	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.412819	0.901531	-3.511288	25871.355130
HLA B*0803	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.516394	1.005094	-3.511300	32839.298725
HLA B*4002	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.642390	1.131046	-3.511344	43892.438219
HLA B*4501	1:176-184	9	VQYHPEVMH	1.181313	-0.103778	-4.589005	1.077535	-3.511469	38815.457405
HLA A*0301	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.355024	0.843518	-3.511506	22647.704815
HLA A*3201	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.474510	0.962975	-3.511535	29820.134996
HLA A*6802	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.431643	0.920085	-3.511558	27017.381251
HLA B*5101	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.415202	0.903619	-3.511582	26013.665724
HLA A*0216	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.434211	0.922498	-3.511713	27177.608511
HLA B*4801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.411851	0.900138	-3.511714	25813.755346
HLA B*4402	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.414125	0.902388	-3.511737	25949.290689
HLA A*3001	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-3.511005	-0.000735	-3.511739	3243.430540
HLA A*0219	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.287556	0.775707	-3.511850	19389.043481
HLA B*1801	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.499092	0.987241	-3.511851	31556.749817
HLA A*2402	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.564481	1.052564	-3.511917	36684.346242
HLA A*8001	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.432022	0.920085	-3.511936	27040.923429
HLA B*5401	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.540493	1.028547	-3.511946	34713.031465
HLA B*1509	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.386665	0.874608	-3.512057	24359.294748
HLA B*7301	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.404739	0.892605	-3.512134	25394.478497
HLA A*2603	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.621251	1.109115	-3.512137	41807.229641
HLA B*0801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.287657	0.775312	-3.512346	19393.554387
HLA A*2601	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.374494	0.862117	-3.512378	23686.144702
HLA B*1503	1:294-302	9	EALSGVSAP	0.479426	0.006871	-3.998678	0.486297	-3.512381	9969.601646
HLA B*2705	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.425215	0.912830	-3.512385	26620.429631
HLA A*2301	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.525230	1.012736	-3.512494	33514.310380
HLA B*5101	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.499842	0.987241	-3.512601	31611.256043
HLA A*3002	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.435104	0.922498	-3.512606	27233.536561
HLA B*2705	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.421188	0.908582	-3.512606	26374.731252
HLA A*3201	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.412819	0.900138	-3.512682	25871.355130
HLA A*6802	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.179395	0.666703	-3.512693	15114.559445
HLA A*0219	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.435327	0.922498	-3.512829	27247.536548
HLA B*1503	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.263133	0.750232	-3.512902	18328.777027
HLA B*7301	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.541207	1.028301	-3.512905	34770.167706
HLA A*6801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.518029	1.005094	-3.512935	32963.181053
HLA B*1801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.424933	0.911989	-3.512944	26603.153611
HLA B*1509	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.454511	0.941565	-3.512946	28478.085451
HLA A*8001	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.405595	0.892605	-3.512989	25444.534564
HLA A*0250	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.564006	1.050933	-3.513073	36644.279572
HLA B*4403	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.547597	1.034513	-3.513084	35285.590087
HLA A*0101	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.332157	0.819048	-3.513109	21486.053776

HLA B*1503	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.447883	0.934761	-3.513122	28046.772492
HLA A*2501	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.440724	0.927581	-3.513143	27588.240980
HLA B*5701	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.394698	0.881518	-3.513180	24814.046952
HLA A*0212	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.261635	0.748391	-3.513244	18265.624132
HLA A*3101	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.306465	0.793168	-3.513297	20251.865754
HLA A*2403	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.405916	0.892605	-3.513311	25463.399893
HLA B*5701	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.411069	0.897730	-3.513339	25767.293907
HLA A*0101	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.370543	0.857166	-3.513376	23471.591837
HLA A*0202	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.279263	0.765882	-3.513381	19022.285804
HLA A*6802	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.413752	0.900138	-3.513614	25926.979424
HLA A*0211	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.540918	1.027198	-3.513720	34747.038764
HLA B*5401	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.411640	0.897730	-3.513910	25801.189945
HLA B*1502	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.557305	1.043307	-3.513999	36083.234158
HLA B*0803	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.425995	0.911989	-3.514006	26668.285101
HLA B*5401	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.292067	0.778023	-3.514045	19591.486795
HLA A*0211	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.416543	0.902388	-3.514155	26094.147394
HLA A*2602	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.593584	1.079304	-3.514280	39226.887919
HLA B*4002	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.640381	1.126026	-3.514355	43689.884524
HLA B*5101	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.407002	0.892605	-3.514397	25527.121919
HLA A*6802	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.215700	0.701295	-3.514405	16432.352220
HLA A*2301	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.535361	1.020917	-3.514444	34305.303566
HLA A*0211	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.543018	1.028547	-3.514471	34915.497805
HLA B*5401	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.435929	0.921448	-3.514481	27285.298666
HLA B*4002	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.637677	1.123169	-3.514507	43418.682355
HLA B*5701	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.416912	0.902388	-3.514524	26116.319941
HLA B*1801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.414372	0.899837	-3.514535	25964.035069
HLA B*1509	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.371856	0.857166	-3.514690	23542.680372
HLA B*3901	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.449509	0.934761	-3.514748	28151.966385
HLA A*0212	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.142043	0.627189	-3.514855	13868.943549
HLA A*1101	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.415105	0.900138	-3.514968	26007.896391
HLA B*4801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.421773	0.906788	-3.514985	26410.283601
HLA A*0206	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-3.805705	0.290570	-3.515135	6393.007360
HLA A*0201	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.372436	0.857166	-3.515270	23574.160133
HLA A*1101	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.420627	0.905240	-3.515386	26340.651724
HLA A*2403	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.301832	0.786323	-3.515509	20036.961119
HLA B*4403	1:451-459	9	LADVRSVGV	1.034616	0.104608	-4.654769	1.139224	-3.515545	45161.581608
HLA A*0216	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.478417	0.962750	-3.515666	30089.626626
HLA B*4801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.417224	0.901531	-3.515694	26135.117794
HLA B*0801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.150910	0.635184	-3.515726	14155.015095
HLA A*2902	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.443506	0.927581	-3.515925	27765.519336
HLA B*0803	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.498533	0.982586	-3.515947	31516.144956
HLA B*7301	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.471444	0.955413	-3.516031	29610.349071
HLA A*2301	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.533338	1.017228	-3.516111	34145.883963
HLA B*3501	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.288797	0.772641	-3.516156	19444.505936
HLA B*1503	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.270715	0.754547	-3.516168	18651.564914
HLA B*2705	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.288936	0.772641	-3.516295	19450.713291
HLA B*4601	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.292025	0.775707	-3.516318	19589.579108
HLA A*0301	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.348366	0.831902	-3.516464	22303.126898
HLA A*3001	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.271058	0.754590	-3.516469	18666.302556
HLA A*0301	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.317717	0.801202	-3.516515	20783.406095
HLA A*1101	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.423526	0.906788	-3.516738	26517.084993
HLA B*7301	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.189790	0.673013	-3.516777	15480.665072
HLA A*2402	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.529574	1.012736	-3.516838	33851.232461
HLA B*0802	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.437740	0.920891	-3.516849	27399.343993
HLA A*3301	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.423702	0.906788	-3.516914	26527.846262
HLA A*3301	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.640144	1.123169	-3.516974	43666.018944
HLA B*3901	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.235323	0.718317	-3.517006	17191.850822
HLA A*6901	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.191274	0.674222	-3.517053	15533.684826
HLA A*0219	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.417297	0.900174	-3.517123	26139.501192
HLA B*0803	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.460908	0.943730	-3.517179	28900.704966
HLA B*3501	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.379405	0.862117	-3.517288	23955.475833
HLA B*3901	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.450399	0.932998	-3.517401	28209.746928
HLA A*3201	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.560917	1.043307	-3.517610	36384.517084
HLA A*3101	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.361149	0.843518	-3.517631	22969.381620
HLA B*1509	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.419193	0.901531	-3.517662	26253.869990

HLA B*4501	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.552233	1.034513	-3.517720	35664.235469
HLA A*1101	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.437820	0.920085	-3.517735	27404.384189
HLA B*5301	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.525038	1.007289	-3.517748	33499.446363
HLA A*2902	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.459325	0.941565	-3.517760	28795.517216
HLA B*5301	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.546080	1.028301	-3.517778	35162.489647
HLA B*5401	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.544994	1.027198	-3.517796	35074.715354
HLA B*1801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.451012	0.933159	-3.517853	28249.606690
HLA B*1509	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.452685	0.934761	-3.517924	28358.629520
HLA A*3101	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.319131	0.801202	-3.517929	20851.202860
HLA A*6802	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.421667	0.903619	-3.518048	26403.854932
HLA A*8001	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.331320	0.813260	-3.518060	21444.713166
HLA B*1502	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.535434	1.017228	-3.518206	34311.057273
HLA A*0212	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.439145	0.920891	-3.518254	27488.127522
HLA B*3801	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.539280	1.020917	-3.518363	34616.265066
HLA A*0101	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.332298	0.813884	-3.518414	21493.029139
HLA A*8001	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.418378	0.899837	-3.518541	26204.631628
HLA B*1502	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.474042	0.955413	-3.518630	29788.048869
HLA A*2603	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.632689	1.113845	-3.518844	42922.863077
HLA B*0702	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.441375	0.922498	-3.518877	27629.614035
HLA B*3901	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.481880	0.962975	-3.518905	30330.525832
HLA A*0211	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.419257	0.900174	-3.519083	26257.705095
HLA B*3501	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.460683	0.941565	-3.519118	28885.699300
HLA A*0202	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.547680	1.028547	-3.519133	35292.271909
HLA B*2705	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.400795	0.881518	-3.519277	25164.859687
HLA A*2603	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.540168	1.020890	-3.519279	34687.125613
HLA B*0702	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.422945	0.903619	-3.519326	26481.675397
HLA A*2301	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.524502	1.005094	-3.519408	33458.151786
HLA B*7301	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.562749	1.043287	-3.519462	36538.373710
HLA A*2402	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.556650	1.036964	-3.519686	36028.812683
HLA B*1502	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.482777	0.962975	-3.519803	30393.271030
HLA B*2705	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.449544	0.929716	-3.519828	28154.250963
HLA A*3301	1:234-242	9	GGVDSAVAA	1.482077	-0.368232	-4.633786	1.113845	-3.519941	43031.441280
HLA B*4403	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.576468	1.056396	-3.520072	37710.983274
HLA A*2603	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.564370	1.044058	-3.520313	36675.019890
HLA B*1501	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.363985	0.843518	-3.520467	23119.856368
HLA B*1503	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.275078	0.754590	-3.520489	18839.885964
HLA B*0702	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.432520	0.911989	-3.520530	27071.954361
HLA B*0803	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.395388	0.874608	-3.520781	24853.545280
HLA B*3901	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.441793	0.920891	-3.520902	27656.233070
HLA B*5301	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.565388	1.044058	-3.521330	36761.031164
HLA B*3501	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.295683	0.774258	-3.521425	19755.282897
HLA B*5101	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.476850	0.955413	-3.521437	29981.246992
HLA B*4601	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.383650	0.862117	-3.521534	24190.805028
HLA B*5801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.334802	0.813260	-3.521542	21617.336279
HLA B*1517	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.484298	0.962750	-3.521547	30499.839903
HLA A*2902	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.311913	0.790294	-3.521620	20507.536613
HLA B*2705	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.335512	0.813884	-3.521628	21652.683258
HLA A*2402	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.465394	0.943730	-3.521664	29200.722919
HLA B*5401	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.555045	1.033365	-3.521680	35895.933509
HLA A*0203	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.329344	0.807656	-3.521689	21347.367411
HLA A*6802	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-3.905897	0.384129	-3.521768	8051.867932
HLA B*5801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.350222	0.828408	-3.521814	22398.650258
HLA A*0301	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.331323	0.809432	-3.521890	21444.829180
HLA B*3501	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.433925	0.911989	-3.521935	27159.677032
HLA A*0203	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.296264	0.774258	-3.522006	19781.698393
HLA B*4801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.396690	0.874608	-3.522082	24928.145044
HLA B*1503	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.258169	0.736037	-3.522132	18120.451982
HLA B*5301	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.601582	1.079304	-3.522277	39955.953728
HLA B*1517	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.415178	0.892605	-3.522573	26012.258452
HLA A*2403	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.443501	0.920891	-3.522610	27765.218921
HLA A*2501	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.457372	0.934761	-3.522611	28666.354126
HLA A*2402	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.565954	1.043307	-3.522647	36808.990840
HLA B*3901	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.491896	0.969193	-3.522702	31038.147609
HLA A*2301	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.444244	0.921448	-3.522796	27812.724851
HLA B*0803	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.503610	0.980728	-3.522883	31886.755110

HLA B*0801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.312372	0.789472	-3.522900	20529.182011
HLA A*6801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-3.793854	0.270903	-3.522952	6220.916930
HLA B*0802	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.449979	0.926967	-3.523012	28182.442673
HLA A*2402	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-3.969577	0.446544	-3.523033	9323.459409
HLA A*0101	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.385274	0.862117	-3.523157	24281.405140
HLA A*0301	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.304332	0.781170	-3.523162	20152.628892
HLA B*5801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.347800	0.824605	-3.523194	22274.067402
HLA B*7301	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.602766	1.079304	-3.523462	40065.045654
HLA A*6801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.492692	0.969193	-3.523499	31095.122323
HLA B*1509	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.438689	0.915104	-3.523585	27459.293357
HLA B*1517	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.438715	0.915104	-3.523611	27460.927475
HLA A*6801	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.576219	1.052564	-3.523655	37689.364176
HLA B*4801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.423500	0.899837	-3.523663	26515.507040
HLA B*0702	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.423556	0.899837	-3.523719	26518.949967
HLA A*3301	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.225098	0.701295	-3.523803	16791.816331
HLA B*3801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.453677	0.929716	-3.523961	28423.445470
HLA A*0201	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.331781	0.807776	-3.524004	21467.463876
HLA A*8001	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.426284	0.902116	-3.524168	26686.036519
HLA A*0211	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.250397	0.726094	-3.524303	17799.054374
HLA B*4402	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.446898	0.922498	-3.524400	27983.269651
HLA A*1101	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.300147	0.775707	-3.524440	19959.390482
HLA A*2402	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.529788	1.005151	-3.524638	33867.901522
HLA A*0201	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.279289	0.754590	-3.524699	19023.417830
HLA A*2402	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.552000	1.027198	-3.524802	35645.139567
HLA A*2602	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.553809	1.028966	-3.524844	35793.933175
HLA A*3001	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.217344	0.692424	-3.524920	16494.698238
HLA A*0206	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.433504	0.908582	-3.524922	27133.389141
HLA B*4403	1:270-278	9	QVQRDFVAA	1.243189	-0.112779	-4.655340	1.130410	-3.524930	45220.990203
HLA B*1801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.437801	0.912830	-3.524972	27403.198177
HLA A*1101	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.480386	0.955413	-3.524973	30226.347236
HLA A*0216	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-3.815578	0.290570	-3.525008	6539.999881
HLA A*0212	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.318217	0.793168	-3.525049	20807.368751
HLA A*2301	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.387196	0.862117	-3.525079	24389.095487
HLA B*5401	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.545990	1.020890	-3.525101	35155.261834
HLA A*3002	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.512414	0.987241	-3.525173	32539.722633
HLA B*4403	1:263-271	9	LRAGERAQV	0.865849	0.254971	-4.646008	1.120820	-3.525188	44259.643698
HLA B*0803	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.458350	0.932998	-3.525352	28730.940803
HLA A*0219	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.318579	0.793168	-3.525411	20824.711070
HLA B*3501	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.440595	0.915104	-3.525491	27580.033488
HLA A*2402	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.440724	0.915104	-3.525620	27588.240980
HLA B*4402	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.400231	0.874608	-3.525623	25132.207505
HLA A*0216	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.278393	0.752770	-3.525624	18984.247757
HLA A*2301	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.530782	1.005151	-3.525632	33945.493001
HLA A*0201	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.400242	0.874608	-3.525635	25132.887326
HLA B*4801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.434256	0.908582	-3.525674	27180.402184
HLA A*3002	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.554343	1.028547	-3.525796	35837.916731
HLA A*2501	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.486196	0.960386	-3.525810	30633.452321
HLA A*2902	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.333623	0.807776	-3.525846	21558.708334
HLA A*3301	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.634998	1.109115	-3.525884	43151.731486
HLA B*1503	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.434510	0.908582	-3.525928	27196.287464
HLA B*1501	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.333602	0.807656	-3.525946	21557.658687
HLA B*0801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.333649	0.807656	-3.525993	21559.991304
HLA A*2403	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.280656	0.754590	-3.526066	19083.408509
HLA A*0211	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.407761	0.881518	-3.526243	25571.766859
HLA A*2501	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.426467	0.900138	-3.526330	26697.299639
HLA A*2501	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.446572	0.920085	-3.526487	27962.234853
HLA B*0801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.351103	0.824605	-3.526498	22444.136713
HLA A*0219	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.428955	0.902388	-3.526567	26850.689377
HLA B*1503	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.433438	0.906788	-3.526651	27129.279371
HLA A*2301	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.456433	0.929716	-3.526717	28604.388476
HLA B*4402	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.388838	0.862117	-3.526721	24481.497757
HLA A*2902	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.340725	0.813884	-3.526842	21914.180283
HLA B*0801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.308636	0.781791	-3.526845	20353.352959
HLA B*4402	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.433206	0.906227	-3.526978	27114.753388
HLA B*4801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.432289	0.905240	-3.527049	27057.605450

HLA B*3901	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.460279	0.933159	-3.527119	28858.833631
HLA A*1101	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.454720	0.927581	-3.527139	28491.800385
HLA B*4001	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.384306	0.857166	-3.527140	24227.345208
HLA A*0301	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.346289	0.819048	-3.527241	22196.720357
HLA B*3501	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.648186	0.120764	-3.527423	4448.220753
HLA B*3901	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.420100	0.892605	-3.527495	26308.751055
HLA B*4403	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.621590	1.094025	-3.527565	41839.811167
HLA A*2403	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.409194	0.881518	-3.527676	25656.293912
HLA B*5401	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-3.458696	-0.069030	-3.527726	2875.382780
HLA B*0802	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.455486	0.927581	-3.527905	28542.093540
HLA B*4002	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.641368	1.113445	-3.527923	43789.267510
HLA A*6801	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.641483	1.113445	-3.528038	43800.876907
HLA B*5101	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.409692	0.881518	-3.528174	25685.735905
HLA A*0206	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.428467	0.900174	-3.528293	26820.492446
HLA B*4501	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.620283	1.091915	-3.528369	41714.150350
HLA A*0216	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.176426	0.647881	-3.528545	15011.557150
HLA B*7301	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.581176	1.052564	-3.528613	38122.048037
HLA A*2902	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.437428	0.908582	-3.528846	27379.636838
HLA A*6802	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.437444	0.908582	-3.528862	27380.673703
HLA B*1501	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.357277	0.828408	-3.528870	22765.508326
HLA A*6901	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.215164	0.686294	-3.528870	16412.096153
HLA B*4403	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.642376	1.113445	-3.528931	43891.013523
HLA A*3001	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.124385	0.595350	-3.529035	13316.333129
HLA A*1101	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.342365	0.813260	-3.529105	21997.086910
HLA B*4403	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.621052	1.091915	-3.529137	41788.009400
HLA A*3002	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.386331	0.857166	-3.529165	24340.589020
HLA B*1517	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.470809	0.941565	-3.529244	29567.129693
HLA B*5801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.361168	0.831902	-3.529266	22970.375735
HLA B*4403	1:347-355	9	GGSGTANIK	1.132293	-0.006267	-4.655317	1.126026	-3.529291	45218.543863
HLA B*5301	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.592346	1.062990	-3.529356	39115.210879
HLA A*2501	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.450293	0.920891	-3.529402	28202.880241
HLA A*0250	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.512054	0.982586	-3.529468	32512.800224
HLA A*0211	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.422095	0.892605	-3.529490	26429.864965
HLA A*2602	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.602333	1.072837	-3.529496	40025.183965
HLA A*0219	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.302161	0.772641	-3.529520	20052.142551
HLA A*2602	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.536907	1.007289	-3.529618	34427.638005
HLA B*2705	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.450528	0.920891	-3.529637	28218.141815
HLA A*0250	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.305347	0.775707	-3.529640	20199.782118
HLA B*1503	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.103249	0.573435	-3.529814	12683.779518
HLA A*2602	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.547005	1.017185	-3.529821	35237.518298
HLA A*1101	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.452413	0.922498	-3.529914	28340.838726
HLA A*6802	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.337645	0.807656	-3.529989	21759.306784
HLA B*3801	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.537351	1.007289	-3.530062	34462.857201
HLA A*0219	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.125470	0.595350	-3.530120	13349.657183
HLA B*3801	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.557324	1.027198	-3.530126	36084.795842
HLA B*5301	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.564932	1.034513	-3.530419	36722.470021
HLA A*3001	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-3.875983	0.345470	-3.530513	7515.934728
HLA A*2602	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.551589	1.020890	-3.530699	35611.409192
HLA A*3002	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.436171	0.905240	-3.530930	27300.506778
HLA B*1503	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.140145	0.609194	-3.530951	13808.452062
HLA B*0702	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.431155	0.900138	-3.531017	26986.996854
HLA B*1503	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.486466	0.955413	-3.531054	30652.516462
HLA B*0803	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.452051	0.920891	-3.531160	28317.237156
HLA A*0201	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.158382	0.627189	-3.531193	14400.636867
HLA B*1502	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.610531	1.079304	-3.531227	40787.838392
HLA B*4501	1:120-128	9	LKVLGGKLH	1.362707	-0.247131	-4.646875	1.115576	-3.531299	44348.085218
HLA A*0212	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.339123	0.807776	-3.531346	21833.475915
HLA B*2705	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.429315	0.897730	-3.531585	26872.923243
HLA A*3002	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.333167	0.801202	-3.531965	21536.093940
HLA A*6802	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.434413	0.902388	-3.532025	27190.255848
HLA A*2403	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.341503	0.809432	-3.532071	21953.456576
HLA A*0202	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.452166	0.920085	-3.532081	28324.744614
HLA B*5101	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.494842	0.962750	-3.532092	31249.426280
HLA B*1517	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.459130	0.926967	-3.532163	28782.590333
HLA A*6801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.465398	0.932998	-3.532401	29201.038866

HLA B*2705	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.459424	0.926967	-3.532457	28802.060743
HLA A*2501	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.425135	0.892605	-3.532530	26615.533620
HLA A*2501	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.455058	0.922498	-3.532560	28514.004830
HLA A*6802	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.322192	0.789472	-3.532721	20998.704036
HLA A*3201	1:372-380	9	VEPLRLLFK	0.894220	0.185084	-4.612305	1.079304	-3.533001	40954.775636
HLA B*3901	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.435400	0.902388	-3.533012	27252.106522
HLA B*1517	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.305805	0.772641	-3.533164	20221.102685
HLA A*0250	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.433088	0.899837	-3.533251	27107.419990
HLA A*0202	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.314474	0.781170	-3.533305	20628.822274
HLA B*5801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.287895	0.754547	-3.533348	19404.153897
HLA A*3101	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.937873	0.404390	-3.533484	8667.086556
HLA A*2501	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.433443	0.899837	-3.533606	27129.572905
HLA A*0250	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.286382	0.752770	-3.533612	19336.668061
HLA B*7301	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.560280	1.026553	-3.533727	36331.213556
HLA A*2402	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.467045	0.933159	-3.533886	29311.989156
HLA A*0202	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.161093	0.627189	-3.533904	14490.821436
HLA A*2902	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.309275	0.775312	-3.533963	20383.324758
HLA A*2501	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.431780	0.897730	-3.534050	27025.859922
HLA A*3301	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.554970	1.020890	-3.534080	35889.719870
HLA A*2301	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.514956	0.980728	-3.534228	32730.752452
HLA A*3101	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.342008	0.807776	-3.534232	21979.006071
HLA A*2603	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.585274	1.050933	-3.534340	38483.425806
HLA B*3501	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.436730	0.902388	-3.534342	27335.680283
HLA A*2501	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.449504	0.915104	-3.534400	28151.661789
HLA B*3901	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.447284	0.912830	-3.534454	28008.108036
HLA A*2403	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.434714	0.900174	-3.534540	27209.090691
HLA B*4403	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.587158	1.052564	-3.534594	38650.757784
HLA B*0801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.437019	0.902388	-3.534631	27353.875945
HLA A*2902	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.344111	0.809432	-3.534678	22085.683188
HLA A*0201	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.378230	0.843518	-3.534712	23890.765157
HLA B*4402	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.328104	0.793168	-3.534936	21286.477338
HLA A*6801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.227386	0.692424	-3.534962	16880.529828
HLA A*3002	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.495427	0.960386	-3.535041	31291.549572
HLA B*4501	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.658265	1.123169	-3.535096	45526.595699
HLA B*0702	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.359702	0.824605	-3.535097	22892.963747
HLA A*1101	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.476692	0.941565	-3.535127	29970.381881
HLA A*6901	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.313234	0.778023	-3.535211	20569.981740
HLA A*3001	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.283736	0.748391	-3.535345	19219.236101
HLA B*3801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.439112	0.903619	-3.535493	27486.045692
HLA A*3201	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.191528	0.656026	-3.535502	15542.763313
HLA B*1509	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.130982	0.595477	-3.535505	13520.165414
HLA A*3002	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.288329	0.752770	-3.535560	19423.583868
HLA A*2603	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.552776	1.017185	-3.535591	35708.832368
HLA B*0802	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.470356	0.934761	-3.535595	29536.274509
HLA B*0801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.316916	0.781170	-3.535746	20745.100789
HLA A*0101	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.319453	0.783681	-3.535772	20866.662557
HLA B*4402	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.437909	0.902116	-3.535793	27410.018446
HLA A*3001	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.163099	0.627189	-3.535911	14557.924578
HLA B*1503	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.319622	0.783681	-3.535942	20874.791956
HLA A*2402	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.442763	0.906788	-3.535976	27718.094036
HLA A*0212	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.262137	0.726094	-3.536043	18286.782788
HLA B*0702	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.433781	0.897730	-3.536051	27150.715729
HLA A*3001	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.286318	0.750232	-3.536087	19333.843819
HLA B*4402	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.442886	0.906788	-3.536098	27725.892628
HLA B*1509	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.463688	0.927581	-3.536107	29086.259687
HLA A*3301	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.630137	1.094025	-3.536112	42671.424606
HLA A*6901	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.360733	0.824605	-3.536128	22947.397806
HLA B*2705	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.437747	0.901531	-3.536216	27399.788679
HLA A*2403	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.360863	0.824605	-3.536258	22954.226681
HLA B*2705	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.458756	0.922498	-3.536258	28757.842988
HLA B*0802	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.451365	0.915104	-3.536261	28272.540080
HLA B*0802	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.411012	0.874608	-3.536405	25763.948567
HLA B*5301	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.469597	0.933159	-3.536437	29484.708061
HLA B*1517	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.458937	0.922498	-3.536439	28769.824893
HLA A*0211	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.331294	0.794851	-3.536443	21443.437056

HLA B*0801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.368369	0.831902	-3.536467	23354.429923
HLA A*3301	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.599514	1.062990	-3.536524	39766.187390
HLA B*0803	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.478154	0.941565	-3.536588	30071.400615
HLA B*4501	1:131-139	9	LPEVQPVWM	1.234481	-0.121036	-4.650061	1.113445	-3.536616	44674.610530
HLA A*3002	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.541801	1.005094	-3.536708	34817.790286
HLA B*3901	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.248964	0.712255	-3.536709	17740.413730
HLA B*1502	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.580838	1.044058	-3.536780	38092.361610
HLA B*0802	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.456997	0.920085	-3.536912	28641.551774
HLA A*3201	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.580260	1.043287	-3.536973	38041.700767
HLA B*3801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.480710	0.943730	-3.536980	30248.921586
HLA B*0802	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.437162	0.900174	-3.536988	27362.904303
HLA B*3501	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.443823	0.906788	-3.537035	27785.804874
HLA B*1801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.470043	0.932998	-3.537046	29515.030353
HLA B*4501	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.624374	1.087303	-3.537071	42108.896016
HLA A*6901	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.350974	0.813884	-3.537090	22437.459590
HLA B*4403	1:222-230	9	QIGDGHAIC	1.130733	0.000313	-4.668159	1.131046	-3.537113	46575.642867
HLA B*3801	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.506315	0.969193	-3.537121	32085.926450
HLA A*0216	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.355828	0.818458	-3.537369	22689.645980
HLA B*3501	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.026806	0.489404	-3.537402	10636.673784
HLA A*0301	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.330606	0.793168	-3.537438	21409.474041
HLA B*5701	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.399718	0.862117	-3.537602	25102.585160
HLA B*5801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.351547	0.813920	-3.537627	22467.096884
HLA B*5701	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.345452	0.807776	-3.537676	22154.012377
HLA A*3301	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.394860	0.857166	-3.537694	24823.311327
HLA B*4801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.435433	0.897730	-3.537703	27254.170632
HLA B*7301	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.558868	1.020917	-3.537951	36213.280130
HLA A*6801	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.629881	1.091915	-3.537966	42646.269626
HLA B*1517	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.458864	0.920891	-3.537973	28765.000409
HLA A*0212	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.395210	0.857166	-3.538044	24843.328807
HLA B*1509	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.518793	0.980728	-3.538065	33021.188358
HLA A*3201	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.450181	0.911989	-3.538191	28195.557618
HLA A*3301	1:22-30	9	FGAQYAQLI	1.065855	0.021448	-4.625523	1.087303	-3.538220	42220.439873
HLA A*2602	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.566804	1.028547	-3.538258	36881.147459
HLA B*1509	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.465333	0.926967	-3.538366	29196.615918
HLA B*4501	1:421-429	9	DTLRHADSI	0.987060	0.113427	-4.639131	1.100487	-3.538644	43564.323144
HLA A*8001	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.328120	0.789472	-3.538648	21287.283455
HLA B*5301	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.519549	0.980728	-3.538822	33078.760881
HLA A*0202	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.441246	0.902388	-3.538857	27621.394234
HLA A*0201	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.328341	0.789472	-3.538869	21298.111422
HLA B*4403	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.662067	1.123169	-3.538897	45926.848315
HLA B*0802	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.480466	0.941565	-3.538900	30231.907468
HLA A*3201	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.551650	1.012736	-3.538914	35616.418542
HLA A*3002	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.439180	0.900138	-3.539043	27490.358228
HLA A*0206	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.313356	0.774258	-3.539098	20575.769182
HLA B*5301	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.590111	1.050933	-3.539178	38914.487547
HLA B*3801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.556436	1.017228	-3.539208	36011.080067
HLA B*1503	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.280997	0.741770	-3.539227	19098.384055
HLA B*3501	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.396469	0.857166	-3.539303	24915.471567
HLA A*0216	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.340643	0.801202	-3.539441	21910.031311
HLA B*1509	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.347285	0.807776	-3.539509	22247.693477
HLA B*4501	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.396791	0.857166	-3.539625	24933.944634
HLA B*5101	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.347428	0.807776	-3.539652	22255.036500
HLA A*3101	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.329201	0.789472	-3.539729	21340.323873
HLA A*3002	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.185706	0.645964	-3.539742	15335.792006
HLA A*3101	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.353708	0.813884	-3.539825	22579.196561
HLA B*1517	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-3.810752	0.270903	-3.539849	6467.730247
HLA B*1801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.502680	0.962750	-3.539930	31818.516721
HLA B*1502	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.596352	1.056396	-3.539955	39477.673228
HLA B*5801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.358501	0.818458	-3.540043	22829.764613
HLA A*1101	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.443668	0.903619	-3.540049	27775.885649
HLA B*0802	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.473079	0.932998	-3.540081	29722.050572
HLA B*4501	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.443762	0.903619	-3.540143	27781.896878
HLA A*1101	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.432825	0.892605	-3.540220	27091.000373
HLA A*6901	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.368708	0.828408	-3.540300	23372.630674
HLA B*4403	1:40-48	9	FSEVIPHTA	1.388808	-0.297332	-4.631855	1.091476	-3.540379	42840.508369

HLA A*0301	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.368893	0.828408	-3.540485	23382.621833
HLA A*3101	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.306397	0.765882	-3.540515	20248.688754
HLA A*2301	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.422097	0.881518	-3.540579	26430.007949
HLA A*0212	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.293435	0.752770	-3.540665	19653.268889
HLA B*1501	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.348662	0.807776	-3.540885	22318.334919
HLA B*4402	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.441210	0.900138	-3.541073	27619.152895
HLA A*0219	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.359594	0.818458	-3.541136	22887.267430
HLA B*4403	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.584468	1.043307	-3.541161	38412.082482
HLA B*1801	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.470884	0.929716	-3.541169	29572.248693
HLA A*0250	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.553908	1.012736	-3.541172	35802.067030
HLA A*8001	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.384776	0.843518	-3.541258	24253.572845
HLA B*5801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.319286	0.778023	-3.541263	20858.649167
HLA B*4403	1:497-505	9	STRITNEVA	1.301822	-0.192924	-4.650185	1.108898	-3.541287	44687.421655
HLA B*1801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.439021	0.897730	-3.541291	27480.247142
HLA A*6801	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.485113	0.943730	-3.541383	30557.148938
HLA B*1502	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.570390	1.028966	-3.541424	37186.879682
HLA B*3501	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.441678	0.900138	-3.541540	27648.902801
HLA B*0803	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.474813	0.933159	-3.541653	29840.953006
HLA A*3001	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.273213	0.731526	-3.541687	18759.133697
HLA B*4001	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.403814	0.862117	-3.541697	25340.407905
HLA A*0206	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.504484	0.962750	-3.541734	31950.991142
HLA B*5401	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.497147	0.955413	-3.541734	31415.711004
HLA A*2603	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.504543	0.962750	-3.541793	31955.312718
HLA B*4601	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.399077	0.857166	-3.541911	25065.538523
HLA A*2902	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.360987	0.819048	-3.541939	22960.809155
HLA A*8001	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.444429	0.902388	-3.542041	27824.614028
HLA A*0301	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.355959	0.813884	-3.542076	22696.520936
HLA A*0202	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.190067	0.647881	-3.542186	15490.550571
HLA B*5301	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.585520	1.043307	-3.542214	38505.292078
HLA A*6901	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.350006	0.807656	-3.542350	22387.505004
HLA B*1502	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.593314	1.050933	-3.542380	39202.491000
HLA A*2902	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.215399	0.673013	-3.542386	16420.977317
HLA A*0216	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.463284	0.920891	-3.542393	29059.207483
HLA B*0803	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.423923	0.881518	-3.542405	26541.339888
HLA B*3901	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.462532	0.920085	-3.542447	29008.944733
HLA B*0803	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.470154	0.927581	-3.542573	29522.535940
HLA A*0211	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-3.640480	0.097746	-3.542734	4369.985754
HLA A*2902	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.435351	0.892605	-3.542746	27249.010649
HLA A*0101	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.361220	0.818458	-3.542762	22973.109776
HLA A*0201	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.306218	0.763388	-3.542831	20240.365185
HLA A*2501	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.484645	0.941565	-3.543080	30524.269793
HLA A*0101	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.375072	0.831902	-3.543171	23717.687983
HLA A*2501	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.449976	0.906788	-3.543189	28182.290210
HLA B*7301	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.506164	0.962975	-3.543190	32074.819170
HLA B*4002	1:506-514	9	EVNRVVLDI	0.826968	0.228866	-4.599100	1.055834	-3.543266	39728.342413
HLA A*2602	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.586730	1.043307	-3.543424	38612.720983
HLA B*3501	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.447249	0.903619	-3.543629	28005.835316
HLA A*3301	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.548760	1.005094	-3.543667	35380.207829
HLA A*2501	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.455657	0.911989	-3.543668	28553.367664
HLA A*0206	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.387205	0.843518	-3.543687	24389.623262
HLA B*5101	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.375928	0.831902	-3.544026	23764.438862
HLA A*3301	1:473-481	9	RPVSSEDAM	0.931240	0.160675	-4.635940	1.091915	-3.544026	43245.444978
HLA B*4402	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.449325	0.905240	-3.544085	28140.089568
HLA A*3301	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.616973	1.072837	-3.544136	41397.391614
HLA B*1517	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.319817	0.775634	-3.544183	20884.167277
HLA A*2301	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.487942	0.943730	-3.544212	30756.832742
HLA B*3801	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.450470	0.906227	-3.544242	28214.325647
HLA B*5101	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.471857	0.927581	-3.544276	29638.555710
HLA A*6801	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.573388	1.028966	-3.544422	37444.469453
HLA B*5101	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.465560	0.920891	-3.544669	29211.941133
HLA A*2603	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.466152	0.921448	-3.544705	29251.792699
HLA A*2602	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.466218	0.921448	-3.544771	29256.224006
HLA B*0802	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.456900	0.911989	-3.544911	28635.199626
HLA A*2403	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.323099	0.778023	-3.545077	21042.599707
HLA B*7301	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.608231	1.062990	-3.545240	40572.385572

HLA A*6801	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.618120	1.072837	-3.545282	41506.826192
HLA A*0201	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.363905	0.818458	-3.545447	23115.604179
HLA A*0206	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-3.640988	0.095477	-3.545510	4375.095224
HLA A*0216	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.318177	0.772641	-3.545536	20805.455224
HLA B*0802	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.454130	0.908582	-3.545548	28453.138133
HLA B*3501	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.358863	0.813260	-3.545603	22848.792538
HLA B*5801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.355057	0.809432	-3.545625	22649.420182
HLA A*6901	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.295876	0.750232	-3.545644	19764.048501
HLA B*3901	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.318384	0.772641	-3.545743	20815.362440
HLA A*6801	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.589851	1.044058	-3.545793	38891.126502
HLA A*6801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.506185	0.960386	-3.545799	32076.380899
HLA B*5801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.339029	0.793168	-3.545861	21828.751759
HLA B*1502	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.574283	1.028301	-3.545982	37521.728380
HLA B*4501	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.590093	1.044058	-3.546035	38912.803399
HLA B*4002	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.572659	1.026553	-3.546106	37381.725247
HLA B*5801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.353788	0.807656	-3.546133	22583.350075
HLA B*1801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.466249	0.920085	-3.546164	29258.281626
HLA A*0202	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.449873	0.903619	-3.546254	28175.582633
HLA A*3201	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.481140	0.934761	-3.546379	30278.883141
HLA B*3501	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.220624	0.674222	-3.546403	16619.741166
HLA B*5701	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.258813	0.712255	-3.546558	18147.332020
HLA B*0802	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.451799	0.905240	-3.546559	28300.850236
HLA A*8001	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.371196	0.824605	-3.546591	23506.918477
HLA A*0211	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.327765	0.781170	-3.546596	21269.901118
HLA A*2402	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.272745	0.726094	-3.546651	18738.949082
HLA B*0801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.356159	0.809432	-3.546727	22706.960117
HLA B*7301	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.564009	1.017228	-3.546781	36644.477814
HLA B*2705	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.449325	0.902388	-3.546937	28140.089568
HLA B*3501	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.279749	0.732703	-3.547046	19043.599786
HLA B*0803	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.476765	0.929716	-3.547049	29975.408532
HLA A*2403	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.448752	0.901531	-3.547221	28102.968791
HLA A*1101	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.459435	0.911989	-3.547446	28802.839833
HLA A*0301	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.365928	0.818458	-3.547470	23223.525838
HLA B*0801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.297774	0.750232	-3.547543	19850.630014
HLA A*0101	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.376099	0.828408	-3.547691	23773.825813
HLA A*0203	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.323433	0.775634	-3.547799	21058.770932
HLA A*6802	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.320477	0.772641	-3.547836	20915.939090
HLA B*7301	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-3.702337	0.154429	-3.547908	5038.917667
HLA A*0301	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.355691	0.807776	-3.547915	22682.527686
HLA B*1517	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.405113	0.857166	-3.547947	25416.331523
HLA A*2402	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.517148	0.969193	-3.547955	32896.376157
HLA A*0216	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.279556	0.731526	-3.548030	19035.153711
HLA A*0219	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.468995	0.920891	-3.548104	29443.902020
HLA A*2402	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.460934	0.912830	-3.548105	28902.424862
HLA B*0803	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.463293	0.915104	-3.548189	29059.836318
HLA A*0212	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.422842	0.874608	-3.548234	26475.372578
HLA B*4002	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-3.755450	0.207166	-3.548284	5694.422940
HLA A*0203	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.175509	0.627189	-3.548321	14979.918303
HLA B*4001	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.366866	0.818458	-3.548407	23273.709024
HLA B*5701	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.367674	0.819048	-3.548626	23317.061767
HLA B*0803	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.509028	0.960386	-3.548642	32287.040526
HLA A*0203	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.312094	0.763388	-3.548707	20516.081042
HLA B*4002	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.585795	1.036964	-3.548832	38529.671988
HLA A*0301	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.324575	0.775707	-3.548868	21114.211632
HLA B*4601	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.392475	0.843518	-3.548957	24687.379140
HLA A*3101	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.367594	0.818458	-3.549136	23312.773309
HLA A*2602	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.605538	1.056396	-3.549142	40321.625741
HLA B*1502	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.576357	1.027198	-3.549159	37701.395918
HLA A*2602	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.586218	1.036964	-3.549255	38567.209688
HLA A*3002	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.530096	0.980728	-3.549368	33891.912058
HLA B*1517	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.456188	0.906788	-3.549401	28588.299359
HLA B*1503	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.144886	0.595477	-3.549409	13960.026969
HLA A*2501	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.357221	0.807776	-3.549444	22762.552705
HLA A*2403	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.344343	0.794851	-3.549493	22097.514985
HLA B*0801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.265154	0.715584	-3.549571	18414.250426

HLA A*8001	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.411717	0.862117	-3.549601	25805.796549
HLA A*3201	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.606085	1.056396	-3.549689	40372.483365
HLA B*1517	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.461686	0.911989	-3.549697	28952.503049
HLA B*0702	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.322348	0.772641	-3.549707	21006.203018
HLA A*2402	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.570768	1.020917	-3.549851	37219.283272
HLA A*0203	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.278182	0.728232	-3.549950	18975.006766
HLA B*5301	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.567218	1.017185	-3.550033	36916.280216
HLA B*5301	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.579191	1.028966	-3.550225	37948.176289
HLA A*2501	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.483525	0.932998	-3.550527	30445.602936
HLA B*5801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.331807	0.781170	-3.550637	21468.741417
HLA B*0801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.369779	0.819048	-3.550731	23430.360014
HLA A*2603	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.579797	1.028966	-3.550831	38001.179490
HLA A*2602	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.594209	1.043287	-3.550922	39283.377242
HLA A*6801	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.585443	1.034513	-3.550930	38498.418483
HLA A*0216	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.345819	0.794851	-3.550968	22172.716985
HLA B*5801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.345925	0.794851	-3.551074	22178.115480
HLA A*6802	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.744233	0.192958	-3.551275	5549.237071
HLA A*2902	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.191326	0.639875	-3.551451	15535.533717
HLA A*6901	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.218223	0.666703	-3.551520	16528.105723
HLA B*5101	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.486288	0.934761	-3.551526	30639.916222
HLA B*4001	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.365014	0.813260	-3.551754	23174.704551
HLA B*1801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.512174	0.960386	-3.551788	32521.771884
HLA A*2603	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.580131	1.028301	-3.551829	38030.383374
HLA B*1517	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.453390	0.901531	-3.551859	28404.692001
HLA A*3301	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-3.833439	0.281539	-3.551900	6814.571073
HLA B*4001	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.370998	0.819048	-3.551950	23496.238638
HLA B*1502	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.595327	1.043287	-3.552040	39384.666511
HLA B*1509	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.464038	0.911989	-3.552048	29109.714801
HLA B*3901	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.452260	0.900138	-3.552122	28330.874626
HLA A*6801	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.615166	1.062990	-3.552176	41225.527732
HLA B*3901	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.300702	0.748391	-3.552311	19984.889585
HLA A*0203	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.264604	0.712255	-3.552350	18390.954316
HLA B*1502	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.334173	0.781791	-3.552382	21586.017087
HLA B*0801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.365858	0.813260	-3.552597	23219.757043
HLA B*4601	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.377215	0.824605	-3.552610	23834.995910
HLA A*0219	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.427370	0.874608	-3.552762	26752.818187
HLA B*4601	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.371330	0.818458	-3.552871	23514.168274
HLA B*0801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.415063	0.862117	-3.552946	26005.363917
HLA A*0216	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.239521	0.686294	-3.553227	17358.858527
HLA B*1517	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.334426	0.781170	-3.553257	21598.632792
HLA B*2705	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.473370	0.920085	-3.553285	29741.995593
HLA A*3001	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.227522	0.674222	-3.553301	16885.827323
HLA B*7301	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.468471	0.915104	-3.553367	29408.402159
HLA A*2402	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.582064	1.028547	-3.553517	38200.085029
HLA A*1101	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.462140	0.908582	-3.553558	28982.748394
HLA A*0206	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.246006	0.692424	-3.553582	17619.993437
HLA A*2601	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.367617	0.813920	-3.553697	23314.034538
HLA B*1509	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.475146	0.921448	-3.553699	29863.885761
HLA A*2601	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.397496	0.843518	-3.553978	24974.444453
HLA A*3301	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.481006	0.926967	-3.554039	30269.547672
HLA A*6801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.454483	0.900174	-3.554308	28476.236752
HLA A*8001	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.368245	0.813920	-3.554325	23347.734604
HLA A*2501	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.368503	0.813920	-3.554583	23361.632691
HLA A*6901	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.958990	0.404390	-3.554601	9098.929603
HLA B*1509	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.487852	0.933159	-3.554693	30750.510532
HLA A*6802	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.959183	0.404390	-3.554793	9102.966883
HLA B*7301	1:291-299	9	TFLEALSGV	0.900311	0.134202	-4.589336	1.034513	-3.554823	38845.076913
HLA A*0212	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.383260	0.828408	-3.554852	24169.090430
HLA A*3002	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.327519	0.772641	-3.554878	21257.822429
HLA B*1509	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.517883	0.962975	-3.554909	32952.126624
HLA A*6802	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.349790	0.794851	-3.554939	22376.365296
HLA A*2603	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.412121	0.857166	-3.554955	25829.820042
HLA A*0301	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.336891	0.781791	-3.555100	21721.552919
HLA B*0801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.199714	0.644580	-3.555133	15838.492355
HLA A*2403	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.383552	0.828408	-3.555144	24185.309130

HLA B*1501	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.270889	0.715584	-3.555306	18659.033223
HLA B*1501	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.305546	0.750232	-3.555315	20209.072933
HLA B*4601	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.383735	0.828408	-3.555327	24195.516791
HLA B*5401	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.560491	1.005151	-3.555341	36348.907168
HLA B*1801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.477841	0.922498	-3.555343	30049.771566
HLA A*3201	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.524596	0.969193	-3.555403	33465.392765
HLA A*6801	1:208-216	9	PANIANALI	0.995189	0.008861	-4.559490	1.004050	-3.555440	36265.233467
HLA A*3001	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.288163	0.732703	-3.555459	19416.124661
HLA B*5101	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.417678	0.862117	-3.555561	26162.419946
HLA B*4501	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.562907	1.007289	-3.555617	36551.619904
HLA A*0216	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.430248	0.874608	-3.555640	26930.700942
HLA B*1801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.417817	0.862117	-3.555700	26170.771890
HLA B*4601	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.387701	0.831902	-3.555799	24417.479586
HLA B*2705	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.374259	0.818458	-3.555801	23673.334225
HLA A*3101	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.339503	0.783681	-3.555823	21852.619205
HLA A*3101	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.387736	0.831902	-3.555834	24419.461105
HLA B*0803	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.490599	0.934761	-3.555838	30945.597925
HLA B*4601	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.345410	0.789472	-3.555938	22151.855168
HLA B*1502	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.525181	0.969193	-3.555988	33510.503114
HLA B*0802	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.459677	0.903619	-3.556058	28818.893783
HLA A*2402	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.543305	0.987241	-3.556064	34938.549867
HLA B*5101	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.476246	0.920085	-3.556161	29939.591784
HLA B*1517	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.456407	0.900174	-3.556233	28602.686315
HLA B*5301	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.516685	0.960386	-3.556299	32861.335580
HLA A*0201	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.380979	0.824605	-3.556374	24042.463020
HLA A*2601	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.331807	0.775312	-3.556495	21468.741417
HLA A*3001	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.297474	0.740887	-3.556587	19836.888890
HLA B*0803	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.449537	0.892605	-3.556932	28153.794033
HLA A*3001	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.213092	0.656026	-3.557066	16333.972005
HLA A*2301	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.463335	0.906227	-3.557108	29062.666245
HLA A*2301	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.539745	0.982586	-3.557159	34653.364423
HLA B*3501	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.197073	0.639875	-3.557198	15742.475213
HLA A*2601	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.370620	0.813260	-3.557360	23475.782509
HLA B*1502	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.490538	0.933159	-3.557378	30941.245512
HLA B*1801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.414553	0.857166	-3.557387	25974.852939
HLA A*3101	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.310217	0.752770	-3.557448	20427.591638
HLA A*2603	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.651517	1.094025	-3.557493	44824.706618
HLA B*0803	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.352372	0.794851	-3.557521	22509.799535
HLA A*3001	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-3.934457	0.376904	-3.557553	8599.178867
HLA B*1503	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.462823	0.905240	-3.557583	29028.411223
HLA A*0202	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.584863	1.027198	-3.557664	38447.009610
HLA B*3901	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.250091	0.692424	-3.557667	17786.540957
HLA B*1501	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.299612	0.741770	-3.557842	19934.786654
HLA B*1517	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.432510	0.874608	-3.557903	27071.368542
HLA B*5701	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.415108	0.857166	-3.557941	26008.037091
HLA A*0101	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.382548	0.824605	-3.557943	24129.504997
HLA A*3201	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.586521	1.028547	-3.557974	38594.134200
HLA A*0216	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.401560	0.843518	-3.558043	25209.280193
HLA A*2601	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.390140	0.831902	-3.558238	24554.980792
HLA B*0702	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.376762	0.818458	-3.558303	23810.122573
HLA B*5401	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-3.786646	0.228245	-3.558401	6118.517156
HLA B*3801	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.563515	1.005094	-3.558421	36602.870515
HLA A*6801	1:403-411	9	PGPGLGIRI	1.268169	-0.145000	-4.681673	1.123169	-3.558504	48047.754491
HLA A*0250	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.467102	0.908582	-3.558520	29315.795194
HLA A*0301	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.336590	0.778023	-3.558567	21706.516693
HLA A*1101	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.460756	0.902116	-3.558640	28890.544028
HLA B*3901	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.500384	0.941565	-3.558819	31650.784831
HLA A*0301	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.366574	0.807656	-3.558919	23258.101644
HLA A*6901	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.348413	0.789472	-3.558941	22305.540178
HLA A*2402	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.576177	1.017228	-3.558949	37685.694240
HLA A*0101	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.402477	0.843518	-3.558959	25262.524313
HLA A*3301	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.564135	1.005151	-3.558985	36655.184477
HLA B*1517	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.459219	0.900138	-3.559082	28788.507944
HLA B*2705	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.465941	0.906788	-3.559153	29237.553760
HLA B*1801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.474268	0.915104	-3.559164	29803.523291

HLA B*4501	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.587581	1.028301	-3.559280	38688.413452
HLA A*2402	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.564431	1.005094	-3.559338	36680.178855
HLA A*6801	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.615747	1.056396	-3.559350	41280.651860
HLA B*5801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.349942	0.790294	-3.559648	22384.235167
HLA A*8001	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.378740	0.819048	-3.559692	23918.828093
HLA B*3801	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.572453	1.012736	-3.559716	37363.933156
HLA B*0802	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.466514	0.906788	-3.559727	29276.173193
HLA B*3801	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.434505	0.874608	-3.559897	27195.993208
HLA B*0803	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.459879	0.899837	-3.560042	28832.304906
HLA A*0203	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.206086	0.645964	-3.560122	16072.581722
HLA A*0101	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.369558	0.809432	-3.560126	23418.448012
HLA A*6802	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-3.990915	0.430602	-3.560313	9792.985403
HLA A*0250	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.588871	1.028547	-3.560324	38803.489973
HLA A*3001	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.246673	0.686294	-3.560379	17647.085752
HLA B*4801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.417617	0.857166	-3.560451	26158.740274
HLA A*1101	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.374389	0.813884	-3.560505	23680.379130
HLA A*3002	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.462997	0.902388	-3.560609	29040.034546
HLA A*3301	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.587868	1.027198	-3.560669	38713.956483
HLA B*1517	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.469352	0.908582	-3.560771	29468.123791
HLA A*3002	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.530183	0.969193	-3.560990	33898.696742
HLA B*0702	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.207030	0.645964	-3.561066	16107.574015
HLA A*3101	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.342875	0.781791	-3.561084	22022.925465
HLA A*2301	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.463331	0.902116	-3.561215	29062.351795
HLA A*0101	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.354402	0.793168	-3.561234	22615.259861
HLA A*8001	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.279582	0.718317	-3.561266	19036.286504
HLA B*4001	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.369091	0.807776	-3.561314	23393.250028
HLA A*2603	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.617927	1.056396	-3.561531	41488.417395
HLA B*2705	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-3.831324	0.269777	-3.561547	6781.472250
HLA A*0203	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.436166	0.874608	-3.561558	27300.211394
HLA A*0301	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.336959	0.775312	-3.561647	21724.961011
HLA B*4002	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.624646	1.062990	-3.561656	42135.329627
HLA A*0201	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.390064	0.828408	-3.561657	24550.730289
HLA A*3201	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.058670	0.496961	-3.561708	11446.416794
HLA B*0801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.405294	0.843518	-3.561776	25426.921193
HLA A*2501	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-3.843391	0.281539	-3.561852	6972.538868
HLA B*7301	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-3.784146	0.222188	-3.561958	6083.399393
HLA B*0801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.289307	0.727191	-3.562116	19467.346138
HLA B*4001	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.386730	0.824605	-3.562125	24362.984898
HLA B*2705	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.462342	0.900174	-3.562167	28996.235768
HLA A*2601	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.381273	0.819048	-3.562225	24058.726901
HLA B*4001	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.405759	0.843518	-3.562241	25454.172036
HLA A*2501	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.470971	0.908582	-3.562389	29578.168641
HLA A*1101	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.462645	0.900174	-3.562471	29016.478599
HLA B*4001	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.357345	0.794851	-3.562495	22769.080213
HLA A*2603	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.606034	1.043307	-3.562727	40367.678616
HLA A*0211	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.504308	0.941565	-3.562743	31938.029923
HLA A*0211	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.338113	0.775312	-3.562801	21782.744770
HLA A*0219	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.235847	0.673013	-3.562834	17212.603677
HLA A*2501	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.338145	0.775312	-3.562834	21784.394624
HLA B*0803	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.482944	0.920085	-3.562859	30404.947393
HLA A*0206	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.215009	0.651841	-3.563168	16406.237216
HLA B*1503	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.198422	0.635184	-3.563238	15791.435928
HLA A*0202	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.550551	0.987241	-3.563310	35526.357949
HLA A*3002	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.395245	0.831902	-3.563343	24845.344883
HLA B*0803	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.518971	0.955413	-3.563559	33034.767863
HLA B*5101	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.490651	0.926967	-3.563684	30949.281214
HLA B*0702	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.377180	0.813260	-3.563919	23833.061818
HLA B*5801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.350262	0.786323	-3.563939	22400.710315
HLA A*6802	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.377981	0.813884	-3.564097	23877.068967
HLA A*2403	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.345894	0.781791	-3.564104	22176.555780
HLA B*4403	1:228-236	9	AICGLSGGV	0.815527	0.247463	-4.627252	1.062990	-3.564262	42388.883208
HLA B*0803	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.466406	0.902116	-3.564290	29268.888580
HLA B*5701	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.407822	0.843518	-3.564304	25575.363963
HLA B*5401	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.290467	0.726094	-3.564373	19519.441915
HLA A*3002	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.282756	0.718317	-3.564440	19175.927838

HLA B*3801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.527436	0.962975	-3.564462	33684.992408
HLA A*0203	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.392872	0.828408	-3.564464	24709.960422
HLA B*3501	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.342539	0.778023	-3.564516	22005.894807
HLA A*0211	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.372375	0.807776	-3.564599	23570.844493
HLA B*4002	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.342638	0.778023	-3.564615	22010.895452
HLA A*2301	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.479730	0.915104	-3.564626	30180.759238
HLA A*2402	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.525045	0.960386	-3.564659	33499.990053
HLA B*5801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.346479	0.781791	-3.564689	22206.449114
HLA A*0206	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.378597	0.813884	-3.564713	23910.936105
HLA B*5801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.328116	0.763388	-3.564728	21287.053133
HLA B*1503	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.357919	0.793168	-3.564751	22799.155540
HLA A*2601	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.342776	0.778023	-3.564753	22017.922087
HLA A*2301	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.527763	0.962975	-3.564788	33710.332193
HLA A*0301	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.317644	0.752770	-3.564874	20779.920874
HLA B*4001	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.397094	0.831902	-3.565192	24951.351501
HLA B*2705	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.138712	0.573435	-3.565277	13762.958829
HLA B*5101	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.467400	0.902116	-3.565284	29335.943705
HLA A*3301	1:208-216	9	PANIANALI	0.995189	0.008861	-4.569431	1.004050	-3.565381	37104.890027
HLA A*6801	1:148-156	9	APDGFDVVA	1.404146	-0.310121	-4.659478	1.094025	-3.565453	45653.860866
HLA B*1509	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.486649	0.920891	-3.565758	30665.453675
HLA A*2603	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.553011	0.987241	-3.565770	35728.155677
HLA A*2301	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.472618	0.906788	-3.565831	29690.551847
HLA B*4601	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.318647	0.752770	-3.565878	20827.978448
HLA B*4601	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.359096	0.793168	-3.565928	22861.033150
HLA B*5801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.355400	0.789472	-3.565928	22667.316753
HLA A*0219	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.201124	0.635184	-3.565940	15889.986576
HLA B*7301	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.599441	1.033365	-3.566076	39759.518899
HLA B*5301	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.593302	1.027198	-3.566104	39201.430609
HLA A*0219	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.385509	0.819048	-3.566461	24294.544665
HLA A*0211	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.359639	0.793168	-3.566471	22889.620085
HLA A*2601	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.298012	0.731526	-3.566486	19861.479339
HLA A*3201	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.496273	0.929716	-3.566557	31352.551128
HLA A*0202	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.508133	0.941565	-3.566568	32220.560056
HLA B*0702	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.469129	0.902388	-3.566741	29452.982850
HLA B*0801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.341010	0.774258	-3.566751	21928.529927
HLA B*5701	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.398732	0.831902	-3.566830	25045.612985
HLA A*2403	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.342553	0.775707	-3.566846	22006.609115
HLA A*1101	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.391599	0.824605	-3.566994	24637.612986
HLA A*2603	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.619644	1.052564	-3.567081	41652.813540
HLA A*3001	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.295408	0.728232	-3.567176	19742.782609
HLA A*0201	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.399103	0.831902	-3.567201	25067.030187
HLA B*5301	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.572387	1.005151	-3.567236	37358.273812
HLA A*3001	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.293336	0.726094	-3.567242	19648.803872
HLA A*0203	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.342657	0.775312	-3.567345	22011.848084
HLA B*1509	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.500352	0.932998	-3.567354	31648.387740
HLA A*0250	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.594639	1.027198	-3.567440	39322.287425
HLA B*0802	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.460072	0.892605	-3.567467	28845.098069
HLA A*2601	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.395884	0.828408	-3.567476	24881.931468
HLA B*5301	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.596093	1.028547	-3.567546	39454.187535
HLA B*0802	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.490061	0.922498	-3.567563	30907.284256
HLA A*0101	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.381714	0.813920	-3.567794	24083.208497
HLA B*4501	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.618747	1.050933	-3.567814	41566.823650
HLA A*2601	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.392510	0.824605	-3.567905	24689.382561
HLA B*0803	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.473220	0.905240	-3.567979	29731.699718
HLA A*2402	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.501059	0.932998	-3.568061	31699.965218
HLA B*5101	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.474331	0.906227	-3.568104	29807.876920
HLA B*1502	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.555550	0.987241	-3.568309	35937.709299
HLA A*3101	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.381888	0.813260	-3.568628	24092.851701
HLA B*5801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.344369	0.775634	-3.568735	22098.830020
HLA A*2301	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.537981	0.969193	-3.568788	34512.859424
HLA B*3901	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.468749	0.899837	-3.568911	29427.181504
HLA A*3101	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.397587	0.828408	-3.569180	24979.714259
HLA A*2301	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.529687	0.960386	-3.569301	33860.023910
HLA B*1801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.476159	0.906788	-3.569371	29933.599498
HLA A*2902	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.471780	0.902388	-3.569391	29633.264919

HLA A*6901	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.359728	0.790294	-3.569434	22894.326120
HLA B*0801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.242524	0.673013	-3.569511	17479.290713
HLA A*0101	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.377257	0.807656	-3.569602	23837.317028
HLA A*0219	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.301172	0.731526	-3.569646	20006.524495
HLA A*6802	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.398090	0.828408	-3.569682	25008.650427
HLA A*0250	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.525141	0.955413	-3.569729	33507.421357
HLA B*4501	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.470013	0.900174	-3.569838	29512.954676
HLA B*0801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.377661	0.807776	-3.569885	23859.507996
HLA A*0101	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.345521	0.775634	-3.569886	22157.488321
HLA A*0201	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.318433	0.748391	-3.570042	20817.727359
HLA B*4002	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.577488	1.007289	-3.570198	37799.628610
HLA A*2902	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.427365	0.857166	-3.570199	26752.528729
HLA A*6801	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.596784	1.026553	-3.570231	39516.989643
HLA B*5401	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.451776	0.881518	-3.570258	28299.319233
HLA B*0801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.342945	0.772641	-3.570305	22026.500002
HLA B*1517	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.371508	0.801202	-3.570306	23523.838149
HLA A*2902	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.371832	0.801202	-3.570630	23541.406774
HLA B*5401	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.498232	0.927581	-3.570652	31494.328658
HLA B*4402	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.427823	0.857166	-3.570657	26780.765623
HLA A*3301	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.614041	1.043287	-3.570754	41118.836796
HLA A*2603	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.497755	0.926967	-3.570789	31459.760335
HLA A*2403	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.427964	0.857166	-3.570798	26789.459892
HLA A*0212	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.372004	0.801202	-3.570802	23550.705627
HLA B*4001	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.384726	0.813884	-3.570843	24250.817609
HLA A*0206	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.402813	0.831902	-3.570911	25282.075320
HLA A*3002	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.468652	0.897730	-3.570922	29420.655118
HLA B*2705	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.352740	0.781791	-3.570950	22528.926413
HLA A*2603	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.372152	0.801202	-3.570950	23558.733618
HLA B*4002	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.614339	1.043287	-3.571052	41147.097444
HLA B*5101	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.468847	0.897730	-3.571117	29433.868571
HLA B*1509	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.476384	0.905240	-3.571144	29949.149531
HLA B*0802	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.470999	0.899837	-3.571162	29580.088878
HLA A*3301	1:277-285	9	AATGANLVT	1.269350	-0.216786	-4.623742	1.052564	-3.571178	42047.661184
HLA B*4801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.433363	0.862117	-3.571247	27124.583253
HLA A*0201	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.378937	0.807656	-3.571282	23929.700013
HLA A*0250	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.352731	0.781170	-3.571562	22528.438903
HLA B*4501	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.554221	0.982586	-3.571634	35827.836433
HLA A*2501	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.474040	0.902388	-3.571652	29787.887719
HLA A*3002	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.381158	0.809432	-3.571725	24052.350149
HLA A*2501	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.475362	0.903619	-3.571743	29878.753009
HLA A*0301	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.362077	0.790294	-3.571783	23018.517514
HLA A*3101	1:495-503	9	RISTRITNE	0.934031	-0.590821	-3.914999	0.343210	-3.571789	8222.399005
HLA B*5801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.373012	0.801202	-3.571810	23605.426579
HLA A*3001	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.178334	0.606435	-3.571899	15077.645419
HLA B*3801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.552644	0.980728	-3.571916	35698.015880
HLA A*3001	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.083687	0.511716	-3.571971	12125.143076
HLA A*6801	1:418-426	9	KRLDTLRHA	1.129735	-0.020620	-4.681112	1.109115	-3.571997	47985.670643
HLA B*5101	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.474535	0.902388	-3.572147	29821.909608
HLA B*4002	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.400592	0.828408	-3.572185	25153.154448
HLA A*2603	1:183-191	9	MHTPHGQQV	0.909550	0.163287	-4.645080	1.072837	-3.572242	44165.165971
HLA A*0219	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.335683	0.763388	-3.572295	21661.236066
HLA A*0201	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.373517	0.801202	-3.572315	23632.898642
HLA A*0211	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.129981	0.557541	-3.572440	13489.042545
HLA B*4601	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.381886	0.809432	-3.572453	24092.721362
HLA B*5801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.356265	0.783681	-3.572584	22712.488686
HLA B*4501	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.288184	0.715584	-3.572600	19417.070035
HLA B*1801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.477949	0.905240	-3.572709	30057.250529
HLA A*0301	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.356516	0.783681	-3.572836	22725.639801
HLA B*1502	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.247068	0.674222	-3.572846	17663.131797
HLA A*2403	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.386991	0.813884	-3.573108	24377.619208
HLA B*1509	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.397740	0.824605	-3.573135	24988.499740
HLA A*2301	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.500192	0.926967	-3.573225	31636.747311
HLA A*0202	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.285632	0.712255	-3.573378	19303.326495
HLA A*3301	1:327-335	9	GKTAEFLVQ	1.236085	-0.179689	-4.629808	1.056396	-3.573412	42639.118167
HLA B*5301	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.590680	1.017228	-3.573452	38965.467492

HLA A*1101	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.494346	0.920891	-3.573455	31213.775830
HLA B*3801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.515022	0.941565	-3.573457	32735.710780
HLA A*0216	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.354651	0.781170	-3.573481	22628.232261
HLA A*2402	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.494934	0.921448	-3.573486	31256.020157
HLA B*1509	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.486344	0.912830	-3.573514	30643.894686
HLA A*0212	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.328155	0.754590	-3.573566	21289.010953
HLA B*4601	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.374800	0.801202	-3.573598	23702.808685
HLA A*8001	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.328210	0.754547	-3.573663	21291.660055
HLA A*0203	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-3.978059	0.404390	-3.573669	9507.333430
HLA B*0802	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.473899	0.900138	-3.573761	29778.220338
HLA B*5401	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.561006	0.987241	-3.573765	36391.997629
HLA B*1502	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.479122	0.905240	-3.573881	30138.500739
HLA A*2601	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.387797	0.813884	-3.573914	24422.896117
HLA A*3001	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.289396	0.715416	-3.573980	19471.348565
HLA A*0211	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.286257	0.712255	-3.574003	19331.124567
HLA A*2602	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.507210	0.933159	-3.574050	32152.129131
HLA A*2602	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.595003	1.020917	-3.574086	39355.274282
HLA A*2602	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.381888	0.807776	-3.574112	24092.851701
HLA A*2601	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.375321	0.801202	-3.574119	23731.292750
HLA B*5701	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.398821	0.824605	-3.574216	25050.762285
HLA A*0201	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.369088	0.794851	-3.574237	23393.123474
HLA B*7301	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.476469	0.902116	-3.574353	29954.982876
HLA B*0702	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.369262	0.794851	-3.574411	23402.490360
HLA B*1501	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.327242	0.752770	-3.574472	21244.256469
HLA B*0702	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.388432	0.813884	-3.574548	24458.595977
HLA A*3002	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.388509	0.813884	-3.574626	24462.962870
HLA A*2301	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.478515	0.903619	-3.574896	30096.464227
HLA B*0803	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.399509	0.824605	-3.574904	25090.501674
HLA A*0212	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.418686	0.843518	-3.575168	26223.209314
HLA A*0211	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.223166	0.647881	-3.575286	16717.310103
HLA B*2705	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.432496	0.857166	-3.575330	27070.489838
HLA B*0801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.359011	0.783681	-3.575331	22856.581260
HLA A*0211	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.418987	0.843518	-3.575469	26241.374279
HLA B*1502	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.588208	1.012736	-3.575472	38744.336939
HLA B*1502	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.457074	0.881518	-3.575556	28646.665502
HLA A*1101	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.478006	0.902388	-3.575617	30061.153336
HLA B*1502	1:208-216	9	PANIANALI	0.995189	0.008861	-4.579729	1.004050	-3.575679	37995.218075
HLA B*2705	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.330324	0.754590	-3.575734	21395.579806
HLA A*0101	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.362084	0.786323	-3.575762	23018.891100
HLA B*4002	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.619952	1.044058	-3.575895	41682.343163
HLA A*0203	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.308622	0.732703	-3.575919	20352.692314
HLA A*0201	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.389968	0.813920	-3.576048	24545.285407
HLA B*7301	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.556817	0.980728	-3.576089	36042.654084
HLA B*5401	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.517750	0.941565	-3.576184	32941.966951
HLA A*0250	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.473997	0.897730	-3.576267	29784.987175
HLA B*0801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.369692	0.793168	-3.576524	23425.670525
HLA A*2602	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.520271	0.943730	-3.576541	33133.744924
HLA A*2301	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.518147	0.941565	-3.576581	32972.098617
HLA A*6801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.483478	0.906788	-3.576690	30442.308968
HLA B*0702	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.384360	0.807656	-3.576704	24230.359942
HLA A*3101	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.350990	0.774258	-3.576732	22438.309295
HLA B*0803	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.476925	0.900174	-3.576751	29986.437688
HLA A*2602	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.610145	1.033365	-3.576781	40751.666580
HLA A*0211	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.539546	0.962750	-3.576795	34637.433063
HLA B*4601	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.371659	0.794851	-3.576808	23531.984286
HLA A*2601	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.366316	0.789472	-3.576844	23244.265149
HLA B*7301	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.434068	0.857166	-3.576902	27168.641292
HLA A*2601	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.386371	0.809432	-3.576939	24342.827681
HLA B*4002	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.605644	1.028547	-3.577097	40331.443035
HLA B*4001	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.386665	0.809432	-3.577232	24359.294748
HLA A*0219	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.391176	0.813884	-3.577292	24613.633047
HLA B*4601	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.352931	0.775634	-3.577297	22538.800775
HLA B*4403	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.598208	1.020890	-3.577318	39646.754451
HLA B*5301	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.590074	1.012736	-3.577337	38911.119324
HLA A*2301	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.512200	0.934761	-3.577439	32523.707273

HLA B*7301	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.582609	1.005151	-3.577459	38248.059837
HLA B*0803	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.479007	0.901531	-3.577476	30130.512546
HLA B*3501	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.309038	0.731526	-3.577512	20372.190376
HLA A*1101	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.475311	0.897730	-3.577581	29875.197124
HLA B*1503	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.358854	0.781170	-3.577684	22848.298106
HLA A*0202	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.479274	0.901531	-3.577743	30149.100589
HLA B*5301	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.598750	1.020890	-3.577861	39696.331353
HLA B*0803	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.484659	0.906788	-3.577872	30525.260606
HLA A*0216	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.213148	0.635184	-3.577964	16336.092902
HLA B*1517	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.135672	0.557541	-3.578130	13666.949105
HLA A*0219	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.352531	0.774258	-3.578273	22518.081794
HLA B*2705	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.314371	0.736037	-3.578334	20623.912474
HLA B*4601	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.392226	0.813884	-3.578342	24673.226264
HLA B*4402	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.392346	0.813884	-3.578462	24680.034653
HLA B*5401	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.392360	0.813884	-3.578476	24680.835764
HLA B*3501	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.396955	0.818458	-3.578497	24943.388713
HLA B*5301	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.541510	0.962975	-3.578535	34794.441430
HLA A*3301	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.599467	1.020917	-3.578550	39761.885010
HLA B*3901	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.501155	0.922498	-3.578657	31706.997223
HLA A*0212	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.342151	0.763388	-3.578764	21986.260412
HLA B*4001	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.354458	0.775634	-3.578824	22618.196357
HLA A*0301	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.365303	0.786323	-3.578980	23190.130510
HLA A*0219	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.294602	0.715584	-3.579019	19706.182028
HLA A*6802	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.410928	0.831902	-3.579026	25758.931372
HLA B*4601	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.392287	0.813260	-3.579027	24676.696973
HLA A*0250	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.386879	0.807776	-3.579102	24371.289779
HLA B*5701	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.372291	0.793168	-3.579123	23566.254376
HLA A*2301	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.541893	0.962750	-3.579142	34825.137116
HLA B*2705	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.441427	0.862117	-3.579310	27632.902640
HLA A*0301	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.352111	0.772641	-3.579470	22496.286510
HLA A*2902	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.461017	0.881518	-3.579499	28907.897943
HLA B*5801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.353828	0.774258	-3.579570	22585.427119
HLA B*4601	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.387381	0.807776	-3.579605	24399.521157
HLA B*1517	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.482019	0.902388	-3.579630	30340.208379
HLA B*4402	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.423319	0.843518	-3.579801	26504.464002
HLA A*6901	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.224407	0.644580	-3.579826	16765.130051
HLA B*4801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.272367	0.692424	-3.579943	18722.634710
HLA B*1502	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.507048	0.926967	-3.580081	32140.129549
HLA B*4002	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.631084	1.050933	-3.580151	42764.557706
HLA B*1509	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.423700	0.843518	-3.580182	26527.702750
HLA B*4403	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.623493	1.043287	-3.580206	42023.555938
HLA B*0801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.358259	0.778023	-3.580237	22817.046987
HLA A*6802	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.404854	0.824605	-3.580249	25401.211073
HLA A*3201	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-3.851187	0.270903	-3.580284	7098.826063
HLA B*5401	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.515160	0.934761	-3.580399	32746.161145
HLA B*0803	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.478137	0.897730	-3.580407	30070.261856
HLA B*4501	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.585520	1.005094	-3.580427	38505.292078
HLA B*0702	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.361605	0.781170	-3.580436	22993.501065
HLA B*0803	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.507466	0.926967	-3.580499	32171.094123
HLA B*0802	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.394420	0.813920	-3.580500	24798.211540
HLA B*4601	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.292906	0.712255	-3.580652	19629.360991
HLA B*5701	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.394580	0.813884	-3.580697	24807.335798
HLA A*6901	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.353398	0.772641	-3.580757	22563.078391
HLA B*4001	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.367126	0.786323	-3.580804	23287.689029
HLA B*5801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.346702	0.765882	-3.580821	22217.864818
HLA B*5101	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.481006	0.900174	-3.580832	30269.547672
HLA A*3301	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.312477	0.731526	-3.580951	20534.180346
HLA B*1509	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.399453	0.818458	-3.580995	25087.244201
HLA B*1517	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.478760	0.897730	-3.581030	30113.402119
HLA A*2601	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.399542	0.818458	-3.581084	25092.402061
HLA B*5701	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.409546	0.828408	-3.581139	25677.122017
HLA A*0216	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.355567	0.774258	-3.581309	22676.024990
HLA B*5401	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.544078	0.962750	-3.581327	35000.790741
HLA B*1501	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.395264	0.813920	-3.581344	24846.420191
HLA B*4601	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.400449	0.819048	-3.581401	25144.855195

HLA B*1517	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.296830	0.715416	-3.581414	19807.506261
HLA B*4801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.395355	0.813884	-3.581472	24851.662983
HLA A*0101	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.362648	0.781170	-3.581479	23048.797627
HLA B*1517	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.485160	0.903619	-3.581540	30560.455333
HLA A*0206	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.022079	0.440475	-3.581603	10521.524632
HLA A*3001	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-3.918340	0.336669	-3.581670	8285.896715
HLA B*4601	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.336231	0.754547	-3.581684	21688.557360
HLA A*3201	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.586784	1.005094	-3.581691	38617.525764
HLA B*4601	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.395926	0.813920	-3.582006	24884.354538
HLA A*3201	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.375197	0.793168	-3.582029	23724.489391
HLA A*0101	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.356382	0.774258	-3.582124	22718.633119
HLA B*1503	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.391624	0.809432	-3.582192	24639.079184
HLA B*1517	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.463937	0.881518	-3.582419	29102.943935
HLA A*0219	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.407093	0.824605	-3.582488	25532.508345
HLA B*0802	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.439711	0.857166	-3.582545	27523.989456
HLA B*1501	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.357891	0.775312	-3.582579	22797.675497
HLA A*2603	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.589888	1.007289	-3.582599	38894.492994
HLA A*1101	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.375812	0.793168	-3.582645	23758.140110
HLA B*1503	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.263115	0.680376	-3.582739	18327.983791
HLA B*3901	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.401297	0.818458	-3.582839	25194.010326
HLA A*0216	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.414819	0.831902	-3.582917	25990.736675
HLA A*0212	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.178319	0.595350	-3.582970	15077.156017
HLA B*5401	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.489278	0.906227	-3.583051	30851.655120
HLA B*3501	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.402261	0.819048	-3.583213	25249.954035
HLA B*4801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.397165	0.813920	-3.583245	24955.401351
HLA A*1101	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.445392	0.862117	-3.583276	27886.399036
HLA A*0216	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.397244	0.813884	-3.583361	24959.991976
HLA A*8001	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.440571	0.857166	-3.583405	27578.541479
HLA B*1502	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.016792	0.433361	-3.583431	10394.230299
HLA B*3901	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.157273	0.573435	-3.583838	14363.912214
HLA B*4801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.302292	0.718317	-3.583976	20058.218344
HLA A*0211	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.485519	0.901531	-3.583988	30585.761092
HLA B*1509	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.486400	0.902388	-3.584012	30647.873666
HLA A*0101	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.378904	0.794851	-3.584053	23927.887683
HLA B*1502	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.496280	0.911989	-3.584290	31353.059974
HLA A*2601	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.391963	0.807656	-3.584307	24658.281097
HLA A*2601	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.370655	0.786323	-3.584333	23477.687607
HLA B*5401	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.486551	0.902116	-3.584435	30658.486805
HLA B*5801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.337490	0.752770	-3.584720	21751.538952
HLA B*5301	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.484692	0.899837	-3.584855	30527.572630
HLA B*4001	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.275764	0.690895	-3.584869	18869.670618
HLA B*0702	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.394420	0.809432	-3.584988	24798.211540
HLA B*1517	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.398976	0.813884	-3.585092	25059.708324
HLA A*2501	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.337882	0.752770	-3.585113	21771.199292
HLA B*4501	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.545544	0.960386	-3.585158	35119.145046
HLA A*0101	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.386406	0.801202	-3.585204	24344.803141
HLA B*2705	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.394641	0.809432	-3.585209	24810.825371
HLA A*0202	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.399190	0.813884	-3.585306	25072.048254
HLA A*0101	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.374781	0.789472	-3.585309	23701.782871
HLA A*0216	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.237181	0.651841	-3.585340	17265.576204
HLA B*7301	1:208-216	9	PANIANALI	0.995189	0.008861	-4.589489	1.004050	-3.585438	38858.738906
HLA A*2402	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.520322	0.934761	-3.585561	33137.688656
HLA A*2902	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.304015	0.718317	-3.585698	20137.916094
HLA A*8001	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.363750	0.778023	-3.585727	23107.352164
HLA A*0301	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.349329	0.763388	-3.585941	22352.651354
HLA B*5401	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.489563	0.903619	-3.585943	30871.857120
HLA B*5701	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.380861	0.794851	-3.586011	24035.960546
HLA B*0801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.361847	0.775707	-3.586140	23006.317041
HLA A*0212	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.410785	0.824605	-3.586179	25750.432244
HLA B*3901	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.395628	0.809432	-3.586196	24867.263467
HLA B*7301	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.488646	0.902388	-3.586258	30806.790588
HLA A*3301	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.629597	1.043307	-3.586290	42618.362659
HLA A*2301	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.541775	0.955413	-3.586363	34815.718383
HLA B*1502	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.614985	1.028547	-3.586438	41208.358342
HLA A*8001	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.367615	0.781170	-3.586446	23313.908412

HLA A*0101	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.301916	0.715416	-3.586500	20040.863817
HLA B*4601	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.394181	0.807656	-3.586525	24784.531446
HLA B*4801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.405012	0.818458	-3.586554	25410.419730
HLA B*4001	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.360849	0.774258	-3.586591	22953.481614
HLA A*2603	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.613808	1.027198	-3.586610	41096.820306
HLA B*2705	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.341289	0.754547	-3.586742	21942.651551
HLA A*3101	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.394402	0.807656	-3.586746	24797.138319
HLA B*4001	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.377044	0.790294	-3.586750	23825.584807
HLA B*3501	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.370463	0.783681	-3.586782	23467.274958
HLA B*1502	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.484523	0.897730	-3.586793	30515.684089
HLA B*4801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.430360	0.843518	-3.586843	26937.695071
HLA A*0216	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.352802	0.765882	-3.586920	22532.095490
HLA A*3301	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.394747	0.807776	-3.586970	24816.866178
HLA A*2403	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.418907	0.831902	-3.587005	26236.547983
HLA B*5401	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.405498	0.818458	-3.587040	25438.891453
HLA B*1517	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.328870	0.741770	-3.587100	21324.051801
HLA B*0802	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.430746	0.843518	-3.587228	26961.605388
HLA B*5801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.362543	0.775312	-3.587231	23043.187195
HLA A*2603	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.630633	1.043287	-3.587346	42720.161276
HLA A*2601	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.382252	0.794851	-3.587401	24113.062820
HLA A*2601	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.361708	0.774258	-3.587450	22998.974977
HLA A*8001	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.395325	0.807776	-3.587548	24849.915263
HLA A*2602	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.574790	0.987241	-3.587549	37565.599500
HLA A*2602	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.342142	0.754547	-3.587595	21985.784644
HLA A*3301	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.604967	1.017185	-3.587782	40268.653635
HLA A*2601	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.363424	0.775634	-3.587789	23089.982554
HLA B*0803	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.487984	0.900138	-3.587846	30759.827927
HLA A*2402	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.568597	0.980728	-3.587870	37033.698075
HLA B*1509	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.508037	0.920085	-3.587952	32213.414153
HLA B*0802	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.490376	0.902388	-3.587988	30929.697847
HLA A*3001	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.234030	0.645964	-3.588066	17140.773544
HLA A*2601	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.300413	0.712255	-3.588158	19971.595736
HLA A*3101	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.369441	0.781170	-3.588271	23412.114309
HLA B*0801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.330052	0.741770	-3.588281	21382.157283
HLA A*3301	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-3.823693	0.235291	-3.588402	6663.353620
HLA A*3101	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.330277	0.741770	-3.588507	21393.264977
HLA A*6802	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.120748	0.532233	-3.588514	13205.281038
HLA A*3201	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.609509	1.020917	-3.588591	40691.965153
HLA A*2501	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.343397	0.754547	-3.588850	22049.390786
HLA A*3001	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.198088	0.609194	-3.588894	15779.309539
HLA B*0702	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.378376	0.789472	-3.588904	23898.779778
HLA A*0212	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.236810	0.647881	-3.588929	17250.824543
HLA B*0702	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.420883	0.831902	-3.588981	26356.188805
HLA A*0250	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.383869	0.794851	-3.589018	24202.978960
HLA A*0203	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-3.640551	0.051389	-3.589162	4370.695045
HLA B*3801	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.549585	0.960386	-3.589199	35447.454108
HLA A*0206	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.198436	0.609194	-3.589242	15791.948516
HLA A*0202	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.315358	0.726094	-3.589264	20670.826445
HLA B*2705	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.379562	0.790294	-3.589268	23964.160370
HLA B*1801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.492946	0.903619	-3.589327	31113.295518
HLA B*0702	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.451482	0.862117	-3.589366	28280.188680
HLA A*0101	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.364934	0.775312	-3.589623	23170.442275
HLA B*3801	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.545055	0.955413	-3.589643	35079.649209
HLA B*1501	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.321283	0.731526	-3.589757	20954.786570
HLA B*4001	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.370928	0.781170	-3.589758	23492.425586
HLA A*1101	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.399286	0.809432	-3.589854	25077.609988
HLA A*6901	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.305279	0.715416	-3.589862	20196.613287
HLA A*2402	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.572542	0.982586	-3.589955	37371.615065
HLA B*5101	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.365785	0.775707	-3.590078	23215.863264
HLA B*4403	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.595250	1.005151	-3.590099	39377.635938
HLA A*0250	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.512710	0.922498	-3.590212	32561.910767
HLA A*2902	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.372004	0.781791	-3.590213	23550.705627
HLA A*2402	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.545847	0.955413	-3.590435	35143.662397
HLA A*2403	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.306023	0.715584	-3.590440	20231.278880
HLA A*3101	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.399956	0.809432	-3.590523	25116.304931

HLA B*4002	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.553509	0.962975	-3.590534	35769.155680
HLA B*1509	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.191340	0.600770	-3.590570	15536.037998
HLA B*0803	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.494212	0.903619	-3.590593	31204.152119
HLA A*0206	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.511556	0.920891	-3.590665	32475.532782
HLA A*0301	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.356551	0.765882	-3.590670	22727.484024
HLA B*1502	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.494379	0.903619	-3.590760	31216.140002
HLA A*0101	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.381169	0.790294	-3.590875	24053.000760
HLA B*4501	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.627839	1.036964	-3.590876	42446.251783
HLA A*6901	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.377368	0.786323	-3.591045	23843.378789
HLA B*5701	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.404314	0.813260	-3.591054	25369.624649
HLA B*4601	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.374828	0.783681	-3.591147	23704.347490
HLA B*1801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.306768	0.715584	-3.591185	20266.003972
HLA B*1502	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.483811	0.892605	-3.591206	30465.703864
HLA A*3002	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.283743	0.692424	-3.591319	19219.548026
HLA B*1801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.365634	0.774258	-3.591376	23207.826560
HLA A*0206	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.372549	0.781170	-3.591379	23580.282540
HLA A*0301	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.365644	0.774258	-3.591386	23208.328772
HLA B*4002	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.612276	1.020890	-3.591387	40952.116992
HLA B*3901	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.377732	0.786323	-3.591409	23863.380629
HLA B*4001	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.380946	0.789472	-3.591474	24040.642150
HLA B*0702	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.435043	0.843518	-3.591525	27229.706240
HLA B*0801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.354951	0.763388	-3.591564	22643.906965
HLA B*3901	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.498418	0.906788	-3.591630	31507.791620
HLA A*0301	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.367307	0.775634	-3.591673	23297.391804
HLA A*6801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.375474	0.783681	-3.591794	23739.639156
HLA A*0216	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.367164	0.775312	-3.591852	23289.704858
HLA A*2402	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.466519	0.874608	-3.591911	29276.489956
HLA A*0250	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.526779	0.934761	-3.592017	33634.006054
HLA A*1101	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.493611	0.901531	-3.592080	31160.966413
HLA A*0216	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.032576	0.440475	-3.592101	10778.942997
HLA A*2602	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.525150	0.932998	-3.592153	33508.146451
HLA A*0201	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.373437	0.781170	-3.592268	23628.552096
HLA B*1509	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.552663	0.960386	-3.592277	35699.560892
HLA A*1101	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.373468	0.781170	-3.592298	23630.213916
HLA B*1509	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.342539	0.750232	-3.592307	22005.894807
HLA A*3201	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.609546	1.017228	-3.592318	40695.487529
HLA A*2403	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.310692	0.718317	-3.592375	20449.927063
HLA A*2902	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.376130	0.783681	-3.592449	23775.497850
HLA A*0212	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.400118	0.807656	-3.592462	25125.682154
HLA A*0202	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.436147	0.843518	-3.592629	27299.029891
HLA A*6901	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.394094	0.801202	-3.592892	24779.570925
HLA B*4403	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.621587	1.028547	-3.593040	41839.584819
HLA B*1502	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.226493	0.633434	-3.593059	16845.863191
HLA B*4801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.401004	0.807776	-3.593227	25176.978985
HLA A*6802	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.375021	0.781791	-3.593230	23714.865330
HLA A*0101	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.347809	0.754547	-3.593262	22274.549408
HLA B*3501	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.285728	0.692424	-3.593304	19307.608553
HLA A*0250	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.580601	0.987241	-3.593360	38071.553675
HLA B*1517	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.260067	0.666703	-3.593365	18199.833297
HLA B*1501	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.284309	0.690895	-3.593414	19244.622493
HLA B*4403	1:93-101	9	CYGFQAMAQ	1.067894	-0.016961	-4.644457	1.050933	-3.593524	44101.895243
HLA A*0202	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.502128	0.908582	-3.593546	31778.090782
HLA A*3002	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.274026	0.680376	-3.593650	18794.280333
HLA B*4801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.401370	0.807656	-3.593714	25198.235881
HLA A*2301	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.526748	0.932998	-3.593750	33631.640706
HLA B*1517	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.189108	0.595350	-3.593758	15456.396996
HLA B*3801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.508946	0.915104	-3.593842	32280.927679
HLA B*5101	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.407206	0.813260	-3.593946	25539.139351
HLA A*0201	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.306310	0.712255	-3.594055	20244.636062
HLA A*1101	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.475581	0.881518	-3.594063	29893.789380
HLA B*4001	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.395278	0.801202	-3.594076	24847.226702
HLA B*5801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.366844	0.772641	-3.594203	23272.575878
HLA A*2902	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.369979	0.775707	-3.594272	23441.136722
HLA B*1801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.286887	0.692424	-3.594463	19359.172131
HLA A*0101	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.376282	0.781791	-3.594492	23783.859803

HLA A*0212	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.408456	0.813920	-3.594536	25612.748428
HLA B*5701	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.413071	0.818458	-3.594612	25886.335310
HLA A*2403	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.402291	0.807656	-3.594635	25251.729890
HLA B*4801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.426575	0.831902	-3.594674	26703.944219
HLA A*0301	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.336517	0.741770	-3.594747	21702.876673
HLA B*3801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.516370	0.921448	-3.594923	32837.522204
HLA B*3801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.522542	0.927581	-3.594962	33307.533744
HLA B*7301	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.577553	0.982586	-3.594967	37805.354814
HLA B*1503	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.457208	0.862117	-3.595091	28655.500455
HLA B*1502	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.600313	1.005094	-3.595219	39839.399127
HLA A*2602	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.622419	1.027198	-3.595221	41919.788614
HLA A*0203	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.427172	0.831902	-3.595270	26740.663648
HLA B*2705	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.402975	0.807656	-3.595319	25291.514434
HLA B*1501	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.313741	0.718317	-3.595425	20594.032554
HLA B*5701	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.405064	0.809432	-3.595631	25413.444197
HLA A*6801	1:140-148	9	SHGDAVTAA	1.303920	-0.260613	-4.638971	1.043307	-3.595665	43548.299976
HLA A*0206	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.452847	0.857166	-3.595681	28369.217272
HLA A*0202	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.424092	0.828408	-3.595684	26551.680072
HLA B*3801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.507767	0.911989	-3.595777	32193.379221
HLA B*3901	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.453172	0.857166	-3.596005	28390.404636
HLA A*0212	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.327540	0.731526	-3.596014	21258.857476
HLA B*7301	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.565216	0.969193	-3.596023	36746.516294
HLA A*2301	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.518602	0.922498	-3.596104	33006.721610
HLA B*1517	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.405555	0.809432	-3.596122	25442.194585
HLA A*0201	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.371654	0.775312	-3.596342	23531.729677
HLA B*4001	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.372053	0.775707	-3.596346	23553.381320
HLA B*3501	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.311975	0.715584	-3.596391	20510.421347
HLA B*7301	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.623613	1.027198	-3.596414	42035.152020
HLA B*5101	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.511775	0.915104	-3.596671	32491.875973
HLA B*5801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.351272	0.754590	-3.596682	22452.880676
HLA B*4402	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.404556	0.807776	-3.596780	25383.765015
HLA B*5101	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.503789	0.906788	-3.597001	31899.868095
HLA A*2602	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.526960	0.929716	-3.597244	33648.019603
HLA B*1502	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.618164	1.020917	-3.597247	41511.092811
HLA A*6901	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.392106	0.794851	-3.597255	24666.419753
HLA B*1801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.497438	0.900138	-3.597301	31436.792558
HLA B*4402	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.416404	0.819048	-3.597357	26085.819903
HLA B*0801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.325705	0.728232	-3.597473	21169.225666
HLA B*0702	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.363372	0.765882	-3.597490	23087.234604
HLA A*0101	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.370141	0.772641	-3.597500	23449.888518
HLA B*4501	1:127-135	9	LHSDLPEVQ	1.043585	-0.000298	-4.640858	1.043287	-3.597571	43737.891439
HLA B*5101	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.472231	0.874608	-3.597623	29664.060944
HLA A*2602	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.560386	0.962750	-3.597635	36340.059285
HLA B*1502	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.518527	0.920891	-3.597636	33001.008098
HLA B*1502	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.270680	0.673013	-3.597667	18650.051431
HLA A*2602	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.602871	1.005094	-3.597778	40074.800477
HLA B*1517	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.278156	0.680376	-3.597780	18973.877620
HLA A*0250	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.441363	0.843518	-3.597845	27628.866679
HLA B*4002	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.618777	1.020917	-3.597860	41569.747087
HLA A*2402	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.560886	0.962975	-3.597912	36381.958303
HLA B*2705	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.405735	0.807776	-3.597959	25452.795031
HLA A*3101	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.361396	0.763388	-3.598008	22982.432816
HLA A*3201	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.472679	0.874608	-3.598072	29694.728328
HLA B*4402	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.430095	0.831902	-3.598193	26921.232620
HLA B*5401	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.455427	0.857166	-3.598261	28538.233562
HLA A*3201	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.625502	1.027198	-3.598303	42218.384252
HLA A*0201	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.372563	0.774258	-3.598305	23581.047953
HLA B*4002	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.631791	1.033365	-3.598426	42834.251241
HLA A*0203	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.412432	0.813920	-3.598512	25848.271842
HLA A*2602	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.615822	1.017228	-3.598594	41287.798839
HLA A*2601	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.353246	0.754590	-3.598656	22555.145642
HLA A*3001	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.300046	0.701295	-3.598752	19954.747964
HLA B*4601	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.376874	0.778023	-3.598852	23816.306262
HLA B*3501	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.430797	0.831902	-3.598896	26964.814483
HLA A*8001	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.406649	0.807656	-3.598994	25506.415487

HLA B*0802	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.406774	0.807776	-3.598997	25513.729840
HLA B*5101	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.499353	0.900138	-3.599215	31575.705264
HLA A*6801	1:35-43	9	REARVFSEV	0.807139	0.210046	-4.616442	1.017185	-3.599257	41346.808645
HLA B*1503	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.500796	0.901531	-3.599265	31680.763786
HLA A*0101	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.362665	0.763388	-3.599277	23049.670483
HLA B*2705	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.443027	0.843518	-3.599509	27734.893729
HLA B*4002	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.604751	1.005151	-3.599600	40248.616518
HLA B*3501	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.443266	0.843518	-3.599748	27750.202307
HLA A*2602	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.086107	0.486297	-3.599810	12192.895215
HLA B*4501	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.393041	0.793168	-3.599874	24719.587124
HLA A*3101	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.386265	0.786323	-3.599943	24336.902262
HLA A*2501	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.419059	0.819048	-3.600011	26245.775498
HLA A*2603	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.612756	1.012736	-3.600019	40997.337409
HLA B*1801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.541599	0.941565	-3.600034	34801.595060
HLA B*3901	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.497943	0.897730	-3.600213	31473.378787
HLA A*2501	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.409697	0.809432	-3.600264	25686.013821
HLA B*1501	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.390577	0.790294	-3.600283	24579.701416
HLA A*3002	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.500215	0.899837	-3.600378	31638.458870
HLA B*4402	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.373028	0.772641	-3.600387	23606.320515
HLA B*4801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.419459	0.819048	-3.600411	26269.924346
HLA A*3002	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.386756	0.786323	-3.600434	24364.434753
HLA A*0203	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.248353	0.647881	-3.600472	17715.478116
HLA B*5301	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.555987	0.955413	-3.600575	35973.889438
HLA B*5801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.348984	0.748391	-3.600593	22334.882392
HLA B*3801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.509282	0.908582	-3.600700	32305.910324
HLA B*2705	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.425340	0.824605	-3.600735	26628.063445
HLA A*2301	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.500986	0.900174	-3.600812	31694.649371
HLA B*4801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.402049	0.801202	-3.600847	25237.663077
HLA B*3501	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.425469	0.824605	-3.600864	26635.987642
HLA A*6901	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.333604	0.732703	-3.600901	21557.775312
HLA B*5401	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.384668	0.783681	-3.600987	24247.537975
HLA B*3801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.534217	0.933159	-3.601058	34215.041219
HLA B*4801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.429592	0.828408	-3.601184	26890.083505
HLA A*8001	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.402430	0.801202	-3.601228	25259.791111
HLA A*2603	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.638224	1.036964	-3.601260	43473.446293
HLA A*2601	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.394446	0.793168	-3.601279	24799.687296
HLA B*1517	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.354070	0.752770	-3.601301	22598.015646
HLA B*5701	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.402543	0.801202	-3.601341	25266.351291
HLA B*1501	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.196786	0.595350	-3.601437	15732.088506
HLA A*1101	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.379461	0.778023	-3.601438	23958.586350
HLA A*2402	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.507682	0.906227	-3.601455	32187.109977
HLA B*1509	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.501468	0.899837	-3.601630	31729.819100
HLA A*2602	1:208-216	9	PANIANALI	0.995189	0.008861	-4.605940	1.004050	-3.601889	40358.944175
HLA A*0219	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.430384	0.828408	-3.601976	26939.152410
HLA A*0202	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.237174	0.635184	-3.601990	17265.295992
HLA B*0702	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.415916	0.813920	-3.601996	26056.483162
HLA A*1101	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.354850	0.752770	-3.602081	22638.640033
HLA B*3801	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.529072	0.926967	-3.602105	33812.065014
HLA A*2601	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.392571	0.790294	-3.602277	24692.855543
HLA B*4501	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.635771	1.033365	-3.602406	43228.603638
HLA A*0201	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.392780	0.790294	-3.602487	24704.747525
HLA A*2403	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.365888	0.763388	-3.602500	23221.390113
HLA B*7301	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.537274	0.934761	-3.602513	34456.705223
HLA B*5401	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.517745	0.915104	-3.602641	32941.610528
HLA B*3901	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.277104	0.674222	-3.602882	18927.947635
HLA A*8001	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.421421	0.818458	-3.602962	26388.860789
HLA A*0219	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.392480	0.789472	-3.603008	24687.646253
HLA B*5301	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.515870	0.912830	-3.603040	32799.705110
HLA B*2705	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.386738	0.783681	-3.603057	24363.380304
HLA A*3001	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.230577	0.627429	-3.603148	17005.001489
HLA A*3301	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.572359	0.969193	-3.603165	37355.848641
HLA B*7301	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.624188	1.020890	-3.603298	42090.903309
HLA A*0201	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.369213	0.765882	-3.603331	23399.831808
HLA B*4403	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.431808	0.828408	-3.603400	27027.614462
HLA B*1502	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.584270	0.980728	-3.603543	38394.630819

HLA A*3001	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.238739	0.635184	-3.603555	17327.614814
HLA A*6801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.505727	0.902116	-3.603611	32042.560456
HLA A*3002	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.379381	0.775634	-3.603747	23954.179903
HLA B*5701	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.417753	0.813920	-3.603833	26166.949483
HLA B*5101	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.461343	0.857166	-3.604177	28929.644123
HLA A*6801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.428962	0.824605	-3.604357	26851.125159
HLA B*4002	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.632731	1.028301	-3.604430	42927.043024
HLA B*1502	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.513013	0.908582	-3.604431	32584.642864
HLA A*8001	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.436594	0.831902	-3.604692	27327.104415
HLA B*1503	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.433126	0.828408	-3.604718	27109.766461
HLA B*4801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.414243	0.809432	-3.604811	25956.310778
HLA A*0212	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.436800	0.831902	-3.604899	27340.117133
HLA A*0201	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.357794	0.752770	-3.605025	22792.619409
HLA A*0201	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.291377	0.686294	-3.605083	19560.351157
HLA A*2902	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.355318	0.750232	-3.605086	22663.025191
HLA B*7301	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.565512	0.960386	-3.605126	36771.572950
HLA B*4402	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-3.812293	0.207166	-3.605127	6490.724270
HLA A*0250	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.546700	0.941565	-3.605135	35212.744971
HLA A*3101	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.380789	0.775634	-3.605154	24031.929896
HLA B*4001	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.398332	0.793168	-3.605165	25022.589595
HLA A*0211	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.526130	0.920891	-3.605239	33583.823604
HLA B*5701	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.412923	0.807656	-3.605267	25877.514154
HLA B*4402	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.383418	0.778023	-3.605395	24177.852409
HLA A*0301	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.332728	0.727191	-3.605537	21514.317983
HLA B*1501	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.214807	0.609194	-3.605613	16398.605982
HLA A*3301	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.639091	1.033365	-3.605726	43560.316799
HLA B*5701	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.383756	0.778023	-3.605733	24196.694875
HLA A*2301	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.525914	0.920085	-3.605829	33567.112765
HLA A*0219	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.437766	0.831902	-3.605864	27400.974544
HLA B*0702	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.383916	0.778023	-3.605893	24205.597811
HLA B*0803	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.514542	0.908582	-3.605961	32699.603009
HLA A*3002	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.527023	0.920891	-3.606132	33652.934827
HLA A*3001	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.254043	0.647881	-3.606163	17949.127002
HLA A*6901	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.318523	0.712255	-3.606268	20822.007420
HLA B*5701	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.388084	0.781791	-3.606293	24439.020707
HLA B*4403	1:54-62	9	RARQPVALV	0.737262	0.289291	-4.632848	1.026553	-3.606295	42938.656121
HLA A*2403	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.419558	0.813260	-3.606297	26275.893955
HLA A*2603	1:208-216	9	PANIANALI	0.995189	0.008861	-4.610406	1.004050	-3.606356	40776.145211
HLA A*6801	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.569372	0.962975	-3.606398	37099.872032
HLA B*4801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.121185	0.514746	-3.606439	13218.575399
HLA B*5801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.356709	0.750232	-3.606477	22735.723379
HLA A*0219	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.450019	0.843518	-3.606501	28185.034678
HLA A*2501	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.414191	0.807656	-3.606536	25953.221705
HLA B*5301	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.593993	0.987241	-3.606752	39263.830385
HLA A*3101	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.355146	0.748391	-3.606755	22654.076833
HLA A*0206	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.481403	0.874608	-3.606795	30297.234905
HLA A*0250	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-3.309757	-0.297084	-3.606841	2040.596391
HLA A*0206	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.335136	0.728232	-3.606904	21633.949189
HLA B*4801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.390708	0.783681	-3.607028	24587.149058
HLA A*3301	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.550772	0.943730	-3.607042	35544.428748
HLA A*6901	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.335368	0.728232	-3.607136	21645.538982
HLA B*3501	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.416677	0.809432	-3.607245	26102.195123
HLA B*1503	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.426301	0.819048	-3.607253	26687.047118
HLA B*1502	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.402145	0.794851	-3.607295	25243.261549
HLA A*6901	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.361903	0.754590	-3.607314	23009.304314
HLA B*4601	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.373219	0.765882	-3.607337	23616.667096
HLA B*1801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.408635	0.801202	-3.607433	25623.281315
HLA A*0219	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.408637	0.801202	-3.607435	25623.419934
HLA A*2501	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.396913	0.789472	-3.607441	24940.959894
HLA B*0803	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.509839	0.902388	-3.607451	32347.357709
HLA B*3801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.489046	0.881518	-3.607528	30835.136045
HLA B*5401	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.534497	0.926967	-3.607530	34237.075161
HLA B*1509	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.435940	0.828408	-3.607533	27286.036728
HLA B*3901	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.383195	0.775634	-3.607560	24165.429649
HLA B*0803	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.408769	0.801202	-3.607567	25631.183823

HLA B*1501	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.394033	0.786323	-3.607710	24776.085747
HLA A*2403	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.360480	0.752770	-3.607710	22933.994292
HLA A*3101	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.362507	0.754590	-3.607918	23041.317355
HLA B*1517	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.402815	0.794851	-3.607964	25282.212094
HLA B*4402	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.432642	0.824605	-3.608037	27079.571159
HLA B*4801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.401380	0.793168	-3.608212	25198.781165
HLA A*8001	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.383930	0.775707	-3.608223	24206.383521
HLA B*0803	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.530740	0.922498	-3.608242	33942.187618
HLA A*2501	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.421660	0.813260	-3.608400	26403.426410
HLA A*0206	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.334497	0.726094	-3.608403	21602.138463
HLA A*0206	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.384123	0.775634	-3.608488	24217.124119
HLA B*1509	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.506282	0.897730	-3.608552	32083.496404
HLA A*6802	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.363215	0.754547	-3.608668	23078.867862
HLA A*6801	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.542041	0.933159	-3.608881	34837.008347
HLA B*1801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.422168	0.813260	-3.608907	26434.297799
HLA A*0206	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.437362	0.828408	-3.608954	27375.489770
HLA A*0101	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.357376	0.748391	-3.608985	22770.681586
HLA A*0203	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.363569	0.754547	-3.609022	23097.728536
HLA A*0301	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.253632	0.644580	-3.609052	17932.142056
HLA A*2602	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.514392	0.905240	-3.609152	32688.283290
HLA A*0216	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.417081	0.807656	-3.609425	26126.494543
HLA B*4501	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.638419	1.028966	-3.609453	43492.971158
HLA B*4002	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.542457	0.932998	-3.609459	34870.382514
HLA A*0250	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.088564	0.479051	-3.609513	12262.087274
HLA B*5401	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-3.675572	0.066046	-3.609526	4737.747697
HLA A*6901	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.364105	0.754547	-3.609558	23126.236117
HLA B*1801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.385279	0.775707	-3.609572	24281.667861
HLA B*1501	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.141837	0.532233	-3.609603	13862.342529
HLA A*3001	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.141865	0.532233	-3.609631	13863.242483
HLA B*4501	1:214-222	9	ALIEQVRTQ	0.889297	0.115854	-4.614882	1.005151	-3.609731	41198.550472
HLA B*4403	1:481-489	9	MTADWTRVP	0.898983	0.129318	-4.638139	1.028301	-3.609838	43464.980402
HLA B*2705	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.396248	0.786323	-3.609926	24902.804534
HLA A*3001	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.177319	0.567351	-3.609967	15042.449019
HLA B*4403	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.638985	1.028966	-3.610019	43549.713548
HLA A*3201	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.536989	0.926967	-3.610023	34434.157362
HLA B*4601	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.391307	0.781170	-3.610138	24621.090971
HLA B*4801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.364775	0.754590	-3.610185	23161.920075
HLA B*3801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.530416	0.920085	-3.610331	33916.857035
HLA B*0802	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.472545	0.862117	-3.610429	29685.572964
HLA A*2601	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.376426	0.765882	-3.610544	23791.709849
HLA A*2301	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.515868	0.905240	-3.610627	32799.527668
HLA B*5701	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.168217	0.557541	-3.610675	14730.471337
HLA B*1801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.322949	0.712255	-3.610694	21035.315328
HLA B*0803	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.423972	0.813260	-3.610712	26544.355359
HLA B*4403	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.644138	1.033365	-3.610773	44069.459431
HLA A*0211	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.485399	0.874608	-3.610792	30577.323511
HLA A*3002	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.285021	0.674222	-3.610800	19276.194079
HLA A*3201	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.598109	0.987241	-3.610868	39637.747124
HLA A*2402	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.537915	0.926967	-3.610949	34507.631919
HLA B*4002	1:484-492	9	DWTRVPYEV	0.872860	0.156106	-4.639972	1.028966	-3.611006	43648.777681
HLA B*5101	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.386822	0.775634	-3.611188	24368.125681
HLA A*2602	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.435807	0.824605	-3.611201	27277.624002
HLA A*2902	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.443172	0.831902	-3.611270	27744.197936
HLA B*4501	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.546082	0.934761	-3.611321	35162.679873
HLA B*4601	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.401809	0.790294	-3.611516	25223.740557
HLA A*3301	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.640188	1.028547	-3.611641	43670.507513
HLA B*0801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.425572	0.813920	-3.611652	26642.328697
HLA A*0201	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.361927	0.750232	-3.611695	23010.549126
HLA A*2902	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.440165	0.828408	-3.611757	27552.742498
HLA B*4001	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.393558	0.781791	-3.611768	24749.025288
HLA B*5301	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.580993	0.969193	-3.611800	38105.965018
HLA B*5701	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.366483	0.754547	-3.611936	23253.195035
HLA A*1101	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.353723	0.741770	-3.611953	22579.929479
HLA A*0201	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.398316	0.786323	-3.611993	25021.642027
HLA A*3002	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.539623	0.927581	-3.612043	34643.617309

HLA A*1101	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.431101	0.819048	-3.612053	26983.639140
HLA B*5101	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.426077	0.813884	-3.612194	26673.335115
HLA B*1517	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.474434	0.862117	-3.612318	29814.973086
HLA A*0219	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.419997	0.807656	-3.612341	26302.489394
HLA A*2301	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.539992	0.927581	-3.612411	34673.054455
HLA A*3201	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.545466	0.932998	-3.612469	35112.875913
HLA A*0212	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.285566	0.673013	-3.612553	19300.402708
HLA B*1509	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.388554	0.775634	-3.612919	24465.477496
HLA B*4601	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.328607	0.715584	-3.613023	21311.135310
HLA A*3301	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.534605	0.921448	-3.613157	34245.596285
HLA B*4001	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.385901	0.772641	-3.613260	24316.503525
HLA B*3801	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.546289	0.932998	-3.613291	35179.423764
HLA A*0301	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.367975	0.754590	-3.613385	23333.213626
HLA A*0201	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.389073	0.775634	-3.613439	24494.745559
HLA B*4402	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.408625	0.794851	-3.613774	25622.726844
HLA B*4601	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.339919	0.726094	-3.613825	21873.554211
HLA A*0101	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.379720	0.765882	-3.613838	23972.848056
HLA A*2402	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.513730	0.899837	-3.613892	32638.452434
HLA A*0101	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.364154	0.750232	-3.613923	23128.863584
HLA B*0803	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.457509	0.843518	-3.613991	28675.350281
HLA A*6802	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.427969	0.813920	-3.614049	26789.749749
HLA B*4601	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.395872	0.781791	-3.614082	24881.258434
HLA A*2402	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.555698	0.941565	-3.614133	35949.959785
HLA A*2602	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.527063	0.912830	-3.614233	33656.029967
HLA B*1801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.516688	0.902388	-3.614299	32861.513356
HLA A*6901	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.340408	0.726094	-3.614314	21898.181433
HLA B*4403	1:192-200	9	LSRFLHDFA	1.183472	-0.170736	-4.627083	1.012736	-3.614347	42372.375443
HLA B*1501	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.341578	0.727191	-3.614387	21957.257409
HLA B*4402	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.423892	0.809432	-3.614460	26539.473339
HLA A*0203	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.400802	0.786323	-3.614479	25165.268108
HLA B*5701	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.398163	0.783681	-3.614482	25012.844894
HLA A*2601	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.396347	0.781791	-3.614556	24908.463476
HLA B*3501	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.295204	0.680376	-3.614828	19733.492650
HLA B*4402	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.396025	0.781170	-3.614856	24890.009288
HLA B*1517	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.433365	0.818458	-3.614907	27124.729994
HLA B*5801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.333235	0.718317	-3.614918	21539.472933
HLA A*2601	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.390743	0.775707	-3.615037	24589.144345
HLA B*3801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.549867	0.934761	-3.615106	35470.473595
HLA A*3301	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.602608	0.987241	-3.615367	40050.526206
HLA A*3101	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.405703	0.790294	-3.615409	25450.867349
HLA B*1503	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.515635	0.900138	-3.615497	32781.965632
HLA A*2403	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.327904	0.712255	-3.615650	21276.691202
HLA B*5701	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.391338	0.775634	-3.615704	24622.822597
HLA B*1502	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.548716	0.932998	-3.615718	35376.571359
HLA A*2902	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.408893	0.793168	-3.615726	25638.533955
HLA A*6801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.515807	0.899837	-3.615969	32794.914505
HLA A*6802	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.019969	0.403979	-3.615989	10470.534177
HLA B*4002	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.621110	1.005094	-3.616017	41793.661494
HLA B*0702	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.328397	0.712255	-3.616143	21300.876891
HLA A*0301	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.366447	0.750232	-3.616216	23251.308154
HLA B*4601	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.402629	0.786323	-3.616307	25271.409259
HLA B*4501	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.546143	0.929716	-3.616427	35167.626102
HLA B*4601	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.371045	0.754590	-3.616456	23498.781017
HLA A*0250	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.509188	0.892605	-3.616583	32298.920224
HLA B*3801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.521840	0.905240	-3.616600	33253.700466
HLA B*1801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.365002	0.748391	-3.616611	23174.077696
HLA A*0202	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.083273	0.466612	-3.616661	12113.603731
HLA B*1503	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.223951	0.607235	-3.616717	16747.543967
HLA B*5701	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.397893	0.781170	-3.616723	24997.288311
HLA A*3002	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.460330	0.843518	-3.616813	28862.268543
HLA B*0802	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.392592	0.775634	-3.616958	24694.057842
HLA A*0211	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.445418	0.828408	-3.617010	27888.058570
HLA A*0301	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.365437	0.748391	-3.617046	23197.282607
HLA A*2402	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.424874	0.807776	-3.617098	26599.555851
HLA B*1502	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.519589	0.902388	-3.617201	33081.803212

HLA A*6801	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.645757	1.028547	-3.617210	44234.031057
HLA A*2402	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.395252	0.778023	-3.617229	24845.748118
HLA B*0702	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.392639	0.775312	-3.617328	24696.729829
HLA B*4402	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.371976	0.754590	-3.617386	23549.176796
HLA B*4002	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.577852	0.960386	-3.617466	37831.338132
HLA A*2603	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.407007	0.789472	-3.617535	25527.398119
HLA A*1101	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.474759	0.857166	-3.617593	29837.240204
HLA A*8001	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.446114	0.828408	-3.617706	27932.752252
HLA B*4002	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.634961	1.017228	-3.617733	43147.996510
HLA B*5401	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.529821	0.911989	-3.617832	33870.466721
HLA A*6801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.475022	0.857166	-3.617856	29855.324292
HLA B*5401	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.530690	0.912830	-3.617861	33938.331744
HLA A*0201	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.349407	0.731526	-3.617881	22356.642247
HLA B*0702	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.411066	0.793168	-3.617899	25767.154509
HLA A*6801	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.533031	0.915104	-3.617927	34121.693502
HLA B*1801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.436469	0.818458	-3.618011	27319.270198
HLA A*6801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.412916	0.794851	-3.618065	25877.094174
HLA A*0202	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.580885	0.962750	-3.618134	38096.483342
HLA B*1517	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.461768	0.843518	-3.618250	28957.985613
HLA A*3002	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.392560	0.774258	-3.618302	24692.187624
HLA A*2501	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.419644	0.801202	-3.618443	26281.154019
HLA B*3501	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.264412	0.645964	-3.618448	18382.797698
HLA A*1101	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.436934	0.818458	-3.618476	27348.549132
HLA B*4402	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.366884	0.748391	-3.618493	23274.716311
HLA B*4801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.394134	0.775634	-3.618500	24781.849960
HLA A*6801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.304802	0.686294	-3.618508	20174.445390
HLA B*1503	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.432430	0.813920	-3.618510	27066.389595
HLA A*0301	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.336914	0.718317	-3.618598	21722.728063
HLA B*4601	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.360388	0.741770	-3.618618	22929.156058
HLA B*4501	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.599378	0.980728	-3.618650	39753.711769
HLA B*7301	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.539546	0.920891	-3.618655	34637.433063
HLA B*1503	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.405000	0.786323	-3.618677	25409.732402
HLA A*6801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.516514	0.897730	-3.618784	32848.360481
HLA A*0219	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.351552	0.732703	-3.618848	22467.339974
HLA B*4002	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.646189	1.027198	-3.618991	44278.084400
HLA B*4001	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.394317	0.775312	-3.619005	24792.309397
HLA B*5701	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.384997	0.765882	-3.619115	24265.909640
HLA A*8001	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.371931	0.752770	-3.619162	23546.756350
HLA B*7301	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.426846	0.807656	-3.619190	26720.562907
HLA B*5701	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.409485	0.790294	-3.619191	25673.510601
HLA A*2501	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.481328	0.862117	-3.619211	30291.990409
HLA A*2902	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.405573	0.786323	-3.619251	25443.295725
HLA B*4402	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.432548	0.813260	-3.619287	27073.711893
HLA B*4601	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.382689	0.763388	-3.619302	24137.338545
HLA B*5801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.360191	0.740887	-3.619304	22918.738713
HLA B*4801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.414189	0.794851	-3.619338	25953.081301
HLA B*7301	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.397388	0.778023	-3.619365	24968.230213
HLA A*2301	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.540305	0.920891	-3.619413	34698.011224
HLA B*5801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.352174	0.732703	-3.619471	22499.572715
HLA A*0203	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.345760	0.726094	-3.619666	22169.718390
HLA A*2601	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.392402	0.772641	-3.619761	24683.239252
HLA B*4801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.409248	0.789472	-3.619776	25659.486457
HLA B*5801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.355825	0.736037	-3.619789	22689.523232
HLA B*3901	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.482246	0.862117	-3.620130	30356.133862
HLA B*5801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.351662	0.731526	-3.620136	22473.053354
HLA B*5801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.362073	0.741770	-3.620303	23018.268461
HLA A*2601	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.370841	0.750232	-3.620609	23487.723675
HLA B*4403	1:308-316	9	IIGRQFIRA	1.236800	-0.192742	-4.664926	1.044058	-3.620868	46230.220691
HLA B*1502	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.562613	0.941565	-3.621048	36526.910733
HLA A*0216	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.435027	0.813920	-3.621107	27228.675092
HLA A*8001	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.434991	0.813884	-3.621108	27226.465620
HLA A*0203	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.254567	0.633434	-3.621133	17970.793991
HLA B*3901	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.396944	0.775707	-3.621237	24942.714017
HLA B*3501	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.449657	0.828408	-3.621249	28161.562859
HLA A*3002	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.277374	0.656026	-3.621348	18939.727081

HLA B*4403	1:377-385	9	LLFKDEVRA	1.151528	-0.114564	-4.658531	1.036964	-3.621567	45554.435411
HLA B*5801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.294732	0.673013	-3.621719	19712.046355
HLA B*2705	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.435088	0.813260	-3.621827	27232.505268
HLA A*3101	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.277931	0.656026	-3.621904	18964.026107
HLA B*4402	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.397674	0.775707	-3.621968	24984.714846
HLA B*4801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.435301	0.813260	-3.622041	27245.915129
HLA B*1801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.363024	0.740887	-3.622137	23068.756894
HLA A*0212	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.396406	0.774258	-3.622148	24911.832505
HLA A*2601	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.374936	0.752770	-3.622167	23710.247167
HLA B*0802	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.441248	0.819048	-3.622200	27621.543663
HLA B*5801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.349397	0.727191	-3.622206	22356.158465
HLA A*2403	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.423408	0.801202	-3.622206	26509.913238
HLA A*0250	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.549818	0.927581	-3.622237	35466.444106
HLA B*1502	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.522636	0.900174	-3.622462	33314.742127
HLA B*4601	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.397808	0.775312	-3.622497	24992.420413
HLA A*0212	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.334807	0.712255	-3.622552	21617.570175
HLA B*4501	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.649971	1.027198	-3.622773	44665.427456
HLA A*3002	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.358819	0.736037	-3.622782	22846.444080
HLA A*2902	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.386258	0.763388	-3.622870	24336.507286
HLA A*2902	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.430607	0.807656	-3.622951	26953.001062
HLA B*5701	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.395701	0.772641	-3.623060	24871.434220
HLA B*4402	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.409466	0.786323	-3.623144	25672.399498
HLA A*0212	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.413475	0.790294	-3.623181	25910.433779
HLA A*1101	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.398494	0.775312	-3.623183	25031.931830
HLA B*2705	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.416390	0.793168	-3.623223	26084.973189
HLA B*3901	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.447946	0.824605	-3.623341	28050.869500
HLA A*0202	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.505067	0.881518	-3.623549	31993.887039
HLA A*2603	1:37-45	9	ARVFSEVIP	0.871286	0.157261	-4.652102	1.028547	-3.623556	44885.128982
HLA A*2603	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.544463	0.920891	-3.623572	35031.857986
HLA B*1501	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.297852	0.674222	-3.623630	19854.174191
HLA A*6802	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.413940	0.790294	-3.623646	25938.202819
HLA A*6901	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.279897	0.656026	-3.623871	19050.091390
HLA A*0101	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.376696	0.752770	-3.623926	23806.516163
HLA B*0803	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.486142	0.862117	-3.624025	30629.640915
HLA B*2705	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.374483	0.750232	-3.624251	23685.504013
HLA A*0101	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.355847	0.731526	-3.624321	22690.627989
HLA A*3201	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.584715	0.960386	-3.624329	38433.908217
HLA B*1502	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.584839	0.960386	-3.624453	38444.929726
HLA A*0211	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.259656	0.635184	-3.624472	18182.611112
HLA A*0216	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.357188	0.732703	-3.624485	22760.828770
HLA A*2902	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.443010	0.818458	-3.624552	27733.843450
HLA B*1517	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.311037	0.686294	-3.624743	20466.196412
HLA B*3901	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.468298	0.843518	-3.624780	29396.631397
HLA A*3301	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.642084	1.017228	-3.624856	43861.580152
HLA B*5801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.340347	0.715416	-3.624931	21895.101514
HLA B*0702	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.408978	0.783681	-3.625297	25643.527700
HLA A*2603	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.420161	0.794851	-3.625310	26312.451829
HLA A*3002	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.367112	0.741770	-3.625342	23286.933139
HLA A*3101	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.130752	0.505350	-3.625401	13512.999339
HLA B*5801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.351531	0.726094	-3.625436	22466.246088
HLA A*1101	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.457424	0.831902	-3.625522	28669.766128
HLA B*1517	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.418726	0.793168	-3.625558	26225.621124
HLA B*4403	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.608181	0.982586	-3.625595	40567.776499
HLA A*2603	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.439547	0.813920	-3.625627	27513.568308
HLA B*5801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.354063	0.728232	-3.625831	22597.648890
HLA B*1503	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-3.924937	0.299099	-3.625838	8412.728422
HLA A*0219	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.374339	0.748391	-3.625948	23677.689010
HLA A*0301	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.358734	0.732703	-3.626031	22841.995031
HLA B*4501	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.569774	0.943730	-3.626045	37134.208671
HLA B*0802	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.450653	0.824605	-3.626048	28226.233797
HLA A*8001	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.401429	0.775312	-3.626117	25201.644103
HLA A*2301	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.526382	0.900138	-3.626244	33603.269501
HLA B*4001	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.380843	0.754590	-3.626253	24034.920314
HLA A*3301	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.581721	0.955413	-3.626309	38169.924840
HLA A*0216	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.454776	0.828408	-3.626368	28495.499925

HLA B*0803	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.440306	0.813920	-3.626386	27561.687387
HLA B*1503	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.389775	0.763388	-3.626388	24534.399265
HLA B*4001	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.392303	0.765882	-3.626422	24677.631478
HLA A*3101	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.271011	0.644580	-3.626431	18664.283013
HLA A*3001	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.278541	0.651841	-3.626700	18990.719128
HLA B*1502	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.554291	0.927581	-3.626710	35833.651644
HLA B*0801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.381261	0.754547	-3.626714	24058.076134
HLA A*2501	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.299832	0.673013	-3.626819	19944.926661
HLA B*0801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.455258	0.828408	-3.626850	28527.119742
HLA B*0801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.392816	0.765882	-3.626934	24706.752355
HLA A*0212	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.402629	0.775634	-3.626995	25271.409259
HLA B*0801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.317959	0.690895	-3.627063	20794.990223
HLA B*7301	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.532366	0.905240	-3.627125	34069.493205
HLA A*1101	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.455540	0.828408	-3.627132	28545.645181
HLA A*3101	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.358664	0.731526	-3.627138	22838.288152
HLA B*4001	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.307633	0.680376	-3.627257	20306.390516
HLA B*4001	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.342859	0.715584	-3.627275	22022.091490
HLA B*1502	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.319754	0.692424	-3.627330	20881.117012
HLA A*0301	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.368249	0.740887	-3.627363	23347.987223
HLA A*2501	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.455777	0.828408	-3.627369	28561.246749
HLA A*2902	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.254685	0.627189	-3.627496	17975.655649
HLA B*1509	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.550043	0.922498	-3.627545	35484.868365
HLA B*4001	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.411254	0.783681	-3.627574	25778.308719
HLA A*2402	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.529708	0.902116	-3.627592	33861.672561
HLA A*2403	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.275598	0.647881	-3.627717	18862.424129
HLA A*0212	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.314094	0.686294	-3.627800	20610.751052
HLA A*2402	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.590555	0.962750	-3.627805	38954.296754
HLA B*0702	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.456217	0.828408	-3.627809	28590.155334
HLA B*5701	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.391234	0.763388	-3.627847	24616.962198
HLA B*5701	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.402141	0.774258	-3.627883	25242.988424
HLA A*2902	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.360736	0.732703	-3.628033	22947.521950
HLA B*4001	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.391573	0.763388	-3.628185	24636.146875
HLA B*1502	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.529746	0.901531	-3.628215	33864.603694
HLA B*5701	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.382821	0.754590	-3.628231	24144.652151
HLA A*6802	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-3.824158	0.195916	-3.628242	6670.494949
HLA A*6802	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.354399	0.726094	-3.628305	22615.137515
HLA A*0219	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.315036	0.686294	-3.628742	20655.511839
HLA A*8001	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.410590	0.781791	-3.628799	25738.872360
HLA A*6901	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.394693	0.765882	-3.628811	24813.778471
HLA A*2301	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.537452	0.908582	-3.628870	34470.875064
HLA A*0216	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.357160	0.728232	-3.628928	22759.351215
HLA A*0301	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.365012	0.736037	-3.628975	23174.579179
HLA A*0206	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.360621	0.731526	-3.629095	22941.439722
HLA B*7301	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.550595	0.921448	-3.629148	35530.009816
HLA A*2301	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.503761	0.874608	-3.629153	31897.797265
HLA B*4001	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.303434	0.674222	-3.629213	20111.024923
HLA A*2501	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.472888	0.843518	-3.629371	29709.029193
HLA A*2402	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.551935	0.922498	-3.629436	35639.740561
HLA A*2603	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.646821	1.017228	-3.629593	44342.567442
HLA B*0802	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.461496	0.831902	-3.629594	28939.818812
HLA B*1502	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.410777	0.781170	-3.629608	25750.014326
HLA A*3201	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.511171	0.881518	-3.629653	32446.732559
HLA A*0202	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.486863	0.857166	-3.629697	30680.553992
HLA B*5301	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.531882	0.902116	-3.629766	34031.546045
HLA A*0250	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.592668	0.962750	-3.629917	39144.212052
HLA A*8001	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.405597	0.775634	-3.629963	25444.672216
HLA A*1101	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.393358	0.763388	-3.629971	24737.647298
HLA A*6801	1:346-354	9	GGGSGTANI	1.043345	-0.009980	-4.663561	1.033365	-3.630196	46085.140500
HLA B*4402	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.207415	0.577199	-3.630216	16121.871347
HLA B*4403	1:208-216	9	PANIANALI	0.995189	0.008861	-4.634343	1.004050	-3.630292	43086.649157
HLA B*4402	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.414029	0.783681	-3.630349	25943.535633
HLA B*7301	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.563619	0.933159	-3.630459	36611.584321
HLA A*3201	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.593236	0.962750	-3.630486	39195.492948
HLA B*4801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.416898	0.786323	-3.630575	26115.472236
HLA B*5101	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.449051	0.818458	-3.630592	28122.283736

HLA B*2705	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.406311	0.775634	-3.630677	25486.553114
HLA A*0219	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.444603	0.813920	-3.630683	27835.755336
HLA B*1801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.420998	0.790294	-3.630704	26363.176350
HLA A*2603	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.185969	0.555251	-3.630719	15345.086895
HLA B*4501	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.593772	0.962975	-3.630797	39243.868642
HLA B*4601	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.405242	0.774258	-3.630984	25423.895122
HLA B*5101	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.385659	0.754590	-3.631069	24302.957692
HLA B*0802	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.426117	0.794851	-3.631266	26675.788324
HLA A*2402	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.533695	0.902388	-3.631307	34173.973778
HLA A*2603	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.531508	0.900174	-3.631334	34002.285635
HLA B*3801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.552226	0.920891	-3.631335	35663.656655
HLA B*4601	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.379832	0.748391	-3.631441	23979.074006
HLA B*5301	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.566264	0.934761	-3.631503	36835.285726
HLA A*0301	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.298211	0.666703	-3.631508	19870.614553
HLA A*2603	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.652516	1.020917	-3.631599	44927.886283
HLA A*0101	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.386282	0.754590	-3.631692	24337.823900
HLA A*2301	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.534081	0.902388	-3.631693	34204.307127
HLA B*4801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.406168	0.774258	-3.631910	25478.143856
HLA A*2403	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.439725	0.807776	-3.631949	27524.882881
HLA B*4002	1:208-216	9	PANIANALI	0.995189	0.008861	-4.636048	1.004050	-3.631998	43256.208158
HLA A*2601	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.267238	0.635184	-3.632054	18502.824872
HLA B*1501	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.406398	0.774258	-3.632140	25491.655163
HLA B*1502	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.531999	0.899837	-3.632162	34040.752635
HLA B*3801	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.532396	0.900174	-3.632222	34071.889348
HLA B*5801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.347884	0.715584	-3.632301	22278.405833
HLA A*0250	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.406574	0.774258	-3.632316	25502.000289
HLA B*5701	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.418641	0.786323	-3.632319	26220.514024
HLA A*2601	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.395715	0.763388	-3.632327	24872.241544
HLA B*5301	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.595149	0.962750	-3.632398	39368.476771
HLA B*5101	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.267654	0.635184	-3.632470	18520.550744
HLA B*4402	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.350830	0.718317	-3.632514	22430.056377
HLA A*2601	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.380941	0.748391	-3.632550	24040.382037
HLA B*0803	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.406997	0.774258	-3.632739	25526.845723
HLA B*4001	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.387316	0.754547	-3.632769	24395.825473
HLA B*3901	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.446736	0.813884	-3.632853	27972.825940
HLA B*3501	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.165195	0.532233	-3.632962	14628.345381
HLA A*0206	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.446910	0.813920	-3.632990	27984.026593
HLA A*2601	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.369076	0.736037	-3.633040	23392.490711
HLA A*8001	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.426214	0.793168	-3.633046	26681.705816
HLA A*0101	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.359401	0.726094	-3.633307	22877.116640
HLA B*1509	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.533580	0.900138	-3.633443	34164.915986
HLA A*2902	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.409083	0.775634	-3.633449	25649.771249
HLA B*1503	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.359707	0.726094	-3.633613	22893.211445
HLA A*3101	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.383942	0.750232	-3.633710	24207.038299
HLA A*3101	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.409506	0.775707	-3.633800	25674.760649
HLA B*5101	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.462215	0.828408	-3.633807	28987.766219
HLA B*1502	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.411924	0.778023	-3.633901	25818.084845
HLA B*0802	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.441589	0.807656	-3.633933	27643.219440
HLA B*4402	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.435273	0.801202	-3.634071	27244.146417
HLA B*5701	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.423709	0.789472	-3.634237	26528.276804
HLA B*4002	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.615096	0.980728	-3.634368	41218.837508
HLA A*3201	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.462800	0.828408	-3.634392	29026.840861
HLA B*4402	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.424764	0.790294	-3.634470	26592.793380
HLA B*0801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.424865	0.790294	-3.634571	26598.980255
HLA A*0206	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.459222	0.824605	-3.634616	28788.663687
HLA A*2402	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.538282	0.903619	-3.634662	34536.766676
HLA B*1509	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.447923	0.813260	-3.634662	28049.352020
HLA B*4403	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.412728	0.778023	-3.634705	25865.897221
HLA B*4501	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.412786	0.778023	-3.634763	25869.395748
HLA A*0202	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.555656	0.920891	-3.634765	35946.459220
HLA B*0802	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.410160	0.775312	-3.634848	25713.403235
HLA A*0219	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.301566	0.666703	-3.634863	20024.715918
HLA A*3201	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.615610	0.980728	-3.634883	41267.701114
HLA B*1509	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.442585	0.807656	-3.634929	27706.700041
HLA B*3901	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.366713	0.731526	-3.635187	23265.526430

HLA A*2403	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.428455	0.793168	-3.635287	26819.766976
HLA B*5701	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.410674	0.775312	-3.635362	25743.885648
HLA B*3901	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.390076	0.754590	-3.635486	24551.394381
HLA A*0201	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.363781	0.728232	-3.635549	23108.977328
HLA B*4801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.416736	0.781170	-3.635566	26105.725611
HLA A*3002	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.544167	0.908582	-3.635585	35007.986796
HLA B*3801	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.492814	0.857166	-3.635648	31103.871055
HLA A*6802	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.368442	0.732703	-3.635739	23358.346943
HLA A*0101	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.271094	0.635184	-3.635910	18667.817357
HLA B*4403	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.598851	0.962750	-3.636101	39705.566795
HLA B*5401	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.543042	0.906788	-3.636254	34917.386746
HLA B*4002	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.541540	0.905240	-3.636300	34796.888559
HLA A*2902	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.284220	0.647881	-3.636339	19240.666672
HLA A*2403	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.425948	0.789472	-3.636476	26665.399807
HLA A*8001	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.422873	0.786323	-3.636550	26477.234618
HLA B*7301	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.556680	0.920085	-3.636595	36031.346626
HLA B*4801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.348890	0.712255	-3.636635	22330.049745
HLA A*0219	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.431782	0.794851	-3.636931	27026.006129
HLA B*4001	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.349193	0.712255	-3.636938	22345.638783
HLA B*4801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.427271	0.790294	-3.636977	26746.740227
HLA A*0301	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.368522	0.731526	-3.636996	23362.643784
HLA A*6802	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.204535	0.567535	-3.637000	16015.296468
HLA A*2501	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.409760	0.772641	-3.637119	25689.765974
HLA A*2902	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.281798	0.644580	-3.637217	19133.648741
HLA B*1502	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.552393	0.915104	-3.637289	35677.357773
HLA A*6901	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.379090	0.741770	-3.637320	23938.116199
HLA A*2601	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.363485	0.726094	-3.637391	23093.230553
HLA A*2602	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.480999	0.843518	-3.637481	30269.056411
HLA B*1517	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.403518	0.765882	-3.637636	25323.140602
HLA B*1502	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.349907	0.712255	-3.637652	22382.418797
HLA A*6802	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.424090	0.786323	-3.637767	26551.536431
HLA B*7301	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.581508	0.943730	-3.637778	38151.138414
HLA A*3301	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.535523	0.897730	-3.637793	34318.111520
HLA A*6802	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.392397	0.754590	-3.637808	24682.972186
HLA A*2402	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.543072	0.905240	-3.637832	34919.842522
HLA A*0201	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.370695	0.732703	-3.637992	23479.846905
HLA B*1501	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.392607	0.754590	-3.638017	24694.859408
HLA A*0216	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.364171	0.726094	-3.638077	23129.739472
HLA A*0101	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.371050	0.732703	-3.638347	23499.035270
HLA B*4403	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.643553	1.005094	-3.638459	44010.135085
HLA B*0702	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.446281	0.807776	-3.638504	27943.483342
HLA B*3801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.540063	0.901531	-3.638532	34678.682233
HLA B*4501	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.538406	0.899837	-3.638569	34546.670620
HLA B*0801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.351032	0.712255	-3.638778	22440.494399
HLA B*4403	1:47-55	9	TASIEEIRA	1.250746	-0.229829	-4.659788	1.020917	-3.638870	45686.474176
HLA B*0801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.425222	0.786323	-3.638899	26620.861675
HLA A*0211	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.470830	0.831902	-3.638928	29568.569322
HLA A*6801	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.656176	1.017228	-3.638949	45308.166156
HLA B*1509	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.452960	0.813920	-3.639040	28376.584996
HLA B*1501	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.371809	0.732703	-3.639106	23540.133244
HLA B*3801	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.536886	0.897730	-3.639156	34425.961798
HLA B*2705	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.471206	0.831902	-3.639304	29594.174431
HLA A*2603	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.559404	0.920085	-3.639319	36257.975131
HLA A*2601	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.381092	0.741770	-3.639322	24048.707049
HLA B*4501	1:208-216	9	PANIANALI	0.995189	0.008861	-4.643414	1.004050	-3.639364	43996.090019
HLA B*4801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.393986	0.754547	-3.639439	24773.405174
HLA B*4402	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.393988	0.754547	-3.639441	24773.539196
HLA B*5801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.340742	0.701295	-3.639447	21915.010172
HLA A*0201	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.394061	0.754547	-3.639514	24777.694230
HLA B*1501	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.325884	0.686294	-3.639590	21177.931216
HLA A*6802	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.405658	0.765882	-3.639776	25448.251442
HLA A*3201	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.545098	0.905240	-3.639857	35083.065362
HLA B*3501	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.392710	0.752770	-3.639940	24700.738352
HLA A*0301	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.368226	0.728232	-3.639994	23346.724157
HLA A*0212	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.426317	0.786323	-3.639994	26688.057755

HLA B*4403	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.561612	0.921448	-3.640165	36442.827275
HLA A*8001	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.449598	0.809432	-3.640166	28157.754343
HLA B*0702	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.415923	0.775707	-3.640216	26056.906054
HLA A*2602	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.560329	0.920085	-3.640244	36335.341295
HLA A*3301	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.540464	0.900174	-3.640290	34710.778015
HLA B*0802	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.468702	0.828408	-3.640294	29423.997720
HLA A*8001	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.412972	0.772641	-3.640331	25880.454206
HLA A*3301	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.415657	0.775312	-3.640346	26040.981879
HLA A*6802	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.441563	0.801202	-3.640361	27641.574474
HLA A*3001	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.013527	0.373125	-3.640402	10316.361472
HLA B*5401	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.560503	0.920085	-3.640418	36349.890400
HLA B*3501	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.307219	0.666703	-3.640516	20287.065181
HLA B*0702	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.422344	0.781791	-3.640553	26445.025472
HLA B*4002	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.573778	0.933159	-3.640618	37478.111247
HLA A*0202	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.368884	0.728232	-3.640652	23382.115848
HLA A*0301	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.296752	0.656026	-3.640726	19803.970415
HLA B*4501	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.560834	0.920085	-3.640749	36377.628469
HLA B*1517	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.418792	0.778023	-3.640769	26229.594001
HLA A*8001	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.415180	0.774258	-3.640922	26012.399176
HLA B*3801	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.543093	0.902116	-3.640977	34921.542776
HLA A*2501	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.368181	0.727191	-3.640990	23344.324520
HLA A*6801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.393908	0.752770	-3.641139	24768.982864
HLA A*3002	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.582807	0.941565	-3.641242	38265.444879
HLA B*4002	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.541082	0.899837	-3.641245	34760.199689
HLA A*0219	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.416905	0.775634	-3.641271	26115.896085
HLA B*1501	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.377469	0.736037	-3.641432	23848.926005
HLA B*4403	1:360-368	9	VGGLPDDLK	0.922845	0.104353	-4.668659	1.027198	-3.641461	46629.343211
HLA A*2501	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.473459	0.831902	-3.641558	29748.110456
HLA A*2603	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.473502	0.831902	-3.641600	29751.007409
HLA A*2902	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.297626	0.656026	-3.641600	19843.865616
HLA A*2403	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.417236	0.775634	-3.641602	26135.824744
HLA B*5801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.334055	0.692424	-3.641631	21580.178979
HLA B*1502	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.541811	0.900138	-3.641673	34818.543735
HLA A*0203	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.431967	0.790294	-3.641674	27037.559006
HLA B*0702	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.432031	0.790294	-3.641737	27041.508589
HLA B*4001	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.334339	0.692424	-3.641915	21594.309915
HLA B*4801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.417636	0.775707	-3.641929	26159.872425
HLA A*2603	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.554831	0.912830	-3.642002	35878.266293
HLA A*3101	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.369286	0.727191	-3.642095	23403.756443
HLA A*2902	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.456198	0.813920	-3.642278	28588.918004
HLA A*3301	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.557402	0.915104	-3.642298	36091.238504
HLA B*3901	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.470706	0.828408	-3.642298	29560.092515
HLA B*5301	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.583913	0.941565	-3.642348	38363.071770
HLA B*5401	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.544818	0.902388	-3.642430	35060.486967
HLA A*0301	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.368581	0.726094	-3.642487	23365.803731
HLA B*0802	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.456628	0.813884	-3.642744	28617.235326
HLA B*1503	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.374306	0.731526	-3.642780	23675.895766
HLA B*4402	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.317007	0.674222	-3.642786	20749.478170
HLA B*1502	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.499997	0.857166	-3.642831	31622.544942
HLA A*1101	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.486419	0.843518	-3.642901	30649.200107
HLA A*2403	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.391305	0.748391	-3.642914	24620.957774
HLA B*1509	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.250296	0.607235	-3.643061	17794.914347
HLA B*1509	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.317308	0.674222	-3.643086	20763.851450
HLA B*0802	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.424437	0.781170	-3.643268	26572.803792
HLA A*3101	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.379459	0.736037	-3.643422	23958.456737
HLA A*3201	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.576602	0.933159	-3.643442	37722.613765
HLA A*2301	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.545051	0.901531	-3.643520	35079.269657
HLA B*5801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.329826	0.686294	-3.643532	21371.055357
HLA A*2402	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.525061	0.881518	-3.643543	33501.258695
HLA B*2705	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.419261	0.775707	-3.643555	26257.989199
HLA B*1502	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.566088	0.922498	-3.643590	36820.343146
HLA A*0301	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.359032	0.715416	-3.643616	22857.694151
HLA B*1509	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.505833	0.862117	-3.643716	32050.362007
HLA A*3301	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.457734	0.813920	-3.643814	28690.246674
HLA A*2601	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.372063	0.728232	-3.643831	23553.891010

HLA B*5101	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.487352	0.843518	-3.643834	30715.096930
HLA B*7301	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.631084	0.987241	-3.643843	42764.557706
HLA A*8001	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.394096	0.750232	-3.643864	24779.704980
HLA B*1501	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.392261	0.748391	-3.643870	24675.228536
HLA B*4002	1:101-109	9	QALGGIVAH	1.110769	-0.128183	-4.626495	0.982586	-3.643909	42315.106716
HLA A*2902	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.418181	0.774258	-3.643923	26192.726145
HLA A*3001	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.296835	0.652880	-3.643955	19807.720575
HLA A*6901	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.385051	0.740887	-3.644164	24268.929173
HLA B*7301	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.577384	0.932998	-3.644386	37790.632041
HLA A*3301	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.557609	0.912830	-3.644779	36108.424559
HLA B*2705	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.473262	0.828408	-3.644854	29734.595073
HLA B*4001	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.363210	0.718317	-3.644893	23078.618155
HLA A*6801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.317959	0.673013	-3.644946	20794.990223
HLA A*3301	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.547125	0.902116	-3.645009	35247.241824
HLA A*0216	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.393436	0.748391	-3.645045	24742.064014
HLA B*4001	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.393441	0.748391	-3.645050	24742.331719
HLA A*0212	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.420396	0.775312	-3.645084	26326.690425
HLA B*4501	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.614532	0.969193	-3.645338	41165.354794
HLA B*2705	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.411355	0.765882	-3.645474	25784.306101
HLA B*4402	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.127166	0.481648	-3.645518	13401.902109
HLA B*5701	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.394042	0.748391	-3.645651	24776.621896
HLA A*2403	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.411534	0.765882	-3.645652	25794.909539
HLA A*2301	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.538303	0.892605	-3.645698	34538.448277
HLA A*0216	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.421430	0.775634	-3.645796	26389.431838
HLA B*0702	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.409431	0.763388	-3.646043	25670.316310
HLA B*4403	1:233-241	9	SGGVDSAVA	1.391452	-0.374224	-4.663274	1.017228	-3.646046	46054.734045
HLA A*3001	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.201297	0.555251	-3.646047	15896.349117
HLA A*0211	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.460006	0.813884	-3.646123	28840.729034
HLA A*8001	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.409544	0.763388	-3.646156	25676.983107
HLA A*8001	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.387966	0.741770	-3.646196	24432.410982
HLA A*2603	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.590036	0.943730	-3.646307	38907.751392
HLA A*0211	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.332622	0.686294	-3.646328	21509.081067
HLA B*0803	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.419010	0.772641	-3.646369	26242.793946
HLA B*1801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.372638	0.726094	-3.646544	23585.130574
HLA B*0801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.399380	0.752770	-3.646611	25083.037258
HLA B*2705	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.378148	0.731526	-3.646622	23886.241962
HLA A*6901	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.292622	0.645964	-3.646658	19616.515883
HLA A*0250	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.521314	0.874608	-3.646706	33213.427534
HLA A*1101	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.433029	0.786323	-3.646707	27103.754034
HLA B*3801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.549096	0.902388	-3.646708	35407.589048
HLA B*3901	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.162855	0.516095	-3.646761	14549.736179
HLA A*3001	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.286699	0.639875	-3.646824	19350.795466
HLA A*3301	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.576677	0.929716	-3.646961	37729.144735
HLA A*8001	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.339405	0.692424	-3.646981	21847.654519
HLA B*4801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.422328	0.775312	-3.647016	26444.024038
HLA A*2403	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.419682	0.772641	-3.647041	26283.428967
HLA B*3901	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.460319	0.813260	-3.647058	28861.487846
HLA A*2602	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.327484	0.680376	-3.647107	21256.097462
HLA A*6801	1:168-176	9	AFDRRLAGV	0.898893	0.121997	-4.668091	1.020890	-3.647201	46568.336337
HLA A*0206	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.437548	0.790294	-3.647254	27387.192041
HLA A*1101	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.454917	0.807656	-3.647262	28504.750876
HLA A*3002	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.430995	0.783681	-3.647314	26977.070907
HLA A*2403	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.428486	0.781170	-3.647316	26821.653238
HLA B*1801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.320332	0.673013	-3.647319	20908.924785
HLA A*0250	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.547541	0.900174	-3.647367	35281.008998
HLA B*5301	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.559357	0.911989	-3.647367	36254.052311
HLA A*0206	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-3.792971	0.145582	-3.647389	6208.275710
HLA A*0101	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.374668	0.727191	-3.647477	23695.628917
HLA B*1502	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.554303	0.906788	-3.647515	35834.620937
HLA A*6901	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.348859	0.701295	-3.647565	22328.479360
HLA A*6801	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.610340	0.962750	-3.647590	40769.969035
HLA A*3201	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.545328	0.897730	-3.647598	35101.670252
HLA B*4402	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.429482	0.781791	-3.647691	26883.247173
HLA B*7301	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.570249	0.922498	-3.647750	37174.811027
HLA A*2501	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.466246	0.818458	-3.647788	29258.123342

HLA A*0202	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.472433	0.824605	-3.647828	29677.865374
HLA B*4001	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.374041	0.726094	-3.647947	23661.426701
HLA B*5101	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.363583	0.715584	-3.648000	23098.478285
HLA A*3301	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.628944	0.980728	-3.648216	42554.314981
HLA A*2601	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.380977	0.732703	-3.648273	24042.332953
HLA B*4403	1:92-100	9	ICYGFQAMA	1.152105	-0.144816	-4.655636	1.007289	-3.648347	45251.825419
HLA B*3901	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.462295	0.813920	-3.648375	28993.098610
HLA B*4402	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.411898	0.763388	-3.648510	25816.548488
HLA B*0803	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.456466	0.807656	-3.648810	28606.555010
HLA B*5301	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.571332	0.922498	-3.648834	37267.639184
HLA B*1517	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.367213	0.718317	-3.648897	23292.350897
HLA A*0250	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.550520	0.901531	-3.648989	35523.859520
HLA A*2603	1:213-221	9	NALIEQVRT	1.197921	-0.192827	-4.654121	1.005094	-3.649027	45094.199840
HLA B*4001	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.390823	0.741770	-3.649053	24593.667595
HLA B*1502	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.583843	0.934761	-3.649082	38356.846077
HLA A*2603	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.361361	0.712255	-3.649106	22980.567905
HLA B*7301	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.555381	0.906227	-3.649154	35923.713855
HLA B*1801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.473795	0.824605	-3.649190	29771.132919
HLA B*4601	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.399871	0.750232	-3.649639	25111.413856
HLA B*1509	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.556450	0.906788	-3.649663	36012.248981
HLA B*0802	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.450902	0.801202	-3.649700	28242.424723
HLA B*3801	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.556561	0.906788	-3.649773	36021.406792
HLA B*5301	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.571381	0.921448	-3.649934	37271.873314
HLA B*0803	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.481845	0.831902	-3.649943	30328.064660
HLA A*0203	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.259165	0.609194	-3.649972	18162.064255
HLA A*0212	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.368339	0.718317	-3.650022	23352.787497
HLA B*0802	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.424311	0.774258	-3.650052	26565.042106
HLA B*0803	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.425394	0.775312	-3.650082	26631.376913
HLA A*2602	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.571001	0.920891	-3.650109	37239.222478
HLA A*0101	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.391906	0.741770	-3.650136	24655.079739
HLA B*5101	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.443499	0.793168	-3.650331	27765.068714
HLA A*0212	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.400715	0.750232	-3.650483	25160.231383
HLA B*0801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.317202	0.666703	-3.650499	20758.797209
HLA A*3002	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.440914	0.790294	-3.650620	27600.332824
HLA A*6801	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.570806	0.920085	-3.650721	37222.505046
HLA B*4801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-3.878417	0.227657	-3.650760	7558.177142
HLA A*0212	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.416952	0.765882	-3.651070	26118.721920
HLA A*6802	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.331597	0.680376	-3.651221	21458.407132
HLA B*7301	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.581038	0.929716	-3.651322	38109.882052
HLA B*3501	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-3.985380	0.334057	-3.651322	9668.959041
HLA A*2301	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.479873	0.828408	-3.651466	30190.720630
HLA A*3301	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.495007	0.843518	-3.651489	31261.262436
HLA B*4001	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.366964	0.715416	-3.651548	23278.997768
HLA B*5401	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-3.571377	-0.080273	-3.651650	3727.150832
HLA B*0803	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.470708	0.819048	-3.651660	29560.252432
HLA A*8001	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.400151	0.748391	-3.651760	25127.585206
HLA B*4601	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.387865	0.736037	-3.651828	24426.728047
HLA B*4402	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.441436	0.789472	-3.651964	27633.500610
HLA B*5701	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.393772	0.741770	-3.652002	24761.212231
HLA A*2902	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.326262	0.674222	-3.652040	21196.385063
HLA B*2705	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.325118	0.673013	-3.652105	21140.614227
HLA A*2301	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.446967	0.794851	-3.652116	27987.660201
HLA A*6801	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.557453	0.905240	-3.652213	36095.534251
HLA B*4001	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.405028	0.752770	-3.652259	25411.382022
HLA B*2705	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.453634	0.801202	-3.652433	28420.677786
HLA A*0301	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.368036	0.715584	-3.652452	23336.495840
HLA A*2902	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.425098	0.772641	-3.652457	26613.229926
HLA B*1503	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.418343	0.765882	-3.652461	26202.505252
HLA A*0219	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.427959	0.775312	-3.652647	26789.170037
HLA A*0219	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.086032	0.433361	-3.652671	12190.784607
HLA A*0203	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.343606	0.690895	-3.652710	22060.009686
HLA B*7301	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.425516	0.772641	-3.652875	26638.869752
HLA A*3001	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.286344	0.633434	-3.652910	19334.994386
HLA B*1502	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.573148	0.920085	-3.653063	37423.812969
HLA B*1517	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.428396	0.775312	-3.653084	26816.139922

HLA A*2602	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.633842	0.980728	-3.653115	43037.028731
HLA A*6901	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.371588	0.718317	-3.653271	23528.165434
HLA A*0202	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.472372	0.819048	-3.653324	29673.691264
HLA B*1502	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.371668	0.718317	-3.653351	23532.493514
HLA B*5801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.208816	0.555251	-3.653565	16173.936891
HLA B*4403	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.551312	0.897730	-3.653582	35588.683301
HLA A*3301	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.614186	0.960386	-3.653801	41132.630907
HLA A*2501	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.429508	0.775634	-3.653873	26884.847010
HLA B*5701	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.406666	0.752770	-3.653896	25507.381413
HLA A*3002	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.386763	0.732703	-3.654060	24364.830183
HLA B*0702	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.440451	0.786323	-3.654129	27570.933489
HLA A*0212	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.408703	0.754547	-3.654156	25627.301584
HLA A*0211	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.249521	0.595350	-3.654171	17763.174078
HLA B*4402	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.385753	0.731526	-3.654227	24308.217313
HLA A*2601	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.395226	0.740887	-3.654340	24844.269622
HLA B*1509	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.455639	0.801202	-3.654437	28552.131927
HLA B*4402	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.396328	0.741770	-3.654558	24907.385483
HLA B*4801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.436497	0.781791	-3.654707	27321.043786
HLA A*0250	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.575702	0.920891	-3.654811	37644.533897
HLA A*0216	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.250251	0.595350	-3.654901	17793.085339
HLA A*2402	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.555104	0.900138	-3.654966	35900.788663
HLA A*3301	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.556535	0.901531	-3.655004	36019.263266
HLA B*5101	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.429397	0.774258	-3.655139	26878.012009
HLA A*0216	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.405432	0.750232	-3.655201	25435.038341
HLA A*2902	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.403614	0.748391	-3.655223	25328.758036
HLA A*2603	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.588391	0.933159	-3.655232	38760.689389
HLA B*1801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.487197	0.831902	-3.655295	30704.131980
HLA A*2902	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.210686	0.555251	-3.655435	16243.736439
HLA B*0801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.373782	0.718317	-3.655466	23647.350263
HLA B*7301	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.555426	0.899837	-3.655589	35927.406568
HLA A*2601	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.348058	0.692424	-3.655634	22287.326373
HLA A*0202	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.307480	0.651841	-3.655639	20299.251175
HLA A*3201	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.557834	0.902116	-3.655718	36127.182317
HLA A*0101	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.371325	0.715584	-3.655741	23513.913858
HLA A*2501	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.430039	0.774258	-3.655781	26917.737466
HLA A*2501	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.450693	0.794851	-3.655842	28228.829830
HLA B*1501	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.307757	0.651841	-3.655916	20312.213682
HLA B*5701	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.406236	0.750232	-3.656004	25482.141354
HLA A*3002	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.329133	0.673013	-3.656120	21336.976121
HLA B*2705	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.437341	0.781170	-3.656171	27374.156917
HLA B*3501	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.470170	0.813920	-3.656250	29523.653957
HLA B*7301	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.488165	0.831902	-3.656263	30772.643955
HLA B*4501	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.643562	0.987241	-3.656321	44011.087455
HLA B*3801	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.556352	0.899837	-3.656514	36004.067375
HLA A*0201	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.397458	0.740887	-3.656572	24972.282803
HLA B*1503	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.409380	0.752770	-3.656610	25667.261274
HLA A*2403	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.406861	0.750232	-3.656629	25518.837330
HLA A*3201	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.560292	0.903619	-3.656672	36332.196308
HLA A*2402	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.577626	0.920891	-3.656735	37811.695552
HLA B*7301	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.583761	0.926967	-3.656794	38349.584044
HLA B*0801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.411461	0.754590	-3.656871	25790.583926
HLA A*0101	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.257951	0.600770	-3.657180	18111.337519
HLA B*4402	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.431441	0.774258	-3.657183	27004.814326
HLA B*1801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.500805	0.843518	-3.657287	31681.449351
HLA A*0201	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.399068	0.741770	-3.657298	25064.996122
HLA A*0301	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.343620	0.686294	-3.657326	22060.725751
HLA B*1801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.446823	0.789472	-3.657351	27978.425706
HLA A*2601	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.358671	0.701295	-3.657376	22838.658813
HLA A*0101	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.358718	0.701295	-3.657423	22841.130038
HLA B*2705	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.324211	0.666703	-3.657508	21096.514094
HLA A*2402	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.577626	0.920085	-3.657541	37811.695552
HLA A*2601	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.331778	0.674222	-3.657557	21467.347740
HLA B*3801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.580149	0.922498	-3.657651	38032.029331
HLA B*5301	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.532485	0.874608	-3.657878	34078.894424
HLA A*6802	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.373442	0.715416	-3.658026	23628.807753

HLA B*0801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.267238	0.609194	-3.658045	18502.824872
HLA A*2603	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.627285	0.969193	-3.658091	42392.093797
HLA A*2602	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.559697	0.901531	-3.658166	36282.502376
HLA A*2603	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.570235	0.911989	-3.658245	37173.604377
HLA A*0201	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.384379	0.726094	-3.658285	24231.408634
HLA B*0803	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.433962	0.775634	-3.658328	27162.028027
HLA A*6802	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-3.893778	0.235291	-3.658487	7830.292750
HLA A*0212	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.310337	0.651841	-3.658496	20433.228477
HLA A*3201	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.477186	0.818458	-3.658727	30004.449882
HLA A*2403	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.400517	0.741770	-3.658747	25148.800400
HLA B*1501	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.293973	0.635184	-3.658789	19677.631716
HLA A*8001	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.442519	0.783681	-3.658838	27702.503434
HLA A*2402	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.567521	0.908582	-3.658939	36942.052182
HLA B*4403	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.646309	0.987241	-3.659068	44290.302602
HLA B*0801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.400022	0.740887	-3.659135	25120.109759
HLA A*0250	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.254579	0.595350	-3.659229	17971.280098
HLA B*4002	1:297-305	9	SGVSAPEGK	0.823175	0.164066	-4.646480	0.987241	-3.659239	44307.797267
HLA B*5101	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.437343	0.778023	-3.659320	27374.305009
HLA B*4001	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.387656	0.728232	-3.659424	24414.969894
HLA A*2402	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.587022	0.927581	-3.659441	38638.632100
HLA A*2301	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.437491	0.778023	-3.659468	27383.636392
HLA B*1509	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.437496	0.778023	-3.659473	27383.932678
HLA B*3801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.552134	0.892605	-3.659529	35656.132928
HLA A*0203	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.395663	0.736037	-3.659626	24869.281486
HLA B*4501	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.568271	0.908582	-3.659689	37005.860143
HLA A*6901	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.352141	0.692424	-3.659717	22497.868697
HLA B*7301	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.174574	0.514746	-3.659828	14947.699202
HLA B*5301	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.586822	0.926967	-3.659855	38620.868574
HLA B*5101	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.386082	0.726094	-3.659988	24326.634953
HLA A*2301	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.435886	0.775634	-3.660252	27282.641807
HLA B*7301	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.446586	0.786323	-3.660263	27963.142504
HLA B*4002	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.623084	0.962750	-3.660334	41984.016907
HLA B*3901	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.435677	0.775312	-3.660366	27269.508919
HLA B*4402	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.352985	0.692424	-3.660561	22541.605395
HLA B*1517	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.442357	0.781791	-3.660566	27692.164508
HLA B*1801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.470031	0.809432	-3.660599	29514.231998
HLA A*6802	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.372885	0.712255	-3.660630	23598.531638
HLA B*5101	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.444387	0.783681	-3.660706	27821.904654
HLA A*2902	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.387985	0.727191	-3.660794	24433.468418
HLA B*5401	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.560994	0.900138	-3.660857	36391.013259
HLA A*0101	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.379285	0.718317	-3.660968	23948.867325
HLA A*0206	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.436338	0.775312	-3.661026	27310.994975
HLA A*1101	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.468822	0.807776	-3.661045	29432.117049
HLA B*4801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.397212	0.736037	-3.661175	24958.101616
HLA A*3301	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.542903	0.881518	-3.661385	34906.243472
HLA B*3501	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.436939	0.775312	-3.661627	27348.845039
HLA B*1503	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.474897	0.813260	-3.661637	29846.765277
HLA A*0202	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.435910	0.774258	-3.661652	27284.117808
HLA B*4403	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.581785	0.920085	-3.661700	38175.500614
HLA A*2603	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.591615	0.929716	-3.661899	39049.455825
HLA A*3101	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.390142	0.728232	-3.661910	24555.113632
HLA B*3901	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.480978	0.819048	-3.661930	30267.582677
HLA B*4801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.427865	0.765882	-3.661984	26783.373607
HLA A*2403	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.437322	0.775312	-3.662010	27372.972213
HLA B*0801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.398067	0.736037	-3.662030	25007.297523
HLA B*0803	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.469860	0.807776	-3.662083	29502.578483
HLA A*3101	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.377643	0.715416	-3.662227	23858.475400
HLA B*5301	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.568543	0.906227	-3.662316	37029.090353
HLA A*6901	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.398516	0.736037	-3.662479	25033.150639
HLA B*0702	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.353412	0.690895	-3.662517	22563.810786
HLA B*4402	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.438158	0.775634	-3.662524	27425.741181
HLA A*0206	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.463744	0.801202	-3.662542	29090.036414
HLA A*0301	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.308565	0.645964	-3.662601	20350.049946
HLA A*2602	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.577755	0.915104	-3.662651	37822.947865
HLA A*0216	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.374990	0.712255	-3.662736	23713.197556

HLA A*3001	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.258416	0.595477	-3.662939	18130.748018
HLA B*4402	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.391199	0.728232	-3.662967	24614.964654
HLA A*8001	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.417767	0.754590	-3.663177	26167.798859
HLA A*0216	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.390396	0.727191	-3.663205	24569.464592
HLA B*1801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.444516	0.781170	-3.663347	27830.184124
HLA B*4402	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.438659	0.775312	-3.663347	27457.362253
HLA B*1501	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.404244	0.740887	-3.663357	25365.507578
HLA A*2501	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.487979	0.824605	-3.663374	30759.495114
HLA A*1101	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.445216	0.781791	-3.663426	27875.086656
HLA A*2403	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.437811	0.774258	-3.663553	27403.791177
HLA A*0201	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.399671	0.736037	-3.663635	25099.869263
HLA B*4002	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.598414	0.934761	-3.663653	39665.633585
HLA A*2501	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.376064	0.712255	-3.663809	23771.896684
HLA A*6901	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.291504	0.627429	-3.664075	19566.066236
HLA A*3002	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.556730	0.892605	-3.664125	36035.440296
HLA A*3301	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.569365	0.905240	-3.664125	37099.269919
HLA A*2403	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.418716	0.754547	-3.664169	26225.053620
HLA A*2902	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.430175	0.765882	-3.664293	26926.184866
HLA B*5301	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.591890	0.927581	-3.664309	39074.180277
HLA B*5401	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.526426	0.862117	-3.664310	33606.723688
HLA A*0219	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.382807	0.718317	-3.664490	24143.868445
HLA A*2602	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.624907	0.960386	-3.664521	42160.639394
HLA A*2603	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.566090	0.901531	-3.664559	36820.542341
HLA B*4601	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.396182	0.731526	-3.664657	24899.032620
HLA B*4801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.428058	0.763388	-3.664670	26795.257639
HLA B*5101	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.472496	0.807656	-3.664840	29682.200647
HLA B*4002	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.634070	0.969193	-3.664877	43059.618736
HLA B*3801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.565134	0.900138	-3.664996	36739.559143
HLA B*0702	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.439263	0.774258	-3.665005	27495.563914
HLA B*0702	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.338171	0.673013	-3.665158	21785.691025
HLA B*5301	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.557815	0.892605	-3.665210	36125.618798
HLA B*4403	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.620692	0.955413	-3.665280	41753.435230
HLA A*3101	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.339503	0.674222	-3.665282	21852.619205
HLA B*3901	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.460187	0.794851	-3.665336	28852.745473
HLA B*0802	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.474792	0.809432	-3.665359	29839.500116
HLA A*6901	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.274646	0.609194	-3.665452	18821.141703
HLA B*0802	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.483971	0.818458	-3.665513	30476.913419
HLA B*5801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.346033	0.680376	-3.665657	22183.635299
HLA B*1517	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.473389	0.807656	-3.665733	29743.282828
HLA B*1503	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.339997	0.674222	-3.665775	21877.459565
HLA B*4801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.414339	0.748391	-3.665948	25962.068668
HLA A*2403	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.339048	0.673013	-3.666035	21829.696508
HLA A*6802	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.312015	0.645964	-3.666050	20512.307739
HLA A*0301	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.367352	0.701295	-3.666057	23299.786617
HLA B*4002	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.609861	0.943730	-3.666132	40724.999407
HLA B*3501	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.448101	0.781791	-3.666311	28060.886926
HLA B*4601	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.384630	0.718317	-3.666313	24245.439242
HLA A*0202	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.399025	0.732703	-3.666322	25062.555461
HLA B*5301	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.586456	0.920085	-3.666370	38588.288523
HLA A*6801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.528496	0.862117	-3.666380	33767.279418
HLA A*3301	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.461237	0.794851	-3.666386	28922.602202
HLA A*3002	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.429860	0.763388	-3.666472	26906.672471
HLA B*1517	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.429862	0.763388	-3.666475	26906.818033
HLA B*4801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.416954	0.750232	-3.666723	26118.863220
HLA B*5701	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.402768	0.736037	-3.666731	25279.476763
HLA B*4801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.419635	0.752770	-3.666865	26280.585312
HLA B*3801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.486020	0.819048	-3.666972	30621.025573
HLA A*0211	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.474651	0.807656	-3.666995	29829.815984
HLA B*0803	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.485505	0.818458	-3.667047	30584.768314
HLA A*2601	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.382746	0.715584	-3.667162	24140.472676
HLA B*3901	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.457488	0.790294	-3.667194	28673.954141
HLA B*0803	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.476732	0.809432	-3.667300	29973.138327
HLA B*7301	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.485787	0.818458	-3.667329	30604.629985
HLA B*0802	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.480611	0.813260	-3.667351	30242.049347
HLA A*2501	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.481351	0.813884	-3.667468	30293.629216

HLA B*3501	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.368799	0.701295	-3.667505	23377.562484
HLA A*0250	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.569917	0.902388	-3.667529	37146.465103
HLA A*0219	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.457854	0.790294	-3.667560	28698.163530
HLA B*0802	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.457873	0.790294	-3.667579	28699.405588
HLA B*1509	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.383028	0.715416	-3.667612	24156.149438
HLA B*1517	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.496151	0.828408	-3.667743	31343.732450
HLA A*0219	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.417995	0.750232	-3.667763	26181.534257
HLA A*1101	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.307659	0.639875	-3.667783	20307.598960
HLA B*5101	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.420622	0.752770	-3.667852	26340.366725
HLA B*1503	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.458493	0.790294	-3.668199	28740.423671
HLA A*0101	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.404267	0.736037	-3.668230	25366.879861
HLA B*4601	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.409232	0.740887	-3.668345	25658.514771
HLA B*5701	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.384134	0.715584	-3.668551	24217.779188
HLA A*2402	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.568754	0.900174	-3.668580	37047.123837
HLA A*3301	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.568468	0.899837	-3.668631	37022.680563
HLA B*1801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.482559	0.813884	-3.668675	30377.983423
HLA B*0802	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.458171	0.789472	-3.668699	28719.130460
HLA A*2501	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.432108	0.763388	-3.668721	27046.336642
HLA A*0206	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.316669	0.647881	-3.668788	20733.320122
HLA B*5701	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.387106	0.718317	-3.668790	24384.082195
HLA B*1801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.497260	0.828408	-3.668852	31423.869928
HLA B*5401	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.476655	0.807776	-3.668878	29967.787810
HLA B*2705	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.410686	0.741770	-3.668916	25744.582015
HLA B*4001	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.401685	0.732703	-3.668982	25216.509338
HLA B*3901	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.500887	0.831902	-3.668985	31687.448679
HLA A*2902	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.397353	0.728232	-3.669121	24966.204165
HLA A*0250	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.423827	0.754590	-3.669237	26535.453526
HLA B*1501	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.224529	0.555251	-3.669278	16769.846984
HLA B*1517	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.296719	0.627429	-3.669291	19802.470550
HLA A*3201	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.589402	0.920085	-3.669317	38850.961490
HLA B*1509	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.423946	0.754547	-3.669399	26542.775783
HLA B*5301	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.178009	0.508560	-3.669449	15066.393182
HLA A*0101	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.410427	0.740887	-3.669541	25729.266286
HLA A*0250	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.462715	0.793168	-3.669548	29021.188260
HLA A*6901	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.237134	0.567535	-3.669599	17263.708208
HLA B*1517	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.459090	0.789472	-3.669618	28779.943374
HLA A*2402	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.571151	0.901531	-3.669620	37252.118155
HLA A*6801	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.650441	0.980728	-3.669714	44713.780612
HLA B*4501	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.632482	0.962750	-3.669732	42902.433643
HLA A*3101	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.342753	0.673013	-3.669740	22016.730974
HLA B*0803	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.200536	0.530534	-3.670002	15868.510336
HLA A*2601	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.388382	0.718317	-3.670066	24455.817451
HLA A*0250	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.006802	0.336669	-3.670133	10157.862382
HLA A*0301	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.013371	0.343210	-3.670162	10312.678645
HLA A*0201	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.388544	0.718317	-3.670228	24464.948080
HLA B*4002	1:344-352	9	ESGGGSGTA	1.308608	-0.353195	-4.625866	0.955413	-3.670453	42253.800599
HLA B*1503	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.315038	0.644580	-3.670458	20655.623583
HLA B*5101	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.495070	0.824605	-3.670465	31265.829009
HLA B*1503	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-3.905145	0.234640	-3.670504	8037.940882
HLA B*2705	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.444831	0.774258	-3.670573	27850.366239
HLA A*0250	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.402258	0.731526	-3.670732	25249.817436
HLA B*5801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.361645	0.690895	-3.670750	22995.615831
HLA B*1501	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.304280	0.633434	-3.670846	20150.230518
HLA A*3301	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.603891	0.932998	-3.670893	40169.002320
HLA A*3301	1:219-227	9	VRTQIGDGH	1.114705	-0.151955	-4.633704	0.962750	-3.670953	43023.294215
HLA A*8001	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.461402	0.790294	-3.671108	28933.557041
HLA B*1801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.446527	0.775312	-3.671215	27959.360822
HLA B*0802	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.464571	0.793168	-3.671404	29145.484795
HLA A*2902	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.413186	0.741770	-3.671416	25893.198288
HLA A*0201	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.398617	0.727191	-3.671426	25038.974659
HLA A*2603	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.652154	0.980728	-3.671427	44890.471419
HLA A*0101	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.383700	0.712255	-3.671445	24193.553445
HLA A*1101	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.461766	0.790294	-3.671472	28957.828953
HLA B*5301	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.592402	0.920891	-3.671511	39120.289824
HLA B*1503	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.445780	0.774258	-3.671522	27911.302433

HLA A*2403	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.404248	0.732703	-3.671545	25365.782028
HLA A*2602	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.575241	0.903619	-3.671622	37604.639112
HLA B*4402	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.407679	0.736037	-3.671642	25566.925402
HLA A*6901	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.229268	0.557541	-3.671727	16953.837303
HLA A*1101	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.461237	0.789472	-3.671766	28922.602202
HLA B*4002	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.569683	0.897730	-3.671953	37126.374712
HLA A*0203	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.346397	0.674222	-3.672175	22202.244807
HLA B*7301	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.398398	0.726094	-3.672304	25026.380226
HLA B*2705	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.461794	0.789472	-3.672322	28959.708918
HLA A*2501	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.450550	0.778023	-3.672527	28219.515761
HLA B*0702	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.317127	0.644580	-3.672547	20755.203831
HLA A*1101	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.446936	0.774258	-3.672678	27985.691938
HLA A*8001	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.312656	0.639875	-3.672781	20542.624743
HLA B*1801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.456510	0.783681	-3.672830	28609.495569
HLA B*1509	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.482265	0.809432	-3.672833	30357.447677
HLA B*3901	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.474035	0.801202	-3.672833	29787.565423
HLA A*2603	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.312874	0.639875	-3.672999	20552.962742
HLA B*5401	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.427630	0.754590	-3.673041	26768.888017
HLA A*2501	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.427649	0.754590	-3.673059	26770.046576
HLA A*0250	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.487063	0.813884	-3.673179	30694.665400
HLA A*3201	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.492276	0.819048	-3.673228	31065.361428
HLA A*2402	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.448900	0.775634	-3.673266	28112.548562
HLA B*3501	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.459614	0.786323	-3.673291	28814.684601
HLA B*4801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.404946	0.731526	-3.673420	25406.570930
HLA A*8001	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.439392	0.765882	-3.673510	27503.746268
HLA B*5101	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.482987	0.809432	-3.673554	30407.908310
HLA B*5101	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.487530	0.813920	-3.673610	30727.728087
HLA A*2501	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.463977	0.790294	-3.673683	29105.620601
HLA B*4002	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.615310	0.941565	-3.673744	41239.134534
HLA A*3301	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.606912	0.933159	-3.673753	40449.437165
HLA A*3301	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.401015	0.727191	-3.673824	25177.660017
HLA B*4601	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.360163	0.686294	-3.673869	22917.250907
HLA B*1501	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.389308	0.715416	-3.673892	24508.000530
HLA B*5301	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.589188	0.915104	-3.674084	38831.839872
HLA A*2601	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.360459	0.686294	-3.674165	22932.877685
HLA A*2902	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.360531	0.686294	-3.674237	22936.724002
HLA B*5401	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.548913	0.874608	-3.674305	35392.651211
HLA B*4403	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.595219	0.920891	-3.674328	39374.866663
HLA A*0101	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.366816	0.692424	-3.674392	23271.065102
HLA B*3501	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.428977	0.754547	-3.674430	26851.996742
HLA B*2705	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.319138	0.644580	-3.674558	20851.541271
HLA B*0802	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.447251	0.772641	-3.674610	28005.986825
HLA A*8001	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.390297	0.715584	-3.674713	24563.882667
HLA A*3002	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.576270	0.901531	-3.674740	37693.850139
HLA A*0206	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.440740	0.765882	-3.674859	27589.285745
HLA B*4403	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.609706	0.934761	-3.674945	40710.461033
HLA B*0702	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.425239	0.750232	-3.675007	26621.869806
HLA A*2602	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.575223	0.900174	-3.675048	37603.011652
HLA B*4001	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.402270	0.727191	-3.675079	25250.500439
HLA B*4801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.416924	0.741770	-3.675154	26117.026383
HLA A*0101	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.348288	0.673013	-3.675275	22299.145558
HLA A*0301	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.349512	0.674222	-3.675291	22362.085523
HLA A*3001	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.276086	0.600770	-3.675316	18883.661149
HLA A*0250	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.494412	0.819048	-3.675364	31218.504354
HLA B*1517	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.489426	0.813920	-3.675507	30862.171866
HLA A*3101	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.401723	0.726094	-3.675629	25218.692129
HLA B*2705	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.450968	0.775312	-3.675656	28246.703122
HLA A*2501	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.425903	0.750232	-3.675672	26662.659068
HLA A*0201	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.310870	0.635184	-3.675686	20458.336812
HLA A*0301	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.366619	0.690895	-3.675724	23260.492418
HLA A*2301	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.489650	0.813920	-3.675730	30878.037231
HLA A*3201	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.451229	0.775312	-3.675917	28263.670296
HLA A*2501	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.350191	0.674222	-3.675970	22397.075049
HLA B*0702	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.394291	0.718317	-3.675974	24790.834081
HLA A*2603	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.581343	0.905240	-3.676103	38136.693609

HLA A*3002	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.557688	0.881518	-3.676171	36115.066818
HLA B*1517	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.173240	0.496961	-3.676278	14901.838154
HLA B*1509	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.394627	0.718317	-3.676310	24810.020042
HLA A*3101	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.377626	0.701295	-3.676332	23857.571915
HLA B*3501	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.442214	0.765882	-3.676332	27683.027512
HLA A*2602	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.578448	0.902116	-3.676333	37883.358354
HLA A*2402	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.568966	0.892605	-3.676361	37065.166104
HLA B*3501	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.402458	0.726094	-3.676364	25261.430997
HLA A*2602	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.578831	0.902388	-3.676443	37916.779085
HLA B*5301	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.580239	0.903619	-3.676619	38039.848599
HLA B*5701	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.417598	0.740887	-3.676711	26157.608171
HLA A*2501	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.452453	0.775707	-3.676746	28343.445299
HLA B*0802	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.458554	0.781791	-3.676764	28744.466501
HLA B*5301	1:20-28	9	VDFGAQYAQ	0.984953	-0.084779	-4.577032	0.900174	-3.676858	37759.978011
HLA A*0201	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.392346	0.715416	-3.676930	24680.034653
HLA B*5701	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.403175	0.726094	-3.677081	25303.147173
HLA B*0802	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.455112	0.778023	-3.677089	28517.552976
HLA A*2602	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.378747	0.701295	-3.677452	23919.216291
HLA A*6802	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.322108	0.644580	-3.677527	20994.614810
HLA A*3201	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.619160	0.941565	-3.677595	41606.419953
HLA B*3801	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.539734	0.862117	-3.677617	34652.427081
HLA B*0803	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.506145	0.828408	-3.677738	32073.431030
HLA B*5701	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.409276	0.731526	-3.677750	25661.152291
HLA B*1501	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.403931	0.726094	-3.677837	25347.263272
HLA A*3101	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.393525	0.715584	-3.677942	24747.150906
HLA B*1509	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.453728	0.775707	-3.678022	28426.828561
HLA B*4403	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.638499	0.960386	-3.678113	43500.971827
HLA A*1101	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.450975	0.772641	-3.678334	28247.161560
HLA B*0802	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.454076	0.775707	-3.678369	28449.598001
HLA B*1801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.473241	0.794851	-3.678390	29733.147360
HLA B*7301	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.591239	0.912830	-3.678409	39015.669933
HLA A*0202	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.553072	0.874608	-3.678464	35733.181449
HLA B*0702	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.433128	0.754590	-3.678538	27109.913123
HLA B*4601	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.411247	0.732703	-3.678544	25777.890349
HLA B*0702	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.414692	0.736037	-3.678655	25983.145005
HLA A*3201	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.581078	0.902388	-3.678689	38113.387107
HLA A*0216	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.433250	0.754547	-3.678703	27117.540600
HLA A*3101	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.419602	0.740887	-3.678715	26278.594937
HLA A*0301	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.351761	0.673013	-3.678748	22478.160156
HLA A*2902	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.404876	0.726094	-3.678782	25402.447863
HLA B*1801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.497929	0.819048	-3.678881	31472.357199
HLA B*1509	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.394514	0.715584	-3.678931	24803.578344
HLA B*4403	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.612117	0.933159	-3.678957	40937.054607
HLA A*3301	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.480263	0.801202	-3.679062	30217.845330
HLA B*4601	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.353328	0.674222	-3.679106	22559.416776
HLA A*2501	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.274519	0.595350	-3.679169	18815.644211
HLA B*0702	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.432099	0.752770	-3.679329	27045.751378
HLA A*0219	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.465713	0.786323	-3.679390	29222.215108
HLA A*0202	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.246837	0.567351	-3.679486	17653.769832
HLA B*4402	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.406292	0.726094	-3.680198	25485.450102
HLA A*2603	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.607831	0.927581	-3.680250	40535.089067
HLA B*4403	1:390-398	9	LGLPEEIVA	1.390750	-0.410022	-4.661056	0.980728	-3.680329	45820.135046
HLA B*5101	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.461526	0.781170	-3.680357	28941.854180
HLA A*1101	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.464426	0.783681	-3.680745	29135.710656
HLA B*5701	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.413463	0.732703	-3.680760	25909.732926
HLA B*3801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.435482	0.754590	-3.680893	27257.267091
HLA A*0212	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.422689	0.741770	-3.680919	26466.064341
HLA B*0801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.413766	0.732703	-3.681063	25927.821010
HLA B*3901	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.470656	0.789472	-3.681185	29556.734453
HLA B*0702	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.413975	0.732703	-3.681272	25940.307746
HLA A*2602	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.622908	0.941565	-3.681343	41966.985697
HLA B*5701	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.397094	0.715416	-3.681678	24951.351501
HLA A*2402	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.506392	0.824605	-3.681787	32091.655145
HLA B*3501	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.432054	0.750232	-3.681823	27042.971545
HLA A*0250	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-3.881946	0.200115	-3.681831	7619.842466

HLA B*4402	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.447733	0.765882	-3.681851	28037.063458
HLA A*0219	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.436514	0.754590	-3.681924	27322.078432
HLA B*5801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.348711	0.666703	-3.682008	22320.870597
HLA A*6802	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.410279	0.728232	-3.682047	25720.498654
HLA B*1517	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.397691	0.715584	-3.682107	24985.661016
HLA B*0802	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.436713	0.754547	-3.682167	27334.645122
HLA A*2603	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.506777	0.824605	-3.682172	32120.140196
HLA B*5401	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.495559	0.813260	-3.682298	31301.030902
HLA A*0203	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.374774	0.692424	-3.682350	23701.398202
HLA A*0211	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.456818	0.774258	-3.682560	28629.778175
HLA A*2602	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.589359	0.906788	-3.682572	38847.178445
HLA B*1503	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.116006	0.433361	-3.682645	13061.900996
HLA B*0702	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.014386	0.331684	-3.682702	10336.808304
HLA A*0201	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.375136	0.692424	-3.682712	23721.152608
HLA A*2501	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.464583	0.781791	-3.682792	29146.273175
HLA B*0702	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.437388	0.754547	-3.682841	27377.118900
HLA A*0301	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.363280	0.680376	-3.682904	23082.364042
HLA A*0206	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.328914	0.645964	-3.682950	21326.243768
HLA B*4402	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.435849	0.752770	-3.683079	27280.280372
HLA A*0212	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.415824	0.732703	-3.683121	26050.986197
HLA B*3901	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.278645	0.595477	-3.683168	18995.240124
HLA B*0802	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.431596	0.748391	-3.683205	27014.458189
HLA B*5701	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.356406	0.673013	-3.683393	22719.862206
HLA B*7301	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.585290	0.901531	-3.683759	38484.883171
HLA B*4403	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.613484	0.929716	-3.683768	41066.150321
HLA A*6801	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.596629	0.912830	-3.683799	39502.882514
HLA A*0216	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.402315	0.718317	-3.683998	25253.096018
HLA A*2601	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.399500	0.715416	-3.684084	25089.958732
HLA A*3001	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.297709	0.613596	-3.684113	19847.623330
HLA B*5101	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.503404	0.819048	-3.684356	31871.578387
HLA B*4002	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.586796	0.902388	-3.684408	38618.570361
HLA A*0203	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.285195	0.600770	-3.684425	19283.912497
HLA B*0802	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.450477	0.765882	-3.684595	28214.783560
HLA B*1509	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.357625	0.673013	-3.684612	22783.743139
HLA A*0201	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.385920	0.701295	-3.684625	24317.555944
HLA B*3801	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.459987	0.775312	-3.684676	28839.480860
HLA A*6901	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.365153	0.680376	-3.684777	23182.102714
HLA B*4601	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.412084	0.727191	-3.684893	25827.584355
HLA A*3001	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.292213	0.607235	-3.684978	19598.059139
HLA A*3002	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.201739	0.516757	-3.684982	15912.524868
HLA A*2602	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.619764	0.934761	-3.685003	41664.307318
HLA A*0206	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.318520	0.633434	-3.685086	20821.894776
HLA B*7301	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.582920	0.897730	-3.685190	38275.382736
HLA B*1517	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-3.684491	-0.000735	-3.685225	4836.047682
HLA A*2603	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.493014	0.807776	-3.685238	31118.177166
HLA B*4801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.401069	0.715584	-3.685486	25180.793004
HLA A*1101	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.403886	0.718317	-3.685570	25344.658014
HLA B*5301	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.585758	0.900138	-3.685620	38526.337072
HLA A*0101	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.352336	0.666703	-3.685633	22507.972976
HLA A*0216	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.472003	0.786323	-3.685680	29648.498538
HLA A*2602	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.613261	0.927581	-3.685680	41045.050228
HLA B*7301	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.547823	0.862117	-3.685706	35303.920395
HLA A*3201	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.499116	0.813260	-3.685855	31558.457049
HLA A*0250	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.313274	0.627189	-3.686085	20571.873609
HLA B*4001	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.359150	0.673013	-3.686137	22863.877867
HLA B*4601	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.414537	0.728232	-3.686305	25973.869310
HLA A*0219	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.440900	0.754547	-3.686353	27599.436950
HLA A*3301	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.606461	0.920085	-3.686376	40407.444199
HLA B*7301	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.595010	0.908582	-3.686428	39355.913010
HLA A*0250	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.452335	0.765882	-3.686454	28335.779591
HLA A*2601	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.366868	0.680376	-3.686492	23273.834932
HLA B*1509	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.500500	0.813884	-3.686616	31659.176077
HLA B*0802	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.450023	0.763388	-3.686635	28185.339636
HLA A*2301	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.402317	0.715584	-3.686733	25253.232635
HLA B*4002	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.588908	0.902116	-3.686792	38806.848879

HLA A*2402	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.468025	0.781170	-3.686855	29378.189412
HLA B*7301	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.561485	0.874608	-3.686878	36432.182640
HLA A*2301	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.544047	0.857166	-3.686881	34998.329273
HLA A*0219	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.452868	0.765882	-3.686987	28370.598574
HLA B*1517	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.879949	0.192958	-3.686991	7584.883778
HLA A*0202	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.494706	0.807656	-3.687050	31239.622574
HLA A*2902	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.418665	0.731526	-3.687139	26221.932563
HLA B*5101	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.460046	0.772641	-3.687405	28843.381583
HLA B*0803	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.473765	0.786323	-3.687442	29769.039232
HLA A*0219	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.414746	0.727191	-3.687555	25986.378223
HLA A*3101	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.373853	0.686294	-3.687559	23651.188461
HLA B*5301	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.549843	0.862117	-3.687727	35468.554734
HLA B*4403	1:155-163	9	VASSAGAPV	0.740279	0.203451	-4.631519	0.943730	-3.687789	42807.379162
HLA A*0301	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.328087	0.639875	-3.688212	21285.671251
HLA A*6802	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.429992	0.741770	-3.688222	26914.825184
HLA A*0203	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.415420	0.727191	-3.688229	26026.757005
HLA B*3501	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.403661	0.715416	-3.688245	25331.498700
HLA A*3001	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.295876	0.607629	-3.688247	19764.048501
HLA B*4801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.362491	0.674222	-3.688269	23040.444814
HLA A*2402	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.483186	0.794851	-3.688335	30421.894316
HLA A*2902	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.323654	0.635184	-3.688470	21069.482664
HLA B*1509	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.462800	0.774258	-3.688542	29026.840861
HLA A*8001	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.420077	0.731526	-3.688551	26307.327820
HLA B*0702	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.420086	0.731526	-3.688560	26307.897105
HLA B*5101	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.489936	0.801202	-3.688734	30898.423663
HLA A*6802	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.246445	0.557541	-3.688904	17637.827710
HLA B*3501	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.298120	0.609194	-3.688926	19866.422580
HLA B*5301	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.464710	0.775707	-3.689003	29154.789037
HLA B*0802	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.472787	0.783681	-3.689107	29702.118927
HLA A*0101	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.369546	0.680376	-3.689170	23417.814565
HLA A*0206	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.416395	0.727191	-3.689204	26085.255424
HLA A*0219	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.337123	0.647881	-3.689243	21733.189644
HLA B*4403	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.622278	0.932998	-3.689280	41906.183938
HLA B*3801	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.484145	0.794851	-3.689294	30489.116739
HLA A*0212	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.417821	0.728232	-3.689589	26171.055054
HLA A*6801	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.610592	0.920891	-3.689701	40793.575895
HLA B*4801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.430696	0.740887	-3.689810	26958.542516
HLA A*1101	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.491017	0.801202	-3.689815	30975.411659
HLA B*5801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.364161	0.674222	-3.689940	23129.238960
HLA B*1501	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.391246	0.701295	-3.689952	24617.628082
HLA B*2705	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.416069	0.726094	-3.689974	26065.647348
HLA B*5401	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.497678	0.807656	-3.690022	31454.144440
HLA B*0801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.416127	0.726094	-3.690033	26069.172893
HLA A*2902	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.356789	0.666703	-3.690086	22739.905687
HLA A*3101	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.317468	0.627189	-3.690279	20771.491304
HLA B*4403	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.405872	0.715584	-3.690288	25460.782698
HLA A*3301	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.466124	0.775634	-3.690490	29249.893773
HLA A*0219	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.418839	0.728232	-3.690607	26232.432138
HLA B*5301	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.593072	0.902388	-3.690684	39180.652729
HLA B*3801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.534360	0.843518	-3.690843	34226.334157
HLA A*2501	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.326144	0.635184	-3.690960	21190.652334
HLA A*0219	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.417135	0.726094	-3.691041	26129.745598
HLA B*5301	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.597858	0.906788	-3.691070	39614.809131
HLA A*0211	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.504994	0.813920	-3.691074	31988.521904
HLA B*0801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.383500	0.692424	-3.691076	24182.430825
HLA A*2602	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.590931	0.899837	-3.691094	38988.029500
HLA B*1502	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.509562	0.818458	-3.691103	32326.714815
HLA B*3801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.504501	0.813260	-3.691240	31952.201125
HLA B*1517	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.439683	0.748391	-3.691292	27522.202693
HLA B*2705	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.439709	0.748391	-3.691318	27523.840555
HLA B*3901	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.445956	0.754547	-3.691409	27922.629509
HLA B*3501	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.318628	0.627189	-3.691440	20827.077051
HLA A*2602	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.603496	0.911989	-3.691507	40132.510851
HLA A*2902	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.446118	0.754590	-3.691529	27933.054480
HLA A*0101	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.331412	0.639875	-3.691537	21449.238171

HLA A*2301	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.481058	0.789472	-3.691586	30273.150494
HLA B*1801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.457544	0.765882	-3.691662	28677.677333
HLA B*3901	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.484840	0.793168	-3.691673	30537.978902
HLA B*4501	1:407-415	9	LGIRIVGEV	0.894772	0.038387	-4.624877	0.933159	-3.691717	42157.674401
HLA B*5701	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.419050	0.727191	-3.691859	26245.207558
HLA B*1502	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.446523	0.754547	-3.691976	27959.058309
HLA A*3201	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.593741	0.901531	-3.692210	39241.108774
HLA B*1502	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.505631	0.813260	-3.692370	32035.454030
HLA B*5301	1:312-320	9	QFIRAFEGA	0.963034	-0.065304	-4.590170	0.897730	-3.692440	38919.750979
HLA B*4801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.419654	0.727191	-3.692463	26281.722738
HLA A*3001	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.250235	0.557541	-3.692693	17792.411541
HLA A*8001	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.420934	0.728232	-3.692702	26359.325841
HLA B*5701	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.421017	0.728232	-3.692785	26364.317350
HLA B*1509	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.241250	0.548275	-3.692976	17428.113703
HLA B*5301	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.486241	0.793168	-3.693073	30636.601231
HLA B*5701	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.394371	0.701295	-3.693076	24795.394433
HLA B*5801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.349103	0.656026	-3.693077	22341.045533
HLA A*2603	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.627891	0.934761	-3.693130	42451.303933
HLA A*3101	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.359958	0.666703	-3.693255	22906.467203
HLA B*5101	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.482855	0.789472	-3.693383	30398.697514
HLA A*3101	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.384320	0.690895	-3.693425	24228.131624
HLA A*0301	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.345356	0.651841	-3.693515	22149.099041
HLA B*4801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.419663	0.726094	-3.693569	26282.291469
HLA B*1517	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.483936	0.790294	-3.693642	30474.440369
HLA A*0250	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.525583	0.831902	-3.693681	33541.517723
HLA B*4801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.409123	0.715416	-3.693707	25652.130318
HLA A*2501	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.409450	0.715584	-3.693866	25671.427323
HLA B*2705	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.457264	0.763388	-3.693877	28659.221251
HLA B*2705	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.446649	0.752770	-3.693880	27967.227294
HLA B*4001	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.425504	0.731526	-3.693978	26638.149195
HLA A*6801	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.621585	0.927581	-3.694004	41839.358472
HLA B*1501	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.422281	0.728232	-3.694049	26441.163008
HLA A*1101	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.444375	0.750232	-3.694143	27821.152097
HLA B*1517	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.386773	0.692424	-3.694349	24365.357432
HLA A*2601	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.361074	0.666703	-3.694371	22965.405586
HLA A*0216	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.484772	0.790294	-3.694478	30533.188273
HLA A*2603	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.594373	0.899837	-3.694536	39298.256370
HLA B*4601	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.329805	0.635184	-3.694621	21370.014847
HLA A*2403	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.380927	0.686294	-3.694633	24039.601715
HLA B*0803	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.508554	0.813884	-3.694670	32251.776597
HLA A*3301	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.519281	0.824605	-3.694676	33058.366593
HLA A*1101	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.449361	0.754590	-3.694771	28142.373182
HLA B*4801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.423011	0.728232	-3.694779	26485.687062
HLA A*8001	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.420878	0.726094	-3.694784	26355.903638
HLA A*0203	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.436627	0.741770	-3.694856	27329.174206
HLA A*3201	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.413435	0.718317	-3.695118	25908.050955
HLA A*0203	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.413498	0.718317	-3.695181	25911.835543
HLA A*0250	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.443593	0.748391	-3.695202	27771.077602
HLA A*3002	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.421306	0.726094	-3.695211	26381.866436
HLA B*4001	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.431256	0.736037	-3.695219	26993.275441
HLA A*0212	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.436232	0.740887	-3.695345	27304.347059
HLA B*5101	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.423589	0.728232	-3.695357	26520.958547
HLA B*4601	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.386535	0.690895	-3.695640	24352.047867
HLA A*6802	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.369993	0.674222	-3.695771	23441.897618
HLA B*3801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.414217	0.718317	-3.695900	25954.766196
HLA B*4403	1:29-37	9	LIARRVREA	1.156929	-0.187736	-4.665170	0.969193	-3.695977	46256.238448
HLA A*2501	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.251280	0.555251	-3.696030	17835.296605
HLA B*5701	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.210799	0.514746	-3.696053	16247.955074
HLA B*0803	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.471768	0.775707	-3.696061	29632.463366
HLA B*4501	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.617001	0.920891	-3.696110	41400.079165
HLA B*4601	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.411619	0.715416	-3.696202	25799.933742
HLA B*4002	1:146-154	9	TAAPDGFDV	0.753416	0.176300	-4.626091	0.929716	-3.696376	42275.750783
HLA B*1517	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.470689	0.774258	-3.696431	29558.973119
HLA B*4501	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.524897	0.828408	-3.696489	33488.574431
HLA B*1503	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.342490	0.645964	-3.696526	22003.394910

HLA B*4501	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.638165	0.941565	-3.696600	43467.567027
HLA A*3201	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.617574	0.920891	-3.696683	41454.763890
HLA A*2403	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.428234	0.731526	-3.696708	26806.131798
HLA B*4002	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.605345	0.908582	-3.696764	40303.742595
HLA B*3501	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.889789	0.192958	-3.696831	7758.693105
HLA B*4601	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.363550	0.666703	-3.696848	23096.728909
HLA A*3301	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.631622	0.934761	-3.696861	42817.570034
HLA B*1509	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.515919	0.819048	-3.696871	32803.431620
HLA A*3201	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.605538	0.908582	-3.696956	40321.625741
HLA A*0216	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.330416	0.633434	-3.696981	21400.094443
HLA A*0203	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.377382	0.680376	-3.697006	23844.152741
HLA B*0802	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.483388	0.786323	-3.697066	30436.051409
HLA B*0803	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.478264	0.781170	-3.697095	30079.047685
HLA B*4601	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.377551	0.680376	-3.697175	23853.442134
HLA A*2603	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.638786	0.941565	-3.697220	43529.692226
HLA B*0803	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.480926	0.783681	-3.697245	30263.980518
HLA A*0101	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.383693	0.686294	-3.697399	24193.160795
HLA A*3201	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.604220	0.906788	-3.697432	40199.437223
HLA B*5301	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.430410	0.732703	-3.697707	26940.755574
HLA A*6901	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.388652	0.690895	-3.697757	24471.037060
HLA A*2301	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.478950	0.781170	-3.697781	30126.600735
HLA A*6802	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-3.968722	0.270903	-3.697819	9305.117721
HLA B*4501	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.612951	0.915104	-3.697847	41015.750200
HLA B*3501	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.138406	0.440475	-3.697931	13753.282941
HLA A*2602	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.620448	0.922498	-3.697950	41729.950166
HLA B*4001	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.399277	0.701295	-3.697982	25077.067325
HLA B*4801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.430689	0.732703	-3.697986	26958.104992
HLA B*3901	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.448238	0.750232	-3.698006	28069.693072
HLA A*3201	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.620572	0.922498	-3.698074	41741.916865
HLA A*0203	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.399399	0.701295	-3.698104	25084.122853
HLA B*0702	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.439878	0.741770	-3.698108	27534.563509
HLA A*2602	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.590722	0.892605	-3.698117	38969.262057
HLA A*3001	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.275457	0.577199	-3.698257	18856.302505
HLA A*1101	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.474030	0.775634	-3.698396	29787.243129
HLA A*2602	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.473814	0.775312	-3.698502	29772.421415
HLA A*2602	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.517674	0.819048	-3.698626	32936.264648
HLA B*7301	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.605435	0.906788	-3.698647	40312.028920
HLA A*3201	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.542292	0.843518	-3.698774	34857.179870
HLA B*1509	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.411031	0.712255	-3.698777	25765.063632
HLA A*6802	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.439796	0.740887	-3.698909	27529.350440
HLA A*0211	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.474597	0.775634	-3.698962	29826.104567
HLA A*3301	1:169-177	9	FDRRLAGVQ	1.054510	-0.133619	-4.619966	0.920891	-3.699075	41683.696167
HLA B*5301	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.512961	0.813884	-3.699078	32580.764950
HLA A*2402	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.482801	0.783681	-3.699120	30394.915317
HLA B*1502	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.465036	0.765882	-3.699155	29176.720942
HLA A*2501	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.485555	0.786323	-3.699232	30588.243176
HLA A*3301	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.640844	0.941565	-3.699279	43736.471759
HLA A*2601	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.390306	0.690895	-3.699411	24564.414224
HLA B*1801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.308627	0.609194	-3.699433	20352.912526
HLA A*3201	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.472221	0.772641	-3.699580	29663.419034
HLA A*2602	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.608181	0.908582	-3.699599	40567.776499
HLA B*5701	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.392101	0.692424	-3.699677	24666.152869
HLA B*3901	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.483468	0.783681	-3.699788	30441.650217
HLA B*1517	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.486170	0.786323	-3.699847	30631.629416
HLA A*2603	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.606699	0.906788	-3.699911	40429.528811
HLA A*0250	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.140577	0.440475	-3.700102	13822.204109
HLA B*5101	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.463512	0.763388	-3.700124	29074.460572
HLA B*4001	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.348098	0.647881	-3.700217	22289.376190
HLA A*2501	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.493390	0.793168	-3.700222	31145.124168
HLA A*0201	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.391176	0.690895	-3.700280	24613.633047
HLA A*0203	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.441239	0.740887	-3.700352	27620.945952
HLA B*4501	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.574959	0.874608	-3.700352	37580.234603
HLA A*3002	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.518882	0.818458	-3.700424	33027.977413
HLA B*5701	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.391345	0.690895	-3.700450	24623.222221
HLA A*0101	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.391385	0.690895	-3.700489	24625.486876

HLA B*0803	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.478515	0.778023	-3.700493	30096.464227
HLA B*0803	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.493724	0.793168	-3.700556	31169.059178
HLA A*2403	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.416273	0.715416	-3.700857	26077.918302
HLA A*3201	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.593694	0.892605	-3.701089	39236.863203
HLA B*4501	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.628189	0.926967	-3.701223	42480.480375
HLA A*0211	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.449704	0.748391	-3.701313	28164.610042
HLA B*4402	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.310534	0.609194	-3.701341	20442.516073
HLA A*0212	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.416827	0.715416	-3.701411	26111.234126
HLA A*3301	1:273-281	9	RDFVAATGA	1.159000	-0.231419	-4.629113	0.927581	-3.701532	42570.893627
HLA A*2403	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.429799	0.728232	-3.701567	26902.888122
HLA B*5801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.354465	0.652880	-3.701585	22618.563445
HLA B*5801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.346190	0.644580	-3.701610	22191.677494
HLA B*3501	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.419964	0.718317	-3.701647	26300.497360
HLA B*5801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.336863	0.635184	-3.701679	21720.142831
HLA B*1801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.454532	0.752770	-3.701762	28479.472055
HLA B*5801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.349677	0.647881	-3.701796	22370.555475
HLA B*4402	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.429033	0.727191	-3.701842	26855.483361
HLA A*2402	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.456524	0.754590	-3.701935	28610.424229
HLA A*6801	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.583486	0.881518	-3.701968	38325.318086
HLA A*0202	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.142480	0.440475	-3.702005	13882.906050
HLA A*3001	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.822899	0.120764	-3.702135	6651.180528
HLA B*7301	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.477844	0.775707	-3.702137	30049.934132
HLA A*6801	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.515513	0.813260	-3.702252	32772.744895
HLA B*4403	1:429-437	9	IVREELTAA	1.079993	-0.117018	-4.665297	0.962975	-3.702323	46269.753443
HLA B*4403	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.443428	0.740887	-3.702542	27760.562902
HLA A*0101	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.347142	0.644580	-3.702561	22240.352877
HLA B*4001	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.354512	0.651841	-3.702671	22621.010856
HLA B*4402	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.414953	0.712255	-3.702698	25998.752510
HLA B*0802	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.434235	0.731526	-3.702709	27179.078829
HLA B*2705	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.431035	0.728232	-3.702803	26979.552051
HLA A*3002	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.197698	0.494882	-3.702816	15765.145423
HLA B*4001	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.389127	0.686294	-3.702833	24497.793567
HLA A*0211	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.421153	0.718317	-3.702836	26372.591074
HLA A*0206	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.303747	0.600770	-3.702976	20125.500320
HLA A*2301	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.451400	0.748391	-3.703009	28274.834443
HLA B*4403	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.602991	0.899837	-3.703154	40085.858814
HLA A*2603	1:240-248	9	VAAALVQRA	1.040381	-0.107383	-4.636168	0.932998	-3.703171	43268.144381
HLA B*5101	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.485031	0.781791	-3.703240	30551.363608
HLA A*2602	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.270948	0.567535	-3.703412	18661.556976
HLA A*2603	1:160-168	9	GAPVAAFEA	1.186353	-0.225967	-4.663826	0.960386	-3.703441	46113.321765
HLA A*6801	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.605167	0.901531	-3.703636	40287.175054
HLA B*1509	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.535552	0.831902	-3.703650	34320.339479
HLA A*3201	1:90-98	9	LGICYGFQA	1.194766	-0.294929	-4.603496	0.899837	-3.703659	40132.510851
HLA A*2501	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.435231	0.731526	-3.703705	27241.493566
HLA B*7301	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.604023	0.900138	-3.703885	40181.173515
HLA A*6901	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.343803	0.639875	-3.703928	22070.036709
HLA B*4002	1:437-445	9	AGLDNQIWQ	0.945390	-0.025305	-4.624144	0.920085	-3.704059	42086.577096
HLA A*2403	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.445047	0.740887	-3.704160	27864.231089
HLA A*2301	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.523250	0.819048	-3.704202	33361.815137
HLA A*6901	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.215921	0.511716	-3.704204	16440.710683
HLA A*2601	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.377316	0.673013	-3.704303	23840.541177
HLA B*0803	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.435999	0.731526	-3.704473	27289.727338
HLA A*2301	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.529192	0.824605	-3.704586	33821.395197
HLA A*0301	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.352600	0.647881	-3.704719	22521.614860
HLA A*6801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.003823	0.299099	-3.704724	10088.420542
HLA B*0802	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.417053	0.712255	-3.704798	26124.798501
HLA B*1509	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.453336	0.748391	-3.704945	28401.157898
HLA A*0250	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.340295	0.635184	-3.705111	21892.495768
HLA B*3501	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.459715	0.754590	-3.705125	28821.388403
HLA B*3901	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.378228	0.673013	-3.705215	23890.635911
HLA B*3801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.537255	0.831902	-3.705353	34455.213999
HLA B*5801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.357341	0.651841	-3.705500	22768.833858
HLA B*3901	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.479939	0.774258	-3.705681	30195.294173
HLA B*0803	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.495162	0.789472	-3.705690	31272.426347
HLA B*5701	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.392022	0.686294	-3.705728	24661.616287

HLA A*8001	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.432919	0.727191	-3.705728	27096.863380
HLA B*5801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.333059	0.627189	-3.705870	21530.735244
HLA A*3101	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.438577	0.732703	-3.705873	27452.163800
HLA A*2603	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.608153	0.902116	-3.706037	40565.142979
HLA B*4501	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.446969	0.740887	-3.706082	27987.811611
HLA B*3801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.507299	0.801202	-3.706097	32158.739510
HLA A*2501	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.434343	0.728232	-3.706111	27185.843318
HLA A*0211	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.456350	0.750232	-3.706119	28598.972859
HLA B*1502	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.525313	0.819048	-3.706265	33520.656785
HLA B*5301	1:51-59	9	EEIRARQPV	0.859860	0.021658	-4.587856	0.881518	-3.706338	38712.909307
HLA B*1509	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.501320	0.794851	-3.706469	31719.006690
HLA A*2301	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.520423	0.813884	-3.706540	33145.398215
HLA A*0203	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.237080	0.530534	-3.706546	17261.560263
HLA B*5801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.346434	0.639875	-3.706559	22204.166677
HLA B*5101	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.501418	0.794851	-3.706567	31726.214554
HLA A*3301	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.629204	0.922498	-3.706706	42579.876423
HLA A*0101	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.362846	0.656026	-3.706819	23059.274088
HLA A*2902	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.442864	0.736037	-3.706828	27724.542714
HLA A*2301	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.538841	0.831902	-3.706939	34581.263254
HLA B*4402	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.439669	0.732703	-3.706966	27521.309355
HLA A*2301	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.488858	0.781791	-3.707067	30821.793759
HLA A*6801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.496555	0.789472	-3.707083	31372.911395
HLA B*7301	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.526278	0.819048	-3.707230	33595.271695
HLA A*2403	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.443299	0.736037	-3.707262	27752.304144
HLA A*2501	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.449128	0.741770	-3.707358	28127.304753
HLA A*6802	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.443398	0.736037	-3.707361	27758.610610
HLA A*0201	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.355318	0.647881	-3.707437	22663.025191
HLA B*4501	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.316664	0.609194	-3.707471	20733.095793
HLA B*0803	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.425828	0.718317	-3.707512	26658.043723
HLA B*5801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.353516	0.645964	-3.707552	22569.182404
HLA A*8001	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.398687	0.690895	-3.707792	25043.038731
HLA A*1101	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.436112	0.728232	-3.707880	27296.814710
HLA B*4601	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.400381	0.692424	-3.707957	25140.910609
HLA A*3101	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.222781	0.514746	-3.708035	16702.484718
HLA B*4501	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.614304	0.906227	-3.708077	41143.758561
HLA B*5101	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.494696	0.786323	-3.708374	31238.946570
HLA B*0803	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.456780	0.748391	-3.708389	28627.300140
HLA B*5401	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.517947	0.809432	-3.708515	32956.940194
HLA B*0801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.409911	0.701295	-3.708616	25698.662156
HLA A*6801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.484406	0.775707	-3.708699	30507.430882
HLA A*2501	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.474653	0.765882	-3.708771	29829.977361
HLA B*4002	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.518309	0.809432	-3.708876	32984.408817
HLA A*0212	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.401438	0.692424	-3.709014	25202.189461
HLA B*4002	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.609201	0.900138	-3.709063	40663.137157
HLA B*4501	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.375787	0.666703	-3.709084	23756.726335
HLA A*0219	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.421383	0.712255	-3.709129	26386.576714
HLA A*2501	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.457530	0.748391	-3.709139	28676.746490
HLA A*0201	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.389818	0.680376	-3.709442	24536.788492
HLA B*1501	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.266984	0.557541	-3.709443	18492.017421
HLA B*4601	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.354115	0.644580	-3.709535	22600.338567
HLA A*0202	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.156192	0.446544	-3.709648	14328.211354
HLA B*1501	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.277078	0.567351	-3.709727	18926.821290
HLA B*3901	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.491640	0.781791	-3.709849	31019.850494
HLA B*4601	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.355828	0.645964	-3.709864	22689.645980
HLA A*0211	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.438102	0.728232	-3.709870	27422.180527
HLA B*5401	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.511258	0.801202	-3.710056	32453.227938
HLA A*2301	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.517905	0.807776	-3.710128	32953.731069
HLA A*3002	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.350140	0.639875	-3.710265	22394.409562
HLA B*4801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.383305	0.673013	-3.710292	24171.574848
HLA A*6901	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.358262	0.647881	-3.710381	22817.170425
HLA B*5101	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.460885	0.750232	-3.710653	28899.141512
HLA A*2602	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.572796	0.862117	-3.710679	37393.456485
HLA B*0802	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.460958	0.750232	-3.710726	28903.988494
HLA B*4403	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.614412	0.903619	-3.710793	41153.998661
HLA A*3201	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.518642	0.807776	-3.710866	33009.757315

HLA A*0101	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.243158	0.532233	-3.710925	17504.840845
HLA B*4501	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.520473	0.809432	-3.711040	33149.164001
HLA B*0801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.385276	0.674222	-3.711055	24281.536500
HLA B*3801	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.525012	0.813920	-3.711092	33497.452912
HLA B*2705	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.426707	0.715584	-3.711123	26712.035506
HLA B*4501	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.623974	0.912830	-3.711145	42070.187061
HLA A*8001	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.447227	0.736037	-3.711191	28004.471773
HLA B*1801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.504473	0.793168	-3.711305	31950.126898
HLA A*0212	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.447418	0.736037	-3.711381	28016.746051
HLA B*0702	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.438600	0.727191	-3.711409	27453.648972
HLA B*5401	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.539900	0.828408	-3.711493	34665.739709
HLA B*0802	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.464668	0.752770	-3.711898	29151.950140
HLA B*0801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.398212	0.686294	-3.711918	25015.686706
HLA A*6802	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.404366	0.692424	-3.711942	25372.644260
HLA A*2402	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.569170	0.857166	-3.712004	37082.615314
HLA A*0101	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.386298	0.674222	-3.712077	24338.745571
HLA B*4001	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.178733	0.466612	-3.712121	15091.518424
HLA A*3301	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.501644	0.789472	-3.712172	31742.695823
HLA B*5401	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.339675	0.627429	-3.712246	21861.250988
HLA B*3801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.453200	0.740887	-3.712313	28392.247763
HLA A*3101	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.207284	0.494882	-3.712402	16116.987905
HLA B*0803	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.494389	0.781791	-3.712598	31216.815513
HLA A*2403	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.368642	0.656026	-3.712616	23369.090528
HLA B*0803	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.503096	0.790294	-3.712802	31848.999146
HLA A*0101	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.364716	0.651841	-3.712875	23158.787701
HLA A*0101	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.358840	0.645964	-3.712876	22847.556477
HLA B*4501	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.014866	0.301939	-3.712927	10348.222482
HLA B*4002	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.639911	0.926967	-3.712944	43642.638602
HLA A*2301	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.439065	0.726094	-3.712971	27483.071924
HLA B*1517	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.072395	0.359286	-3.713109	11813.953226
HLA A*2301	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.496858	0.783681	-3.713177	31394.813429
HLA A*6801	1:81-89	9	ALLDLGVPV	0.769820	0.151628	-4.634629	0.921448	-3.713182	43115.096011
HLA A*3002	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.461639	0.748391	-3.713248	28949.370622
HLA A*0219	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.428775	0.715416	-3.713358	26839.506744
HLA A*3201	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.538051	0.824605	-3.713446	34518.461201
HLA B*4403	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.532262	0.818458	-3.713804	34061.384435
HLA B*0801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.369838	0.656026	-3.713812	23433.529120
HLA B*1502	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.575956	0.862117	-3.713839	37666.534821
HLA A*3301	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.625838	0.911989	-3.713848	42251.057628
HLA A*2902	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.429540	0.715584	-3.713957	26886.883304
HLA B*3901	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.429543	0.715416	-3.714127	26887.028759
HLA B*3901	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.455928	0.741770	-3.714157	28571.137305
HLA B*4501	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.576646	0.862117	-3.714530	37726.491392
HLA A*2403	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.441725	0.727191	-3.714534	27651.894512
HLA A*2601	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.360611	0.645964	-3.714647	22940.943285
HLA A*8001	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.447420	0.732703	-3.714717	28016.897619
HLA A*3301	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.487573	0.772641	-3.714932	30730.720437
HLA B*1502	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.498639	0.783681	-3.714958	31523.818338
HLA B*1517	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.455918	0.740887	-3.715031	28570.519045
HLA A*0206	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.342508	0.627429	-3.715080	22004.347218
HLA B*5101	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.505436	0.790294	-3.715142	32021.072674
HLA A*2603	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.607876	0.892605	-3.715271	40539.255797
HLA B*0702	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.441438	0.726094	-3.715344	27633.650104
HLA B*4403	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.656952	0.941565	-3.715387	45389.125413
HLA A*1101	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.441523	0.726094	-3.715429	27639.032448
HLA A*3101	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.395835	0.680376	-3.715459	24879.104850
HLA A*2501	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.407918	0.692424	-3.715494	25581.037347
HLA B*1501	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.342995	0.627429	-3.715566	22029.002524
HLA B*1801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.457342	0.741770	-3.715572	28664.338133
HLA B*4001	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.382377	0.666703	-3.715674	24119.977608
HLA A*0201	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.389980	0.674222	-3.715758	24545.949352
HLA B*5401	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.468549	0.752770	-3.715779	29413.652802
HLA A*0301	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.368729	0.652880	-3.715849	23373.768692
HLA A*3101	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.355734	0.639875	-3.715859	22684.736573
HLA A*0201	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.311293	0.595350	-3.715943	20478.268435

HLA A*3002	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.481913	0.765882	-3.716031	30332.823106
HLA B*0801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.363943	0.647881	-3.716062	23117.605112
HLA B*0702	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.408520	0.692424	-3.716096	25616.489879
HLA A*0203	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.431540	0.715416	-3.716124	27010.950931
HLA A*0219	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.457955	0.741770	-3.716185	28704.840223
HLA B*1517	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.407150	0.690895	-3.716255	25535.823633
HLA B*5801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.349754	0.633434	-3.716320	22374.549565
HLA A*6901	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-3.987231	0.270903	-3.716328	9710.265725
HLA A*2301	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.534811	0.818458	-3.716353	34261.903476
HLA B*5401	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.505833	0.789472	-3.716361	32050.362007
HLA A*3301	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.616698	0.900138	-3.716561	41371.197135
HLA B*0702	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.444901	0.728232	-3.716669	27854.886627
HLA B*5801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.344207	0.627429	-3.716778	22090.582456
HLA B*5101	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.448390	0.731526	-3.716864	28079.565313
HLA B*0801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.362888	0.645964	-3.716924	23061.519663
HLA B*1517	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.418221	0.701295	-3.716926	26195.135151
HLA B*0803	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.482813	0.765882	-3.716931	30395.737494
HLA A*2402	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.507308	0.790294	-3.717015	32159.435419
HLA B*4002	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.630107	0.912830	-3.717277	42668.423691
HLA B*4002	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.531276	0.813884	-3.717392	33984.079600
HLA A*8001	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.458432	0.740887	-3.717545	28736.381410
HLA B*0801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.433065	0.715416	-3.717649	27105.953548
HLA A*8001	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.418951	0.701295	-3.717657	26239.244921
HLA B*4002	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.640275	0.922498	-3.717777	43679.249734
HLA B*4002	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.574959	0.857166	-3.717793	37580.234603
HLA A*0219	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.351293	0.633434	-3.717859	22453.973911
HLA B*3801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.546268	0.828408	-3.717860	35177.710954
HLA A*0301	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.345149	0.627189	-3.717961	22138.557023
HLA A*0211	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.450688	0.732703	-3.717985	28228.524402
HLA B*2705	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.433577	0.715416	-3.718161	27137.939970
HLA B*3501	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.445423	0.727191	-3.718232	27888.360315
HLA A*0201	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.008818	0.290570	-3.718248	10205.121575
HLA B*5301	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.525926	0.807656	-3.718270	33568.020749
HLA A*3301	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.492551	0.774258	-3.718293	31085.030691
HLA B*1501	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.911371	0.192958	-3.718413	8154.004428
HLA A*2602	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.466853	0.748391	-3.718462	29298.988921
HLA B*0802	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.454508	0.736037	-3.718472	28477.931388
HLA A*0203	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.370322	0.651841	-3.718480	23459.658873
HLA A*8001	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.374539	0.656026	-3.718513	23688.579476
HLA B*1509	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.509056	0.790294	-3.718763	32289.136626
HLA A*2402	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.493125	0.774258	-3.718867	31126.090428
HLA A*2501	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.420319	0.701295	-3.719024	26321.990836
HLA A*2301	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.527014	0.807656	-3.719358	33652.206601
HLA A*6801	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.562885	0.843518	-3.719368	36549.840285
HLA B*1517	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.365538	0.645964	-3.719574	23202.679508
HLA B*0802	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.461385	0.741770	-3.719615	28932.461371
HLA A*2301	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.509916	0.790294	-3.719622	32353.133080
HLA A*2402	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.548086	0.828408	-3.719678	35325.317790
HLA A*0101	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.372615	0.652880	-3.719735	23583.854679
HLA A*0212	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.186496	0.466612	-3.719883	15363.693575
HLA A*1101	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.435630	0.715584	-3.720047	27266.558578
HLA B*4002	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.364643	0.644580	-3.720063	23154.904146
HLA B*4601	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.421505	0.701295	-3.720211	26394.000678
HLA B*4402	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.368167	0.647881	-3.720286	23343.566791
HLA B*4002	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.635489	0.915104	-3.720385	43200.549311
HLA B*4403	1:210-218	9	NIANALIEQ	0.827718	0.099249	-4.647411	0.926967	-3.720444	44402.820323
HLA B*0801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.372295	0.651841	-3.720454	23566.509359
HLA B*3801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.538951	0.818458	-3.720493	34590.057170
HLA A*6801	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.643069	0.922498	-3.720570	43961.115874
HLA B*5101	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.486497	0.765882	-3.720615	30654.672285
HLA A*0216	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.275938	0.555251	-3.720687	18877.226260
HLA B*5401	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-3.593645	-0.127048	-3.720694	3923.244613
HLA A*3201	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.577870	0.857166	-3.720704	37832.975474
HLA B*0702	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.407058	0.686294	-3.720764	25530.436508
HLA A*0211	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.507346	0.786323	-3.721023	32162.219203

HLA A*6801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.514272	0.793168	-3.721105	32679.265695
HLA B*2705	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-3.586198	-0.135106	-3.721304	3856.537154
HLA A*2902	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.462292	0.740887	-3.721406	28992.941761
HLA B*3901	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.484864	0.763388	-3.721476	30539.631018
HLA B*1509	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.505159	0.783681	-3.721478	32000.638003
HLA B*0803	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.474336	0.752770	-3.721566	29808.199437
HLA B*7301	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.457661	0.736037	-3.721625	28685.435535
HLA A*8001	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.408017	0.686294	-3.721723	25586.850412
HLA B*0702	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.437181	0.715416	-3.721765	27364.088571
HLA A*0212	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.402153	0.680376	-3.721776	25243.671242
HLA B*0702	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.437371	0.715584	-3.721788	27376.082170
HLA A*2301	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.535126	0.813260	-3.721866	34286.749796
HLA A*6801	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.614518	0.892605	-3.721913	41164.018616
HLA B*3801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.508293	0.786323	-3.721970	32232.415293
HLA A*2602	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.494612	0.772641	-3.721971	31232.863190
HLA A*0202	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.512374	0.790294	-3.722080	32536.730153
HLA B*5401	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.565714	0.843518	-3.722196	36788.684922
HLA B*4801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.423493	0.701295	-3.722198	26515.076706
HLA A*8001	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.389002	0.666703	-3.722300	24490.770466
HLA B*1509	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.464123	0.741770	-3.722352	29115.384645
HLA B*5401	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.541461	0.819048	-3.722413	34790.488739
HLA B*0802	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.438137	0.715584	-3.722554	27424.405881
HLA A*3001	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.290247	0.567535	-3.722711	19509.518225
HLA B*1502	1:397-405	9	VARQPFFPGP	0.713125	0.118777	-4.554754	0.831902	-3.722852	35871.861650
HLA B*4002	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.629352	0.906227	-3.723125	42594.391099
HLA B*4501	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.645695	0.922498	-3.723197	44227.809663
HLA B*0802	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.477940	0.754590	-3.723350	30056.600111
HLA B*0802	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.415831	0.692424	-3.723407	26051.409000
HLA A*0212	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.358617	0.635184	-3.723433	22835.817233
HLA A*3002	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.450660	0.727191	-3.723469	28226.691903
HLA B*5401	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.499290	0.775707	-3.723583	31571.093432
HLA A*1101	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.455272	0.731526	-3.723746	28528.045728
HLA B*2705	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.176703	0.452913	-3.723790	15021.143091
HLA A*6802	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.442113	0.718317	-3.723796	27676.588490
HLA B*0702	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.464790	0.740887	-3.723903	29160.152152
HLA B*5301	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-3.952177	0.228245	-3.723932	8957.293369
HLA A*2402	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.537899	0.813920	-3.723979	34506.325167
HLA B*3901	1:430-438	9	VREELTAAG	0.822860	-0.547544	-3.999317	0.275316	-3.724001	9984.282613
HLA B*0802	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.442369	0.718317	-3.724052	27692.913576
HLA B*4501	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.543117	0.819048	-3.724069	34923.432044
HLA B*4402	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.439521	0.715416	-3.724105	27511.931058
HLA B*0802	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.465072	0.740887	-3.724185	29179.088681
HLA B*0702	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.351380	0.627189	-3.724192	22458.468881
HLA B*1509	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.513788	0.789472	-3.724316	32642.866992
HLA B*5101	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.410620	0.686294	-3.724326	25740.682601
HLA A*0301	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.351812	0.627429	-3.724384	22480.835612
HLA A*2602	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.624635	0.900138	-3.724497	42134.189905
HLA A*0250	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.229898	0.505350	-3.724547	16978.435657
HLA B*5401	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.510875	0.786323	-3.724552	32424.622908
HLA A*0301	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.056268	0.331684	-3.724584	11383.305253
HLA B*0803	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.474914	0.750232	-3.724682	29847.895573
HLA B*5801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.239444	0.514746	-3.724698	17355.759790
HLA B*7301	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.553121	0.828408	-3.724713	35737.241244
HLA A*2902	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.325501	0.600770	-3.724730	21159.264495
HLA A*3002	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.517930	0.793168	-3.724763	32955.692163
HLA B*2705	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.380890	0.656026	-3.724864	24037.520979
HLA B*4501	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.627038	0.902116	-3.724922	42368.020300
HLA B*1503	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.325703	0.600770	-3.724932	21169.111143
HLA A*6801	1:472-480	9	LRPVSSEDA	1.067554	-0.125989	-4.666754	0.941565	-3.725189	46425.208833
HLA A*0101	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.373073	0.647881	-3.725192	23608.747084
HLA A*0301	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.360386	0.635184	-3.725202	22929.032014
HLA A*1101	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.491109	0.765882	-3.725227	30981.947716
HLA B*1502	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.533033	0.807776	-3.725256	34121.878097
HLA A*3301	1:293-301	9	LEALSGVSA	1.219193	-0.326588	-4.617899	0.892605	-3.725293	41485.724109
HLA B*1801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.488917	0.763388	-3.725529	30825.962603

HLA B*1801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.507621	0.781791	-3.725830	32182.582949
HLA B*3801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.452041	0.726094	-3.725947	28316.624391
HLA B*1501	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.373876	0.647881	-3.725996	23652.467998
HLA B*4403	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.600611	0.874608	-3.726004	39866.780428
HLA B*0702	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.379003	0.652880	-3.726123	23933.325084
HLA B*5701	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.382172	0.656026	-3.726146	24108.627962
HLA B*0803	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.441871	0.715584	-3.726287	27661.170876
HLA B*4801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.406837	0.680376	-3.726461	25517.456826
HLA A*2603	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.649203	0.922498	-3.726705	44586.482656
HLA A*3002	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.540664	0.813920	-3.726744	34726.743109
HLA A*0250	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.545224	0.818458	-3.726766	35093.315816
HLA B*2705	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.242916	0.516095	-3.726822	17495.089540
HLA B*4501	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.570651	0.843518	-3.727133	37209.217023
HLA A*0216	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.468025	0.740887	-3.727138	29378.189412
HLA A*2902	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.428509	0.701295	-3.727214	26823.104299
HLA A*3001	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.222156	0.494882	-3.727274	16678.466618
HLA A*0212	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.454656	0.727191	-3.727465	28487.638977
HLA B*1517	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.477846	0.750232	-3.727614	30050.096699
HLA A*2902	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.373592	0.645964	-3.727628	23636.990240
HLA B*0803	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.463690	0.736037	-3.727653	29086.417040
HLA A*3301	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.636272	0.908582	-3.727690	43278.444945
HLA B*4501	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.632987	0.905240	-3.727747	42952.363618
HLA B*0702	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.401969	0.674222	-3.727748	25233.021383
HLA A*0202	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.503382	0.775634	-3.727748	31870.026630
HLA B*1502	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.518053	0.790294	-3.727759	32964.964373
HLA B*3801	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.552367	0.824605	-3.727762	35675.234720
HLA B*3901	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.493721	0.765882	-3.727840	31168.890557
HLA B*1801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.514225	0.786323	-3.727903	32675.730062
HLA B*4001	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.372511	0.644580	-3.727931	23578.241561
HLA B*1517	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.379774	0.651841	-3.727932	23975.831122
HLA A*3201	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.590062	0.862117	-3.727945	38910.066814
HLA B*5301	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.571541	0.843518	-3.728023	37285.587133
HLA A*3301	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.631730	0.903619	-3.728111	42828.226722
HLA B*4402	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.401154	0.673013	-3.728141	25185.697592
HLA A*2601	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.384193	0.656026	-3.728167	24221.054797
HLA A*3001	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.071517	0.343210	-3.728307	11790.074237
HLA B*1509	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.521567	0.793168	-3.728400	33232.838748
HLA B*5401	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.553039	0.824605	-3.728434	35730.475176
HLA B*3801	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.509604	0.781170	-3.728434	32329.862880
HLA B*1517	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.483024	0.754590	-3.728434	30410.540479
HLA B*1503	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.455639	0.727191	-3.728448	28552.131927
HLA B*1509	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.491903	0.763388	-3.728515	31038.651352
HLA A*6802	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.337962	0.609194	-3.728769	21775.204173
HLA A*3002	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.395527	0.666703	-3.728824	24861.479387
HLA B*4501	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.631248	0.902388	-3.728860	42780.755379
HLA B*1502	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.572460	0.843518	-3.728942	37364.539565
HLA A*0301	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.335378	0.606435	-3.728943	21646.007387
HLA A*0202	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.456134	0.727191	-3.728943	28584.742411
HLA B*0803	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.483567	0.754547	-3.729020	30448.567813
HLA A*2902	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.444537	0.715416	-3.729121	27831.539181
HLA A*0101	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.356345	0.627189	-3.729156	22716.666720
HLA A*3001	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.303021	0.573435	-3.729586	20091.885515
HLA A*2902	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.241431	0.511716	-3.729715	17435.375096
HLA B*4403	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.631253	0.901531	-3.729722	42781.218260
HLA B*1509	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.505199	0.775312	-3.729887	32003.581177
HLA A*2301	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.483005	0.752770	-3.730236	30409.224366
HLA A*0216	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.472092	0.741770	-3.730322	29654.594178
HLA B*4402	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.410846	0.680376	-3.730469	25754.054480
HLA A*2602	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.531680	0.801202	-3.730478	34015.716535
HLA A*2501	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.463183	0.732703	-3.730480	29052.448364
HLA A*6901	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.331252	0.600770	-3.730482	21441.349038
HLA A*2603	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.645663	0.915104	-3.730559	44224.460044
HLA A*0212	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.021158	0.290570	-3.730588	10499.235524
HLA A*0301	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.364128	0.633434	-3.730694	23127.487254
HLA A*3002	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.417025	0.686294	-3.730731	26123.102569

HLA A*1101	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.479335	0.748391	-3.730944	30153.341573
HLA A*0211	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.225943	0.494882	-3.731062	16824.551268
HLA B*5401	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.397808	0.666703	-3.731105	24992.420413
HLA B*3801	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.506987	0.775707	-3.731280	32135.609129
HLA B*4403	1:85-93	9	LGVPVLGIC	1.057395	-0.134897	-4.653804	0.922498	-3.731305	45061.277990
HLA B*4403	1:1-9	9	VVQPADIDV	0.757996	0.154834	-4.644258	0.912830	-3.731428	44081.620064
HLA A*1101	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.404450	0.673013	-3.731437	25377.586216
HLA B*4002	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.633046	0.901531	-3.731515	42958.173199
HLA B*7301	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.539322	0.807776	-3.731546	34619.636093
HLA A*0206	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.464329	0.732703	-3.731626	29129.248913
HLA A*6901	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.383803	0.651841	-3.731962	24199.313046
HLA B*4402	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.433323	0.701295	-3.732029	27122.088771
HLA A*2602	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.464752	0.732703	-3.732049	29157.628210
HLA A*2301	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.541538	0.809432	-3.732106	34796.700312
HLA A*0202	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.406497	0.674222	-3.732275	25497.447916
HLA B*4002	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.639119	0.906788	-3.732332	43563.144769
HLA A*1101	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.473234	0.740887	-3.732347	29732.664805
HLA A*3002	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.510405	0.778023	-3.732382	32389.559158
HLA A*6801	1:200-208	9	AGLGAQWTP	0.981428	-0.046667	-4.667144	0.934761	-3.732383	46466.919328
HLA A*3301	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.487004	0.754547	-3.732457	30690.514312
HLA A*2902	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.109404	0.376904	-3.732501	12864.838387
HLA A*2403	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.424975	0.692424	-3.732551	26605.744299
HLA B*3901	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.485439	0.752770	-3.732670	30580.135779
HLA A*6802	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.372671	0.639875	-3.732796	23586.916942
HLA B*1509	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.505504	0.772641	-3.732863	32026.096751
HLA A*0219	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.473779	0.740887	-3.732892	29770.005531
HLA A*0203	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.173381	0.440475	-3.732906	14906.675977
HLA A*1101	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.448348	0.715416	-3.732932	28076.831114
HLA B*0702	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.413345	0.680376	-3.732969	25902.725434
HLA A*2602	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.451433	0.718317	-3.733116	28276.976016
HLA B*4403	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.641835	0.908582	-3.733253	43836.435016
HLA B*0803	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.487864	0.754590	-3.733274	30751.342327
HLA B*1517	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.460530	0.727191	-3.733339	28875.543638
HLA B*4002	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.474251	0.740887	-3.733364	29802.394676
HLA A*3002	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.515207	0.781791	-3.733417	32749.704399
HLA A*0202	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.379388	0.645964	-3.733424	23954.568675
HLA B*0803	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.474399	0.740887	-3.733512	29812.553749
HLA B*5401	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.506357	0.772641	-3.733716	32089.051066
HLA B*5701	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.400459	0.666703	-3.733756	25145.399324
HLA B*1501	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.361015	0.627189	-3.733827	22962.299788
HLA B*4501	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.509587	0.775707	-3.733881	32328.638596
HLA A*2602	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.552376	0.818458	-3.733918	35676.006724
HLA B*5401	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.509616	0.775634	-3.733981	32330.737396
HLA A*3001	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.239375	0.505350	-3.734025	17353.037114
HLA B*4002	1:289-297	9	AETFLEALS	0.785461	-0.921388	-3.598161	-0.135927	-3.734088	3964.250570
HLA B*7301	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.547355	0.813260	-3.734095	35265.933778
HLA A*0216	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.164702	0.430602	-3.734100	14611.735895
HLA A*0206	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.408433	0.674222	-3.734211	25611.362844
HLA B*0702	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.435513	0.701295	-3.734218	27259.184123
HLA A*2601	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.386256	0.651841	-3.734415	24336.375628
HLA A*0202	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.068537	0.334057	-3.734480	11709.474163
HLA B*3801	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.542351	0.807776	-3.734574	34861.894526
HLA A*0206	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-3.925895	0.191274	-3.734622	8431.317797
HLA B*1517	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.390776	0.656026	-3.734750	24591.006759
HLA B*0802	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.450279	0.715416	-3.734863	28201.964810
HLA B*5301	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.592052	0.857166	-3.734886	39088.768701
HLA B*5401	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.548836	0.813920	-3.734916	35386.333255
HLA A*2402	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.566901	0.831902	-3.734999	36889.328806
HLA B*3801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.548908	0.813884	-3.735025	35392.268273
HLA A*3101	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.382929	0.647881	-3.735048	24150.661414
HLA B*3501	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.476133	0.740887	-3.735246	29931.818239
HLA A*0216	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.471397	0.736037	-3.735360	29607.145470
HLA A*2403	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.409582	0.674222	-3.735360	25679.205757
HLA B*5701	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.415749	0.680376	-3.735373	26046.476733
HLA A*2601	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.383260	0.647881	-3.735380	24169.090430

HLA A*0206	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.415780	0.680376	-3.735403	26048.308609
HLA B*4601	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.391641	0.656026	-3.735615	24640.012264
HLA A*3201	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.451417	0.715584	-3.735833	28275.905209
HLA A*0201	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.388892	0.652880	-3.736012	24484.544117
HLA A*6901	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.389024	0.652880	-3.736144	24491.962926
HLA A*2403	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.402902	0.666703	-3.736199	25287.273237
HLA B*1801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.490792	0.754590	-3.736202	30959.328775
HLA B*1517	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.202848	0.466612	-3.736236	15953.208907
HLA B*4801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.427193	0.690895	-3.736298	26741.965656
HLA A*0250	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.544000	0.807656	-3.736345	34994.542736
HLA B*0801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.376245	0.639875	-3.736370	23781.801203
HLA B*4501	1:79-87	9	DPALLDLGV	1.007438	-0.105907	-4.638034	0.901531	-3.736503	43454.400358
HLA A*2601	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.381143	0.644580	-3.736563	24051.569438
HLA B*0803	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.500023	0.763388	-3.736635	31624.426817
HLA B*3501	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.253489	0.516757	-3.736732	17926.225367
HLA B*4501	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.500135	0.763388	-3.736748	31632.639947
HLA B*1509	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.502640	0.765882	-3.736758	31815.590567
HLA A*3002	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.389688	0.652880	-3.736809	24529.488806
HLA A*2301	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.538451	0.801202	-3.737249	34550.221782
HLA A*0201	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.389150	0.651841	-3.737309	24499.118907
HLA B*7301	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.551314	0.813884	-3.737431	35588.875832
HLA B*4501	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.637573	0.900138	-3.737436	43408.348413
HLA A*2602	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.569344	0.831902	-3.737442	37097.463636
HLA B*5101	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.512914	0.775312	-3.737602	32577.239975
HLA A*0212	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.438901	0.701295	-3.737606	27472.666268
HLA B*7301	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.551582	0.813920	-3.737662	35610.831235
HLA A*6901	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.371106	0.633434	-3.737672	23502.086520
HLA B*0803	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.430156	0.692424	-3.737732	26925.019549
HLA A*2402	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.550992	0.813260	-3.737732	35562.508738
HLA B*5101	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.410857	0.673013	-3.737844	25754.751122
HLA B*1801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.456186	0.718317	-3.737869	28588.144700
HLA A*6802	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.305241	0.567351	-3.737890	20194.865180
HLA A*0206	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.141888	0.403979	-3.737909	13863.992490
HLA B*0802	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.464036	0.726094	-3.737942	29109.557321
HLA A*6901	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.930956	0.192958	-3.737998	8530.141785
HLA B*4501	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.644850	0.906788	-3.738062	44141.757169
HLA A*2603	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.510934	0.772641	-3.738293	32429.008545
HLA A*0250	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.471035	0.732703	-3.738331	29582.489351
HLA A*0216	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.339207	0.600770	-3.738437	21837.728530
HLA B*2705	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.465739	0.727191	-3.738548	29223.954138
HLA B*0803	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.464738	0.726094	-3.738644	29156.681788
HLA A*0211	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.217711	0.479051	-3.738660	16508.624694
HLA A*1101	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.465943	0.727191	-3.738752	29237.711932
HLA A*0216	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.413028	0.674222	-3.738807	25883.814673
HLA B*5301	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.425189	0.686294	-3.738895	26618.845529
HLA A*3101	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.296475	0.557541	-3.738934	19791.332250
HLA A*2601	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.306564	0.567535	-3.739028	20256.467812
HLA A*2402	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.558085	0.819048	-3.739038	36148.100884
HLA B*0801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.143124	0.403979	-3.739145	13903.500075
HLA A*0301	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.334739	0.595350	-3.739389	21614.178930
HLA B*0802	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.440825	0.701295	-3.739530	27594.659447
HLA B*1509	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.431979	0.692424	-3.739555	27038.290367
HLA A*8001	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.413785	0.674222	-3.739563	25928.943167
HLA A*6901	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.172963	0.433361	-3.739601	14892.328350
HLA B*3501	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.430544	0.690895	-3.739648	26949.064406
HLA A*0202	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.494515	0.754547	-3.739969	31225.936339
HLA A*2403	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.373442	0.633434	-3.740007	23628.807753
HLA B*0802	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.472719	0.732703	-3.740016	29697.459422
HLA B*4002	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.602486	0.862117	-3.740370	40039.261007
HLA A*0211	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.530674	0.790294	-3.740380	33937.046550
HLA B*4001	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.386451	0.645964	-3.740487	24347.305621
HLA B*4001	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.375683	0.635184	-3.740499	23751.072072
HLA A*0211	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.861360	0.120764	-3.740596	7267.077725
HLA A*2602	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-3.582504	-0.158117	-3.740621	3823.878894
HLA A*3201	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.541886	0.801202	-3.740684	34824.571920

HLA B*3801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.495244	0.754547	-3.740697	31278.348220
HLA B*3801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.531092	0.790294	-3.740798	33969.742317
HLA B*1503	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-3.968703	0.227657	-3.741046	9304.715012
HLA B*3501	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.348483	0.607235	-3.741249	22309.160587
HLA B*4801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.385896	0.644580	-3.741316	24316.240427
HLA B*7301	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.584940	0.843518	-3.741422	38453.874027
HLA A*0203	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.368853	0.627429	-3.741425	23380.471476
HLA A*3301	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.643830	0.902388	-3.741442	44038.238668
HLA A*0219	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.433906	0.692424	-3.741482	27158.501610
HLA A*2602	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.554841	0.813260	-3.741580	35879.042692
HLA A*2301	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.515938	0.774258	-3.741680	32804.851354
HLA A*2601	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.349317	0.607629	-3.741689	22352.046735
HLA B*1517	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.474517	0.732703	-3.741813	29820.618970
HLA B*4601	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.393781	0.651841	-3.741940	24761.748058
HLA A*0212	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.375488	0.633434	-3.742054	23740.409741
HLA A*2603	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.645677	0.903619	-3.742057	44225.895564
HLA B*4601	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.299689	0.557541	-3.742148	19938.345856
HLA B*0702	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.390109	0.647881	-3.742228	24553.253936
HLA A*2603	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.585915	0.843518	-3.742397	38540.303959
HLA B*5101	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.433438	0.690895	-3.742543	27129.279371
HLA A*2402	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.556521	0.813884	-3.742637	36018.094124
HLA A*0201	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.147062	0.404390	-3.742672	14030.135986
HLA B*3801	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.455089	0.712255	-3.742834	28516.010250
HLA A*2402	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.518560	0.775707	-3.742853	33003.507638
HLA B*7301	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.497452	0.754590	-3.742863	31437.812992
HLA B*1502	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.529199	0.786323	-3.742876	33821.944112
HLA B*5801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.352085	0.609194	-3.742891	22494.947823
HLA A*0219	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.478938	0.736037	-3.742902	30125.785838
HLA A*0212	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.433805	0.690895	-3.742909	27152.184592
HLA B*3901	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.470109	0.727191	-3.742918	29519.501537
HLA A*3001	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.015467	0.272539	-3.742928	10362.563991
HLA A*2602	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.550656	0.807656	-3.743001	35535.007717
HLA B*4403	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.605136	0.862117	-3.743020	40284.341814
HLA B*3801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.552480	0.809432	-3.743047	35684.499878
HLA B*1503	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.518454	0.775312	-3.743143	32995.474076
HLA A*3002	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.111749	0.368545	-3.743204	12934.484384
HLA B*4402	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.429529	0.686294	-3.743235	26886.156038
HLA B*0702	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.275520	0.532233	-3.743286	18859.056990
HLA A*0212	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.238245	0.494882	-3.743364	17307.940492
HLA A*2301	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.536557	0.793168	-3.743389	34399.897981
HLA B*5801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.349914	0.606435	-3.743480	22382.782060
HLA B*5401	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.344313	0.600770	-3.743543	22095.960953
HLA B*0803	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.471848	0.728232	-3.743616	29637.914351
HLA B*4403	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.646095	0.902388	-3.743707	44268.503856
HLA B*4801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.430024	0.686294	-3.743730	26916.863748
HLA A*1101	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.410444	0.666703	-3.743741	25730.240652
HLA B*2705	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.484634	0.740887	-3.743747	30523.444139
HLA A*0212	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.417974	0.674222	-3.743752	26180.259535
HLA A*2501	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.434900	0.690895	-3.744004	27220.721831
HLA B*5401	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.518313	0.774258	-3.744055	32984.765703
HLA B*7301	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.418322	0.674222	-3.744100	26201.229509
HLA A*2902	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.311467	0.567351	-3.744116	20486.468178
HLA B*1503	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-3.526309	-0.217813	-3.744122	3359.766898
HLA A*0201	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.390149	0.645964	-3.744185	24555.512157
HLA A*2603	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.652838	0.908582	-3.744256	44961.197145
HLA A*3201	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.526168	0.781791	-3.744377	33586.730686
HLA A*6901	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.091868	0.347374	-3.744494	12355.712057
HLA B*4001	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.397435	0.652880	-3.744555	24970.931866
HLA A*0101	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.372190	0.627429	-3.744761	23560.772908
HLA B*3801	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.528463	0.783681	-3.744783	33764.722033
HLA B*5801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.352517	0.607629	-3.744889	22517.350884
HLA B*5401	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.526234	0.781170	-3.745064	33591.818685
HLA A*2601	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.398001	0.652880	-3.745121	25003.509782
HLA B*5301	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.573533	0.828408	-3.745126	37457.030926
HLA A*6802	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.436025	0.690895	-3.745130	27291.351365

HLA A*3101	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.380319	0.635184	-3.745135	24005.941942
HLA B*4403	1:89-97	9	VLGICYGFQ	1.051973	-0.145185	-4.651954	0.906788	-3.745167	44869.833704
HLA A*2602	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.520851	0.775634	-3.745217	33178.049240
HLA A*3001	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.293569	0.548275	-3.745294	19659.330178
HLA B*7301	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.354587	0.609194	-3.745394	22624.927264
HLA B*5801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.352957	0.607235	-3.745722	22540.142072
HLA A*2902	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.426268	0.680376	-3.745891	26685.025959
HLA B*1517	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.000261	0.254355	-3.745906	10006.019813
HLA A*0201	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.385871	0.639875	-3.745995	24314.793440
HLA A*3101	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.341573	0.595477	-3.746096	21957.019838
HLA B*3501	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.390685	0.644580	-3.746104	24585.818956
HLA B*5301	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.381298	0.635184	-3.746115	24060.158649
HLA A*2403	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.426521	0.680376	-3.746145	26700.621722
HLA A*0211	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.212937	0.466612	-3.746324	16328.140958
HLA A*3201	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.500932	0.754547	-3.746385	31690.705932
HLA A*0101	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.379893	0.633434	-3.746459	23982.447070
HLA A*2603	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.648858	0.902388	-3.746470	44551.039185
HLA B*0802	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.437404	0.690895	-3.746509	27378.155670
HLA A*2403	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.447838	0.701295	-3.746544	28043.889772
HLA B*4601	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.394575	0.647881	-3.746695	24807.067389
HLA A*3001	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.301684	0.554890	-3.746794	20030.133225
HLA B*3801	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.539969	0.793168	-3.746801	34671.178732
HLA B*0802	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.475034	0.728232	-3.746802	29856.131873
HLA A*3201	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.560914	0.813884	-3.747031	36384.320248
HLA A*2601	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.374328	0.627189	-3.747139	23677.048550
HLA B*0801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.427522	0.680376	-3.747146	26762.227277
HLA A*0211	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.474399	0.727191	-3.747208	29812.553749
HLA A*8001	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.391841	0.644580	-3.747260	24651.345347
HLA A*0216	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.151347	0.403979	-3.747368	14169.265598
HLA B*0803	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.489241	0.741770	-3.747471	30848.984771
HLA A*0216	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.463058	0.715416	-3.747642	29044.119520
HLA A*0211	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.502208	0.754547	-3.747661	31783.936461
HLA A*8001	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.421157	0.673013	-3.748144	26372.876421
HLA B*1501	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.152658	0.404390	-3.748269	14212.103242
HLA B*5301	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.561720	0.813260	-3.748460	36451.897380
HLA B*5301	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.580615	0.831902	-3.748713	38072.789472
HLA B*4601	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.376256	0.627429	-3.748828	23782.444497
HLA B*1801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-3.544922	-0.203931	-3.748853	3506.886960
HLA A*0250	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.400696	0.651841	-3.748855	25159.142495
HLA A*8001	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.401906	0.652880	-3.749026	25229.335940
HLA B*4001	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.376491	0.627429	-3.749063	23795.314016
HLA B*5701	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.423385	0.674222	-3.749163	26508.479120
HLA B*1502	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.563118	0.813920	-3.749198	36569.420856
HLA B*4801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.415906	0.666703	-3.749203	26055.919317
HLA B*1503	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.382664	0.633434	-3.749229	24135.902204
HLA B*5801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.344602	0.595350	-3.749252	22110.668860
HLA A*2403	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.440177	0.690895	-3.749281	27553.487795
HLA A*2501	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.467722	0.718317	-3.749405	29357.694240
HLA A*0202	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.481034	0.731526	-3.749508	30271.512795
HLA B*1501	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.356016	0.606435	-3.749581	22699.467983
HLA A*2602	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.559305	0.809432	-3.749873	36249.737698
HLA A*8001	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.395957	0.645964	-3.749993	24886.104681
HLA A*8001	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.430375	0.680376	-3.749998	26938.569465
HLA B*2705	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.482888	0.732703	-3.750185	30400.999952
HLA A*3001	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.247176	0.496961	-3.750214	17667.527901
HLA B*5801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.363854	0.613596	-3.750258	23112.853180
HLA A*2501	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.430821	0.680376	-3.750445	26966.273289
HLA B*5101	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.483186	0.732703	-3.750483	30421.894316
HLA B*5801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.351260	0.600770	-3.750490	22452.273347
HLA B*4403	1:172-180	9	RLAGVQYHP	0.691508	0.223596	-4.665657	0.915104	-3.750553	46308.067375
HLA A*0206	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.536886	0.786323	-3.750563	34425.961798
HLA B*4601	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.403496	0.652880	-3.750617	25321.907674
HLA B*3501	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.478957	0.728232	-3.750725	30127.089683
HLA B*0702	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.359998	0.609194	-3.750805	22908.573965
HLA A*2601	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.390685	0.639875	-3.750810	24585.818956

HLA A*8001	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.378256	0.627429	-3.750827	23892.186910
HLA B*3501	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.092963	0.342132	-3.750831	12386.900206
HLA B*3901	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.487042	0.736037	-3.751005	30693.170944
HLA A*3101	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.306256	0.555251	-3.751005	20242.117230
HLA A*2602	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.407061	0.656026	-3.751034	25530.574625
HLA A*2301	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.505760	0.754590	-3.751170	32044.987402
HLA B*5101	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.505997	0.754547	-3.751450	32062.501529
HLA B*5401	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.533376	0.781791	-3.751585	34148.839698
HLA B*1502	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.514998	0.763388	-3.751610	32733.939863
HLA A*0250	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.580039	0.828408	-3.751631	38022.360354
HLA A*0202	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-3.849439	0.097746	-3.751692	7070.311014
HLA B*1503	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.484408	0.732703	-3.751705	30507.595924
HLA A*2602	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.546571	0.794851	-3.751720	35202.269192
HLA A*0101	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.358321	0.606435	-3.751886	22820.256593
HLA B*1501	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.391805	0.639875	-3.751930	24649.345013
HLA A*0211	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.192407	0.440475	-3.751932	15574.242799
HLA A*2902	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.248961	0.496961	-3.752000	17740.317756
HLA A*1101	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.484852	0.732703	-3.752149	30538.804949
HLA B*4601	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.319538	0.567351	-3.752187	20870.726861
HLA B*1517	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.478330	0.726094	-3.752236	30083.604311
HLA A*6801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.398306	0.645964	-3.752342	25021.100575
HLA A*3002	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.483908	0.731526	-3.752382	30472.462073
HLA B*4601	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.385878	0.633434	-3.752443	24315.188065
HLA B*1801	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.506996	0.754547	-3.752449	32136.304537
HLA A*3101	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.404340	0.651841	-3.752499	25371.134410
HLA B*0803	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.464910	0.712255	-3.752655	29168.198675
HLA B*1509	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.480903	0.728232	-3.752671	30262.343314
HLA B*1517	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.484260	0.731526	-3.752734	30497.200005
HLA B*4001	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.408903	0.656026	-3.752876	25639.088767
HLA A*2902	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.405827	0.652880	-3.752947	25458.165773
HLA A*2501	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.489027	0.736037	-3.752990	30833.801556
HLA A*0301	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.360665	0.607629	-3.753037	22943.797945
HLA A*0301	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.366633	0.613596	-3.753037	23261.247451
HLA A*8001	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.380276	0.627189	-3.753088	24003.604405
HLA A*2402	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.539480	0.786323	-3.753157	34632.186689
HLA B*1501	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-3.456102	-0.297084	-3.753186	2858.260688
HLA B*1503	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.494104	0.740887	-3.753218	31196.387779
HLA B*0702	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.265006	0.511716	-3.753290	18407.975495
HLA A*3002	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.507990	0.754590	-3.753400	32209.928921
HLA B*0802	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.480705	0.727191	-3.753514	30248.594301
HLA B*4001	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.393450	0.639875	-3.753575	24742.867138
HLA B*1501	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.259170	0.505350	-3.753820	18162.260765
HLA A*3301	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.585758	0.831902	-3.753856	38526.337072
HLA A*2601	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.360303	0.606435	-3.753869	22924.690902
HLA A*2601	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.387433	0.633434	-3.753999	24402.425301
HLA A*2301	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.529349	0.775312	-3.754037	33833.656409
HLA A*0219	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.455399	0.701295	-3.754104	28536.380958
HLA A*2301	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.540439	0.786323	-3.754116	34708.712480
HLA A*3301	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.507041	0.752770	-3.754271	32139.607929
HLA B*5101	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.495258	0.740887	-3.754371	31279.363511
HLA B*5301	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.562181	0.807776	-3.754404	36490.569220
HLA B*7301	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.579104	0.824605	-3.754499	37940.581119
HLA B*1517	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.490604	0.736037	-3.754567	30945.932751
HLA B*1503	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.406595	0.651841	-3.754754	25503.241986
HLA B*3501	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.491050	0.736037	-3.755013	30977.757777
HLA A*0216	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.456343	0.701295	-3.755049	28598.508711
HLA B*7301	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.564504	0.809432	-3.755072	36686.330878
HLA A*3101	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.382504	0.627429	-3.755075	24127.024904
HLA B*0801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.322547	0.567351	-3.755196	21015.864744
HLA B*0702	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.390466	0.635184	-3.755282	24573.452458
HLA B*7301	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.538996	0.783681	-3.755315	34593.612792
HLA A*2301	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.531034	0.775707	-3.755327	33965.148315
HLA B*4601	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.395210	0.639875	-3.755335	24843.328807
HLA A*0201	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.388784	0.633434	-3.755349	24478.451776
HLA A*3201	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.539118	0.783681	-3.755437	34603.345836

HLA B*0702	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.395438	0.639875	-3.755563	24856.368994
HLA A*8001	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.471014	0.715416	-3.755597	29581.049044
HLA A*0201	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.383072	0.627429	-3.755644	24158.632526
HLA B*5401	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.519180	0.763388	-3.755793	33050.677278
HLA A*3002	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.403753	0.647881	-3.755872	25336.843847
HLA B*5401	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.484189	0.728232	-3.755958	30492.250812
HLA B*5801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.351535	0.595477	-3.756058	22466.489169
HLA B*4403	1:69-77	9	SVYADGAPK	0.472549	0.433678	-4.662440	0.906227	-3.756213	45966.370317
HLA B*1502	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.570134	0.813884	-3.756250	37164.957864
HLA A*0101	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.365458	0.609194	-3.756265	23198.412087
HLA B*4002	1:133-141	9	EVQPVWMSH	1.211821	-0.337213	-4.630967	0.874608	-3.756359	42752.991695
HLA B*5701	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.408217	0.651841	-3.756375	25598.618989
HLA B*0801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.352069	0.595350	-3.756719	22494.095973
HLA B*5701	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.404655	0.647881	-3.756774	25389.533251
HLA A*8001	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.392003	0.635184	-3.756819	24660.548977
HLA A*3301	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.392040	0.635184	-3.756856	24662.683643
HLA A*0101	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.314409	0.557541	-3.756867	20625.697720
HLA A*2603	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.657015	0.900138	-3.756878	45395.755751
HLA B*4403	1:257-265	9	FVDHGLLRA	1.173536	-0.268296	-4.662273	0.905240	-3.757033	45948.717926
HLA B*4402	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.311925	0.554890	-3.757036	20508.091338
HLA A*1101	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.403005	0.645964	-3.757041	25293.293213
HLA A*0301	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.366638	0.609194	-3.757444	23261.499133
HLA A*2501	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.498458	0.740887	-3.757571	31510.689465
HLA B*4402	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.413735	0.656026	-3.757709	25925.997608
HLA B*1517	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.397646	0.639875	-3.757771	24983.092924
HLA A*0202	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.589698	0.831902	-3.757796	38877.453122
HLA B*3801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.565484	0.807656	-3.757828	36769.185866
HLA B*5401	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.548150	0.790294	-3.757856	35330.478031
HLA A*2602	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.586376	0.828408	-3.757968	38581.191392
HLA B*1502	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.473734	0.715584	-3.758151	29766.945692
HLA B*5701	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.411099	0.652880	-3.758220	25769.106147
HLA B*0803	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.485414	0.727191	-3.758223	30578.316047
HLA B*5301	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.539395	0.781170	-3.758226	34625.442520
HLA A*0201	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.367472	0.609194	-3.758278	23306.216016
HLA B*7301	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.551479	0.793168	-3.758311	35602.355615
HLA B*5401	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-3.795461	0.037065	-3.758397	6243.979231
HLA B*1503	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.474051	0.715416	-3.758635	29788.693476
HLA A*2602	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.511545	0.752770	-3.758775	32474.654349
HLA A*6901	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.366464	0.607629	-3.758835	23252.188680
HLA B*4402	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.425553	0.666703	-3.758850	26641.175665
HLA A*0203	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.270610	0.511716	-3.758893	18647.024836
HLA A*2603	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.534264	0.775312	-3.758952	34218.743411
HLA A*3101	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.255942	0.496961	-3.758980	18027.757784
HLA B*1517	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.487241	0.728232	-3.759010	30707.288155
HLA B*1509	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.540967	0.781791	-3.759177	34750.986518
HLA A*3002	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.587616	0.828408	-3.759208	38691.553080
HLA A*0301	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.360005	0.600770	-3.759235	22908.945767
HLA B*4403	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.659379	0.900138	-3.759241	45643.488786
HLA B*4801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.354918	0.595477	-3.759441	22642.192015
HLA A*1101	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.404063	0.644580	-3.759482	25354.943485
HLA B*1801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.354876	0.595350	-3.759526	22639.987271
HLA B*5701	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.404135	0.644580	-3.759555	25359.196032
HLA B*5301	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.578157	0.818458	-3.759699	37857.953725
HLA A*2601	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.387191	0.627429	-3.759762	24388.831604
HLA B*5401	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.554742	0.794851	-3.759891	35870.891349
HLA A*2501	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.327479	0.567535	-3.759943	21255.867477
HLA A*2403	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.367747	0.607629	-3.760118	23320.972519
HLA A*0203	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.366638	0.606435	-3.760203	23261.499133
HLA A*1101	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.496247	0.736037	-3.760210	31350.685431
HLA A*2501	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.475781	0.715416	-3.760365	29907.538919
HLA A*2601	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.369577	0.609194	-3.760383	23419.461564
HLA B*4002	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.515026	0.754590	-3.760437	32736.064975
HLA A*0212	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.361213	0.600770	-3.760443	22972.736933
HLA A*0206	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.478765	0.718317	-3.760448	30113.727942
HLA B*4801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.400369	0.639875	-3.760494	25140.230570

HLA B*4403	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.453002	0.692424	-3.760578	28379.348386
HLA B*4403	1:138-146	9	WMSHGDAVT	1.150060	-0.247944	-4.662708	0.902116	-3.760592	45994.727778
HLA B*1801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.487796	0.727191	-3.760605	30746.518227
HLA B*7301	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.513560	0.752770	-3.760791	32625.741840
HLA A*0301	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.368043	0.607235	-3.760808	23336.874587
HLA B*5101	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.502635	0.741770	-3.760865	31815.246331
HLA B*7301	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.562399	0.801202	-3.761197	36508.932963
HLA A*2402	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.579764	0.818458	-3.761306	37998.301449
HLA A*0211	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.395212	0.633434	-3.761778	24843.463207
HLA B*5101	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.389522	0.627429	-3.762093	24520.068787
HLA B*0802	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.435123	0.673013	-3.762110	27234.715230
HLA A*6802	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.389604	0.627429	-3.762175	24524.712006
HLA B*0802	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.402101	0.639875	-3.762226	25240.666981
HLA A*2902	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.052810	0.290570	-3.762240	11293.015912
HLA A*2402	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.551728	0.789472	-3.762256	35622.777579
HLA B*1501	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-3.902128	0.139834	-3.762294	7982.300423
HLA A*2301	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.534983	0.772641	-3.762342	34275.436924
HLA A*6801	1:463-471	9	GRTYGHPIV	0.832746	0.070873	-4.665990	0.903619	-3.762371	46343.655097
HLA B*0702	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.395809	0.633434	-3.762374	24877.624369
HLA A*2403	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.408395	0.645964	-3.762431	25609.146066
HLA A*6801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.436775	0.674222	-3.762553	27338.490205
HLA A*0250	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.488682	0.726094	-3.762588	30809.290609
HLA A*3101	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.415608	0.652880	-3.762728	26038.023592
HLA B*3501	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-3.998175	0.235291	-3.762884	9958.066355
HLA B*4001	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.363959	0.600770	-3.763189	23118.480574
HLA A*0301	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.358678	0.595477	-3.763200	22839.029479
HLA A*0219	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.415096	0.651841	-3.763255	26007.333598
HLA B*3901	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.504155	0.740887	-3.763269	31926.801119
HLA A*3301	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.582374	0.819048	-3.763327	38227.373657
HLA A*6802	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.411266	0.647881	-3.763385	25779.006017
HLA A*2403	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.408409	0.644580	-3.763829	25609.977335
HLA A*0202	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.577812	0.813920	-3.763892	37827.859015
HLA A*2403	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.391561	0.627429	-3.764132	24635.480490
HLA B*1801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.492460	0.728232	-3.764228	31078.472887
HLA B*3901	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.492561	0.728232	-3.764329	31085.703365
HLA A*8001	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.416245	0.651841	-3.764403	26076.225413
HLA B*1502	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.572239	0.807656	-3.764583	37345.543422
HLA B*3801	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.554077	0.789472	-3.764605	35816.015082
HLA A*8001	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.398050	0.633434	-3.764616	25006.350534
HLA A*2403	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.404554	0.639875	-3.764679	25383.627692
HLA B*1509	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.466324	0.701295	-3.765029	29263.347154
HLA B*5101	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.492615	0.727191	-3.765424	31089.571520
HLA B*1501	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.342760	0.577199	-3.765561	22017.088301
HLA B*1503	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.451950	0.686294	-3.765656	28310.650619
HLA B*3501	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.393121	0.627429	-3.765692	24724.134370
HLA A*0211	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.366614	0.600770	-3.765844	23260.240746
HLA A*3201	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.555351	0.789472	-3.765879	35921.187481
HLA B*3801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.507938	0.741770	-3.766168	32206.095602
HLA B*3801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.514571	0.748391	-3.766180	32701.725893
HLA A*2301	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.529612	0.763388	-3.766224	33854.162690
HLA B*1501	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.374008	0.607629	-3.766379	23659.634689
HLA A*0101	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.379985	0.613596	-3.766389	23987.507557
HLA B*1517	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.361899	0.595477	-3.766422	23009.055360
HLA B*4002	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.494692	0.728232	-3.766460	31238.608573
HLA A*6801	1:334-342	9	VQGTLYPDV	0.766962	0.145027	-4.678527	0.911989	-3.766538	47700.961742
HLA A*0206	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.521217	0.754547	-3.766670	33206.061431
HLA A*0212	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.375991	0.609194	-3.766797	23767.910316
HLA A*0202	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.553243	0.786323	-3.766920	35747.296052
HLA B*7301	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.459581	0.692424	-3.767157	28812.502304
HLA A*0212	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.407143	0.639875	-3.767268	25535.409198
HLA B*2705	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.453580	0.686294	-3.767286	28417.141694
HLA A*8001	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.368141	0.600770	-3.767371	23342.177685
HLA A*0216	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.458310	0.690895	-3.767415	28728.298594
HLA B*5701	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.413486	0.645964	-3.767522	25911.134652
HLA B*3501	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.401013	0.633434	-3.767579	25177.523809

HLA B*4402	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.402792	0.635184	-3.767608	25280.844391
HLA A*6901	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.888416	0.120764	-3.767653	7734.219164
HLA A*2403	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.394886	0.627189	-3.767697	24824.788576
HLA B*5301	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.577267	0.809432	-3.767834	37780.411267
HLA B*3801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.531297	0.763388	-3.767909	33985.734291
HLA B*5401	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.381592	0.613596	-3.767996	24076.434500
HLA B*1517	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.335646	0.567351	-3.768295	21659.361189
HLA B*3801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.543974	0.775634	-3.768340	34992.460315
HLA A*2402	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.521177	0.752770	-3.768408	33203.007673
HLA B*4001	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.395637	0.627189	-3.768449	24867.801590
HLA B*1509	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.401903	0.633434	-3.768469	25229.199453
HLA A*0203	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.421503	0.652880	-3.768623	26393.857890
HLA A*2603	1:39-47	9	VFSEVIPHT	1.013493	-0.151376	-4.630781	0.862117	-3.768664	42734.723772
HLA B*0803	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.501449	0.732703	-3.768746	31728.445891
HLA B*2705	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.420735	0.651841	-3.768893	26347.207540
HLA A*0201	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.369777	0.600770	-3.769006	23430.233259
HLA B*3801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.547050	0.778023	-3.769027	35241.140474
HLA A*3101	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.402498	0.633434	-3.769063	25263.754350
HLA A*0203	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.226954	0.457680	-3.769274	16863.734978
HLA A*6801	1:438-446	9	GLDNQIWQC	0.973180	-0.073042	-4.669465	0.900138	-3.769328	46715.948573
HLA B*5801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.336691	0.567351	-3.769340	21711.566764
HLA B*1509	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.522115	0.752770	-3.769345	33274.755292
HLA A*2402	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.551474	0.781791	-3.769683	35601.970408
HLA A*2402	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.579156	0.809432	-3.769723	37945.096983
HLA A*3301	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.582985	0.813260	-3.769725	38281.181012
HLA A*3101	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.415841	0.645964	-3.769877	26051.972747
HLA A*0216	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.423023	0.652880	-3.770143	26486.403495
HLA A*6801	1:2-10	9	VQPADIDVP	0.784967	0.117421	-4.672656	0.902388	-3.770268	47060.417129
HLA B*4402	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-3.848795	0.078424	-3.770371	7059.838388
HLA B*1517	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.444673	0.674222	-3.770452	27840.273353
HLA A*2603	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.578124	0.807656	-3.770469	37855.086531
HLA A*0219	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.461442	0.690895	-3.770546	28936.218128
HLA A*6801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.544940	0.774258	-3.770682	35070.351368
HLA B*2705	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.366168	0.595477	-3.770691	23236.344318
HLA B*1501	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.366269	0.595477	-3.770792	23241.750307
HLA B*5401	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.502332	0.731526	-3.770806	31793.050989
HLA A*2402	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.578486	0.807656	-3.770830	37886.637612
HLA A*0212	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.416891	0.645964	-3.770927	26115.048394
HLA A*3301	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.554620	0.783681	-3.770939	35860.801776
HLA B*4501	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.415580	0.644580	-3.770999	26036.333293
HLA A*0206	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.512787	0.741770	-3.771017	32567.724445
HLA B*5701	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.398245	0.627189	-3.771057	25017.581427
HLA B*5701	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.398685	0.627429	-3.771256	25042.903251
HLA B*5101	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.507391	0.736037	-3.771354	32165.525259
HLA A*2602	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.319822	0.548275	-3.771547	20884.393240
HLA B*3901	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.504365	0.732703	-3.771661	31942.176941
HLA A*6901	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.385351	0.613596	-3.771755	24285.740397
HLA B*0801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.399000	0.627189	-3.771811	25061.064063
HLA B*1501	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.268984	0.496961	-3.772022	18577.347531
HLA A*2601	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.327338	0.555251	-3.772087	21248.969083
HLA A*2602	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.498279	0.726094	-3.772185	31497.736459
HLA A*0101	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.379659	0.607235	-3.772424	23969.476341
HLA B*7301	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.284180	0.511716	-3.772464	19238.897225
HLA A*3301	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.484725	0.712255	-3.772471	30529.884828
HLA A*2301	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.538458	0.765882	-3.772576	34550.782525
HLA A*6901	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.213068	0.440475	-3.772593	16333.088379
HLA B*0801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.425511	0.652880	-3.772631	26638.581527
HLA B*5801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.349909	0.577199	-3.772710	22382.539884
HLA B*4002	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.616433	0.843518	-3.772915	41345.913928
HLA B*1509	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.513903	0.740887	-3.773017	32651.521260
HLA A*6901	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.380380	0.607235	-3.773145	24009.318786
HLA B*5301	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.551310	0.778023	-3.773287	35588.490770
HLA A*6901	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.340850	0.567351	-3.773499	21920.464508
HLA A*0250	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.549162	0.775634	-3.773528	35412.952886
HLA A*2902	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.425455	0.651841	-3.773613	26635.123069

HLA A*0301	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.279009	0.505350	-3.773659	19011.174936
HLA B*1501	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.426604	0.652880	-3.773724	26705.677860
HLA B*2705	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.475144	0.701295	-3.773849	29863.724201
HLA A*0101	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.369250	0.595350	-3.773900	23401.857344
HLA A*2301	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.528552	0.754547	-3.774006	33771.663956
HLA A*0212	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.426968	0.652880	-3.774088	26728.080839
HLA B*1509	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.465008	0.690895	-3.774113	29174.826890
HLA A*6801	1:404-412	9	GPGLGIRIV	1.117151	-0.208569	-4.682737	0.908582	-3.774156	48165.648553
HLA B*4601	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.383373	0.609194	-3.774180	24175.367346
HLA B*0803	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.465175	0.690895	-3.774280	29186.035155
HLA B*0802	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.454666	0.680376	-3.774290	28488.255444
HLA B*5301	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.593370	0.819048	-3.774322	39207.581278
HLA A*0250	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.502678	0.728232	-3.774446	31818.344587
HLA A*2601	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.388105	0.613596	-3.774509	24440.210648
HLA B*1503	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.430687	0.656026	-3.774661	26957.959152
HLA A*0219	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.375531	0.600770	-3.774760	23742.721647
HLA B*1517	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.409986	0.635184	-3.774802	25703.111403
HLA B*4403	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.547496	0.772641	-3.774855	35277.382723
HLA A*0250	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.525092	0.750232	-3.774860	33503.614873
HLA B*4002	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.556652	0.781791	-3.774862	36029.007595
HLA A*2403	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.426735	0.651841	-3.774894	26713.769672
HLA A*2403	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.370387	0.595477	-3.774910	23463.212738
HLA B*1503	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.283647	0.508560	-3.775087	19215.285498
HLA A*0101	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.352376	0.577199	-3.775177	22510.043087
HLA A*3101	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.384386	0.609194	-3.775192	24231.801904
HLA B*2705	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.449502	0.674222	-3.775280	28151.509492
HLA B*4801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.421268	0.645964	-3.775304	26379.582967
HLA B*3801	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.528076	0.752770	-3.775306	33734.596019
HLA A*2602	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.589242	0.813920	-3.775322	38836.671920
HLA B*4501	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.607251	0.831902	-3.775349	40480.960526
HLA A*8001	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.330618	0.555251	-3.775367	21410.053163
HLA B*5701	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.415288	0.639875	-3.775413	26018.873294
HLA B*3901	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.423375	0.647881	-3.775495	26507.905494
HLA A*3001	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.292006	0.516095	-3.775912	19588.731306
HLA A*8001	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.382386	0.606435	-3.775952	24120.499560
HLA B*3801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.548596	0.772641	-3.775955	35366.812155
HLA A*0201	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.383258	0.607235	-3.776023	24168.959679
HLA B*3801	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.550344	0.774258	-3.776086	35509.448933
HLA B*0702	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.432125	0.656026	-3.776099	27047.360885
HLA A*2601	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.383366	0.607235	-3.776131	24174.974991
HLA A*0101	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.343484	0.567351	-3.776132	22053.804764
HLA A*2603	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.503427	0.727191	-3.776236	31873.302651
HLA A*2403	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.411449	0.635184	-3.776266	25789.886315
HLA B*1501	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.389935	0.613596	-3.776339	24543.426455
HLA A*0219	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.075628	0.299099	-3.776529	11902.224520
HLA A*6802	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.067259	0.290570	-3.776689	11675.064078
HLA B*1801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.509395	0.732703	-3.776692	32314.300440
HLA B*5701	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.411938	0.635184	-3.776754	25818.922897
HLA B*4001	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.258435	0.481648	-3.776786	18131.532718
HLA B*5401	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.463117	0.686294	-3.776823	29048.047923
HLA B*4001	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.386066	0.609194	-3.776872	24325.713740
HLA A*3001	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.285437	0.508560	-3.776877	19294.660845
HLA A*0250	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.590910	0.813920	-3.776990	38986.131258
HLA B*5101	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.241187	0.463883	-3.777304	17425.568217
HLA B*0702	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.404805	0.627429	-3.777376	25398.325465
HLA A*3201	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.585121	0.807656	-3.777465	38469.895766
HLA A*0211	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.519277	0.741770	-3.777507	33058.008911
HLA A*3002	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.585260	0.807656	-3.777604	38482.176680
HLA B*5801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.351075	0.573435	-3.777640	22442.679716
HLA B*0802	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.451922	0.674222	-3.777700	28308.812788
HLA A*6802	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.430638	0.652880	-3.777758	26954.896695
HLA B*2705	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.417758	0.639875	-3.777883	26167.232605
HLA B*4002	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.571083	0.793168	-3.777915	37246.274248
HLA A*0250	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.505128	0.727191	-3.777937	31998.387524
HLA B*5701	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.411494	0.633434	-3.778060	25792.537339

HLA B*4801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.434249	0.656026	-3.778223	27179.961059
HLA B*1502	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.373670	0.595350	-3.778320	23641.210442
HLA B*5401	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.532883	0.754547	-3.778336	34110.066025
HLA A*6801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.528656	0.750232	-3.778424	33779.703755
HLA B*0702	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.430283	0.651841	-3.778442	26932.886412
HLA A*0301	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.333832	0.555251	-3.778581	21569.090923
HLA A*2902	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.469580	0.690895	-3.778685	29483.591519
HLA B*7301	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.560710	0.781791	-3.778919	36367.199621
HLA B*1502	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.287493	0.508560	-3.778933	19386.211588
HLA B*1509	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.514998	0.736037	-3.778961	32733.939863
HLA A*0301	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.336506	0.557541	-3.778964	21702.289630
HLA B*5301	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.562655	0.783681	-3.778975	36530.467824
HLA B*1509	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.511742	0.732703	-3.779039	32489.415182
HLA A*3201	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.557249	0.778023	-3.779226	36078.549511
HLA B*3801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.561086	0.781791	-3.779295	36398.692051
HLA A*3201	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.611304	0.831902	-3.779402	40860.499413
HLA B*0801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.274331	0.494882	-3.779449	18807.502729
HLA A*3001	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.258507	0.479051	-3.779456	18134.573750
HLA A*2501	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.446163	0.666703	-3.779460	27935.925807
HLA A*2402	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.527925	0.748391	-3.779534	33722.918014
HLA B*1502	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.554860	0.775312	-3.779548	35880.595538
HLA A*3301	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.569845	0.790294	-3.779551	37140.235919
HLA B*4801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.432440	0.652880	-3.779560	27066.975306
HLA B*4801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.413009	0.633434	-3.779575	25882.694469
HLA A*6901	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.294469	0.514746	-3.779723	19700.106294
HLA A*0250	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-3.831131	0.051389	-3.779742	6778.464582
HLA A*2501	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.466059	0.686294	-3.779765	29245.463426
HLA A*0202	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.472287	0.692424	-3.779863	29667.912697
HLA A*3301	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.472379	0.692424	-3.779955	29674.172862
HLA A*2603	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.599119	0.819048	-3.780071	39730.061858
HLA A*0219	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.419999	0.639875	-3.780124	26302.631688
HLA A*3101	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.154900	0.374749	-3.780150	14285.641998
HLA B*7301	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.055507	0.275316	-3.780191	11363.370026
HLA A*6802	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.413848	0.633434	-3.780414	25932.730807
HLA B*1801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.516455	0.736037	-3.780418	32843.918131
HLA B*5401	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.546503	0.765882	-3.780621	35196.746855
HLA A*1101	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.461007	0.680376	-3.780631	28907.272395
HLA A*3002	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.387106	0.606435	-3.780672	24384.082195
HLA B*5101	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.499066	0.718317	-3.780750	31554.871970
HLA B*3801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.516932	0.736037	-3.780895	32880.007382
HLA A*0203	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.388248	0.607235	-3.781014	24448.277327
HLA B*0802	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.467452	0.686294	-3.781158	29339.435405
HLA B*4403	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.588953	0.807776	-3.781177	38810.837959
HLA B*1517	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.414682	0.633434	-3.781248	25982.582748
HLA A*6802	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.115311	0.334057	-3.781253	13041.001357
HLA A*3001	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.298014	0.516757	-3.781257	19861.586787
HLA A*0219	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.461820	0.680376	-3.781444	28961.432326
HLA B*0801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.293165	0.511716	-3.781448	19641.045661
HLA A*2602	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.557237	0.775707	-3.781530	36077.573620
HLA B*5401	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.472442	0.690895	-3.781547	29678.507596
HLA A*2402	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.574764	0.793168	-3.781597	37563.364084
HLA A*6901	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.388032	0.606435	-3.781598	24436.112208
HLA B*0801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.290315	0.508560	-3.781755	19512.579251
HLA B*5301	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.606379	0.824605	-3.781774	40399.793930
HLA B*4402	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.434904	0.652880	-3.782025	27221.016355
HLA B*1502	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.513565	0.731526	-3.782039	32626.094845
HLA A*0201	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.248722	0.466612	-3.782109	17730.531195
HLA B*4801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.430086	0.647881	-3.782205	26920.650063
HLA A*2402	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.583455	0.801202	-3.782253	38322.622816
HLA A*6901	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.378002	0.595477	-3.782525	23878.231546
HLA A*6801	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.601612	0.819048	-3.782564	39958.763871
HLA A*2603	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.500885	0.718317	-3.782568	31687.277253
HLA A*2301	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.532847	0.750232	-3.782616	34107.298162
HLA A*2403	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.383479	0.600770	-3.782709	24181.253435
HLA A*0201	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.396333	0.613596	-3.782737	24907.654977

HLA B*5401	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.457058	0.674222	-3.782836	28645.580695
HLA A*6802	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.434681	0.651841	-3.782840	27207.029995
HLA A*3002	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.416350	0.633434	-3.782916	26082.574313
HLA B*2705	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.473840	0.690895	-3.782945	29774.193189
HLA B*4501	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.475395	0.692424	-3.782971	29881.016065
HLA B*1517	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.157785	0.374749	-3.783035	14380.862371
HLA B*5701	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.383834	0.600770	-3.783063	24201.015009
HLA A*1101	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.473962	0.690895	-3.783067	29782.570271
HLA B*1509	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.510365	0.727191	-3.783174	32386.580488
HLA B*0801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.410745	0.627429	-3.783316	25748.064134
HLA B*5801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.069590	0.286262	-3.783328	11737.888019
HLA B*1501	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.384200	0.600770	-3.783430	24221.447900
HLA A*3101	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.390769	0.607235	-3.783535	24590.607658
HLA A*6901	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.241220	0.457680	-3.783540	17426.888052
HLA A*0101	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.391218	0.607629	-3.783589	24616.029991
HLA B*1502	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.612283	0.828408	-3.783876	40952.781637
HLA B*1502	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.536769	0.752770	-3.783999	34416.651026
HLA A*2902	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.379377	0.595350	-3.784027	23953.920726
HLA B*1801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.065619	0.281539	-3.784080	11631.060970
HLA B*0801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.397700	0.613596	-3.784104	24986.201700
HLA A*0203	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.250733	0.466612	-3.784121	17812.829302
HLA A*0206	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.292866	0.508560	-3.784306	19627.555799
HLA A*0216	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.476796	0.692424	-3.784372	29977.516734
HLA A*3101	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-3.930223	0.145582	-3.784641	8515.756027
HLA B*7301	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.574154	0.789472	-3.784682	37510.565680
HLA B*3501	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.436725	0.651841	-3.784884	27335.384519
HLA B*4601	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.392712	0.607629	-3.785084	24700.871980
HLA B*0801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.251828	0.466612	-3.785215	17857.792245
HLA B*4801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.437089	0.651841	-3.785248	27358.315749
HLA B*3901	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.271702	0.486297	-3.785405	18693.992313
HLA B*3901	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.431392	0.645964	-3.785428	27001.746546
HLA B*5101	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.497690	0.712255	-3.785435	31454.995269
HLA B*2705	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.465831	0.680376	-3.785454	29230.120624
HLA A*3201	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.561130	0.775634	-3.785496	36402.433588
HLA B*4801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.394726	0.609194	-3.785532	24815.657899
HLA A*2501	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.441565	0.656026	-3.785539	27641.724013
HLA A*0216	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.431507	0.645964	-3.785543	27008.905241
HLA B*3801	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.512787	0.727191	-3.785596	32567.724445
HLA B*5401	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.560975	0.775312	-3.785664	36389.438322
HLA B*1503	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.487054	0.701295	-3.785759	30694.001188
HLA B*0702	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.393034	0.607235	-3.785800	24719.185936
HLA A*0219	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.431768	0.645964	-3.785804	27025.128897
HLA A*0203	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.425704	0.639875	-3.785829	26650.401314
HLA A*2902	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.392484	0.606435	-3.786050	24687.913370
HLA B*0803	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.501592	0.715416	-3.786176	31738.918109
HLA A*2403	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.439124	0.652880	-3.786244	27486.789185
HLA A*2601	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.387076	0.600770	-3.786306	24382.367358
HLA B*5301	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.600426	0.813920	-3.786506	39849.745754
HLA B*4402	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.413806	0.627189	-3.786617	25930.205652
HLA A*0216	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.395821	0.609194	-3.786627	24878.297304
HLA B*3501	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.434592	0.647881	-3.786711	27201.437463
HLA B*4601	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.413945	0.627189	-3.786756	25938.483466
HLA B*0802	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.442794	0.656026	-3.786768	27720.043478
HLA B*0801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.387640	0.600770	-3.786870	24414.045336
HLA A*0301	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.301627	0.514746	-3.786881	20027.532735
HLA A*0212	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.414797	0.627429	-3.787369	25989.471242
HLA A*0206	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.488759	0.701295	-3.787465	30814.791370
HLA A*0203	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.354829	0.567351	-3.787478	22637.537807
HLA B*0801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.420962	0.633434	-3.787528	26361.037109
HLA B*3801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.427435	0.639875	-3.787560	26756.870928
HLA A*0211	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.355048	0.567351	-3.787697	22648.930064
HLA A*0206	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-3.980765	0.192958	-3.787807	9566.769978
HLA A*0201	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.343089	0.555251	-3.787838	22033.770018
HLA B*4501	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-3.995111	0.207166	-3.787945	9888.064425
HLA A*3201	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.133501	0.345470	-3.788031	13598.802079

HLA A*2603	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.480456	0.692424	-3.788032	30231.253270
HLA B*5301	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.563682	0.775634	-3.788048	36616.932456
HLA B*4801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.423234	0.635184	-3.788051	26499.302601
HLA B*5101	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.503500	0.715416	-3.788084	31878.648461
HLA B*4801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.415582	0.627429	-3.788153	26036.474147
HLA A*2301	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.519732	0.731526	-3.788207	33092.722116
HLA A*0206	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.303004	0.514746	-3.788258	20091.124666
HLA B*5101	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.397458	0.609194	-3.788265	24972.282803
HLA A*0206	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.479173	0.690895	-3.788278	30142.087963
HLA B*1801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.455187	0.666703	-3.788485	28522.490261
HLA A*3101	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.165402	0.376904	-3.788498	14635.311159
HLA A*3002	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.346115	0.557541	-3.788574	22187.836082
HLA B*3901	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.423845	0.635184	-3.788661	26536.601982
HLA B*7301	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.583542	0.794851	-3.788691	38330.294466
HLA B*4001	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.395137	0.606435	-3.788702	24839.162767
HLA A*0301	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.366020	0.577199	-3.788821	23228.426187
HLA B*3801	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.481283	0.692424	-3.788859	30288.876919
HLA A*1101	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.436756	0.647881	-3.788875	27337.307045
HLA B*1503	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.193469	0.404390	-3.789079	15612.372626
HLA A*2402	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.561793	0.772641	-3.789152	36458.011115
HLA B*0801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.396406	0.607235	-3.789171	24911.832505
HLA B*2705	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.437101	0.647881	-3.789220	27359.055786
HLA B*2705	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.133435	0.344171	-3.789264	13596.742331
HLA A*6901	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.337542	0.548275	-3.789267	21754.127921
HLA A*0219	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.463711	0.674222	-3.789490	29087.833264
HLA B*4002	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.521018	0.731526	-3.789492	33190.795447
HLA A*0206	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.121250	0.331684	-3.789566	13220.577859
HLA A*2501	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.429555	0.639875	-3.789679	26887.756048
HLA A*6801	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.531492	0.741770	-3.789722	34000.998020
HLA A*3101	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.397381	0.607629	-3.789752	24967.824990
HLA A*3001	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.279169	0.489404	-3.789765	19018.169911
HLA A*2301	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.522545	0.732703	-3.789842	33307.713935
HLA B*5101	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.491355	0.701295	-3.790061	30999.551650
HLA A*3201	1:118-126	9	TELKVLGGK	0.614308	0.199612	-4.604107	0.813920	-3.790187	40188.999802
HLA B*1502	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.565959	0.775707	-3.790252	36809.389107
HLA A*2402	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.521856	0.731526	-3.790330	33254.959781
HLA A*2301	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.463345	0.673013	-3.790332	29063.295155
HLA B*0801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.133599	0.343210	-3.790390	13601.892287
HLA B*0803	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.463472	0.673013	-3.790459	29071.786772
HLA A*0301	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.322806	0.532233	-3.790572	21028.374751
HLA B*4402	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.435172	0.644580	-3.790592	27237.809479
HLA B*7301	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.571905	0.781170	-3.790736	37316.865433
HLA B*4601	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.404352	0.613596	-3.790756	25371.820694
HLA B*0803	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.477099	0.686294	-3.790805	29998.444616
HLA A*2902	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.424271	0.633434	-3.790836	26562.599082
HLA A*2402	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.506552	0.715584	-3.790968	32103.462953
HLA A*6802	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.277268	0.486297	-3.790971	18935.116860
HLA A*0201	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.397428	0.606435	-3.790993	24970.526600
HLA A*2402	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.566454	0.775312	-3.791143	36851.430522
HLA B*4001	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.398908	0.607629	-3.791279	25055.777096
HLA A*6901	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.368564	0.577199	-3.791365	23364.918902
HLA B*1503	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.519732	0.728232	-3.791501	33092.722116
HLA B*4402	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.431434	0.639875	-3.791559	27004.376050
HLA A*2603	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.426752	0.635184	-3.791568	26714.781321
HLA A*0301	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.365073	0.573435	-3.791638	23177.839077
HLA A*0206	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-3.935007	0.143276	-3.791730	8610.071582
HLA B*1801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.478102	0.686294	-3.791808	30067.821803
HLA A*0211	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.527963	0.736037	-3.791926	33725.837136
HLA A*0212	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.347301	0.555251	-3.792051	22248.535996
HLA A*0216	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.419651	0.627429	-3.792223	26281.580557
HLA A*6802	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.393098	0.600770	-3.792327	24722.796857
HLA B*5801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.359874	0.567535	-3.792338	22902.006466
HLA A*0101	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.347668	0.555251	-3.792417	22267.320411
HLA B*7301	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.483339	0.690895	-3.792444	30432.593837
HLA A*2902	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.399700	0.607235	-3.792465	25101.498766

HLA B*5301	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.545340	0.752770	-3.792570	35102.619745
HLA A*0219	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.445470	0.652880	-3.792590	27891.377937
HLA B*3801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.558631	0.765882	-3.792749	36193.498642
HLA B*0702	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.388145	0.595350	-3.792795	24442.458471
HLA A*3301	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.586019	0.793168	-3.792851	38549.478997
HLA B*4501	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.428046	0.635184	-3.792862	26794.532852
HLA A*0301	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.360256	0.567351	-3.792905	22922.210635
HLA A*2902	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.366553	0.573435	-3.793118	23256.969258
HLA B*4002	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.625060	0.831902	-3.793158	42175.467486
HLA B*5301	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.588011	0.794851	-3.793160	38726.734323
HLA B*3801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.508826	0.715584	-3.793243	32272.022459
HLA A*2602	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.439218	0.645964	-3.793254	27492.737848
HLA B*3901	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.460088	0.666703	-3.793386	28846.190431
HLA B*4403	1:177-185	9	QYHPEVMHT	0.996873	-0.153355	-4.636925	0.843518	-3.793407	43343.582496
HLA B*3901	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.427083	0.633434	-3.793648	26735.166980
HLA B*1509	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.446598	0.652880	-3.793718	27963.898901
HLA B*3501	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-3.859927	0.066046	-3.793880	7243.135659
HLA A*2902	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.421376	0.627429	-3.793947	26386.148472
HLA A*0206	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.535138	0.740887	-3.794251	34287.677246
HLA A*6802	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.401518	0.607235	-3.794284	25206.825483
HLA B*4002	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.613399	0.819048	-3.794351	41058.153220
HLA B*1501	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.280710	0.486297	-3.794413	19085.783157
HLA A*2501	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.439058	0.644580	-3.794478	27482.625887
HLA B*4501	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.607862	0.813260	-3.794601	40537.939941
HLA A*3001	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.206551	0.411911	-3.794640	16089.807221
HLA B*3901	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.434646	0.639875	-3.794771	27204.822279
HLA A*2403	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.401224	0.606435	-3.794790	25189.785479
HLA B*1517	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-3.908303	0.113362	-3.794941	8096.596856
HLA B*3501	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.447850	0.652880	-3.794970	28044.648354
HLA B*1502	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.569278	0.774258	-3.795020	37091.844653
HLA B*5301	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.584599	0.789472	-3.795128	38423.721331
HLA A*2301	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.531191	0.736037	-3.795154	33977.461641
HLA A*0219	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.404361	0.609194	-3.795168	25372.369735
HLA B*2705	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.134440	0.339229	-3.795212	13628.261147
HLA B*3501	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.350689	0.555251	-3.795439	22422.776912
HLA A*0203	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.391032	0.595477	-3.795555	24605.511809
HLA B*0801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.402303	0.606435	-3.795868	25252.412945
HLA A*0212	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.199958	0.403979	-3.795979	15847.406049
HLA A*0206	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.511399	0.715416	-3.795983	32463.763750
HLA B*1503	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.448989	0.652880	-3.796110	28118.328415
HLA B*5801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.351180	0.554890	-3.796291	22448.143940
HLA B*5401	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.423488	0.627189	-3.796300	26514.789820
HLA A*0219	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.351554	0.555251	-3.796303	22467.461520
HLA A*6801	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.610249	0.813884	-3.796365	40761.368062
HLA B*1503	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.200400	0.403979	-3.796420	15863.531998
HLA B*1501	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.403661	0.607235	-3.796426	25331.498700
HLA B*0801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.391925	0.595477	-3.796448	24656.146812
HLA A*2301	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.538406	0.741770	-3.796636	34546.670620
HLA A*2902	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.404312	0.607629	-3.796683	25369.487403
HLA B*1502	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.546979	0.750232	-3.796748	35235.421418
HLA B*7301	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.562838	0.765882	-3.796957	36545.885887
HLA A*6801	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.599295	0.801202	-3.798094	39746.185271
HLA B*4402	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.444248	0.645964	-3.798284	27813.025780
HLA A*3001	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.202336	0.403979	-3.798356	15934.405487
HLA A*0250	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.588753	0.790294	-3.798459	38792.995263
HLA A*3002	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.548772	0.750232	-3.798540	35381.164857
HLA A*3301	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.606299	0.807656	-3.798644	40392.363628
HLA A*0216	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.310480	0.511716	-3.798764	20439.972621
HLA B*4601	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.394270	0.595477	-3.798793	24789.627070
HLA A*0219	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.426261	0.627429	-3.798832	26684.592873
HLA A*0101	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.394427	0.595477	-3.798950	24798.614010
HLA A*2602	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.580984	0.781791	-3.799193	38105.140431
HLA A*3001	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.285503	0.486297	-3.799206	19297.583762
HLA B*5701	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.394937	0.595477	-3.799460	24827.743337
HLA A*0301	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.367070	0.567535	-3.799535	23284.665614

HLA B*3901	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.485834	0.686294	-3.799540	30607.941518
HLA A*1101	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.455585	0.656026	-3.799558	28548.579479
HLA B*0802	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.432994	0.633434	-3.799560	27101.554699
HLA B*4601	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.406819	0.607235	-3.799584	25516.352477
HLA B*1503	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.131325	0.331684	-3.799641	13530.848451
HLA B*7301	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.590078	0.790294	-3.799785	38911.540336
HLA A*1101	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.357470	0.557541	-3.799929	22775.609594
HLA B*1502	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.439836	0.639875	-3.799961	27531.882379
HLA A*3101	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.406396	0.606435	-3.799961	25491.517257
HLA B*4402	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.427506	0.627429	-3.800077	26761.213832
HLA A*2301	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.528362	0.728232	-3.800130	33756.868420
HLA B*4001	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.395482	0.595350	-3.800132	24858.924059
HLA A*2601	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.395703	0.595477	-3.800226	24871.568772
HLA A*0201	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.395708	0.595477	-3.800231	24871.837879
HLA B*3901	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.295129	0.494882	-3.800247	19730.076754
HLA A*2902	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.332516	0.532233	-3.800283	21503.845425
HLA A*3201	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.515736	0.715416	-3.800320	32789.592431
HLA A*8001	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.448247	0.647881	-3.800366	28070.300495
HLA A*3201	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.566318	0.765882	-3.800437	36839.869331
HLA A*2403	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.367824	0.567351	-3.800473	23325.136299
HLA B*1801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.515903	0.715416	-3.800487	32802.189403
HLA B*5701	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.409814	0.609194	-3.800621	25692.962685
HLA B*1801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.501919	0.701295	-3.800624	31762.793945
HLA A*3201	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.590985	0.790294	-3.800691	38992.880983
HLA A*2402	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.555292	0.754547	-3.800745	35916.329569
HLA A*2603	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.578770	0.778023	-3.800747	37911.446195
HLA B*4801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.428032	0.627189	-3.800844	26793.663134
HLA A*8001	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.396218	0.595350	-3.800868	24901.053217
HLA A*0211	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.247589	0.446544	-3.801045	17684.357881
HLA B*0801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.408748	0.607629	-3.801119	25629.935896
HLA B*4501	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.582330	0.781170	-3.801160	38223.444547
HLA B*4001	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.414772	0.613596	-3.801176	25987.924687
HLA A*1101	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.487493	0.686294	-3.801199	30725.068464
HLA B*1502	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.447331	0.645964	-3.801367	28011.138615
HLA B*4402	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.402155	0.600770	-3.801385	25243.807808
HLA A*2602	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.488024	0.686294	-3.801730	30762.656980
HLA A*0202	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.402507	0.600770	-3.801737	25264.301052
HLA A*6801	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.579802	0.778023	-3.801779	38001.590657
HLA A*0250	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.514051	0.712255	-3.801797	32662.651546
HLA A*2603	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.620267	0.818458	-3.801809	41712.570697
HLA B*4402	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.397369	0.595477	-3.801892	24967.149633
HLA A*2603	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.630302	0.828408	-3.801894	42687.587003
HLA A*3301	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.579922	0.778023	-3.801899	38012.076908
HLA B*5301	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.603193	0.801202	-3.801991	40104.513117
HLA A*2402	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.565411	0.763388	-3.802023	36763.019949
HLA B*3501	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.232696	0.430602	-3.802094	17088.183924
HLA A*2602	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.616033	0.813884	-3.802150	41307.906351
HLA B*3801	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.552400	0.750232	-3.802168	35677.936809
HLA A*3101	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.403005	0.600770	-3.802235	25293.293213
HLA A*2403	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.357540	0.555251	-3.802290	22779.306300
HLA A*8001	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.411583	0.609194	-3.802390	25797.840205
HLA A*3001	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.261498	0.458831	-3.802667	18259.893761
HLA B*0802	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.469399	0.666703	-3.802697	29471.312349
HLA A*6801	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.634618	0.831902	-3.802716	43113.929788
HLA A*2403	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.412086	0.609194	-3.802893	25827.724080
HLA A*2403	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.416538	0.613596	-3.802943	26093.865063
HLA B*5401	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.518497	0.715416	-3.803081	32998.687266
HLA A*0211	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.358351	0.555251	-3.803100	22821.861565
HLA A*0101	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.376632	0.573435	-3.803197	23803.039071
HLA B*5701	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.416888	0.613596	-3.803293	26114.907115
HLA B*1503	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.358555	0.555251	-3.803305	22832.605439
HLA B*5301	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.575960	0.772641	-3.803319	37666.942367
HLA B*5301	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.577654	0.774258	-3.803396	37814.150316
HLA A*8001	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.410665	0.607235	-3.803430	25743.328568
HLA B*0801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.380739	0.577199	-3.803540	24029.199839

HLA B*3801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.399237	0.595477	-3.803760	25074.761141
HLA B*4402	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.455681	0.651841	-3.803840	28554.912412
HLA A*0211	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.140573	0.336669	-3.803903	13822.054557
HLA A*3101	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.381111	0.577199	-3.803911	24049.747878
HLA A*0211	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.318772	0.514746	-3.804026	20833.951188
HLA A*3002	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.431481	0.627429	-3.804052	27007.298022
HLA B*1501	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.319061	0.514746	-3.804315	20847.819053
HLA A*0203	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.361856	0.557541	-3.804315	23006.814893
HLA A*2301	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.545372	0.740887	-3.804486	35105.278464
HLA A*6901	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.086083	0.281539	-3.804544	12192.235611
HLA A*0216	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.485329	0.680376	-3.804953	30572.361316
HLA B*4601	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.405747	0.600770	-3.804977	25453.483524
HLA A*3101	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.418573	0.613596	-3.804977	26216.400695
HLA B*3501	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.362575	0.557541	-3.805034	23044.932516
HLA B*0801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.291466	0.486297	-3.805169	19564.372705
HLA A*2501	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.438678	0.633434	-3.805243	27458.550609
HLA B*4001	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.412504	0.607235	-3.805270	25852.607131
HLA A*3001	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.180044	0.374749	-3.805295	15137.144295
HLA B*0802	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.458199	0.652880	-3.805320	28720.994928
HLA A*0250	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.360576	0.555251	-3.805325	22939.081741
HLA B*4601	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.411839	0.606435	-3.805405	25813.057108
HLA B*1801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.485858	0.680376	-3.805481	30609.597418
HLA A*0250	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.591970	0.786323	-3.805647	39081.368095
HLA A*0301	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.300580	0.494882	-3.805698	19979.268342
HLA B*1502	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.560569	0.754590	-3.805979	36355.396985
HLA A*6901	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.379435	0.573435	-3.806000	23957.160646
HLA A*6801	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.634481	0.828408	-3.806074	43100.403898
HLA A*0216	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.446027	0.639875	-3.806152	27927.161627
HLA B*1503	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.317900	0.511716	-3.806184	20792.177948
HLA B*3901	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.486565	0.680376	-3.806189	30659.481976
HLA B*1502	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.497137	0.690895	-3.806242	31415.031189
HLA B*1501	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.096867	0.290570	-3.806298	12498.775943
HLA B*2705	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.441753	0.635184	-3.806569	27653.689695
HLA A*0201	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.318290	0.511716	-3.806574	20810.858575
HLA A*6801	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.616040	0.809432	-3.806608	41308.576770
HLA B*5801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.355085	0.548275	-3.806811	22650.890600
HLA A*0250	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.454797	0.647881	-3.806917	28496.887376
HLA A*0101	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.374490	0.567535	-3.806954	23685.888424
HLA A*3001	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.264642	0.457680	-3.806962	18392.546274
HLA A*0206	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.459886	0.652880	-3.807007	28832.772849
HLA B*4601	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.402507	0.595350	-3.807157	25264.301052
HLA A*3301	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.621066	0.813884	-3.807182	41789.365833
HLA A*2402	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.519476	0.712255	-3.807222	33073.213821
HLA A*2602	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.549009	0.741770	-3.807239	35400.502365
HLA B*4402	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.414595	0.607235	-3.807361	25977.382441
HLA A*8001	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.374903	0.567351	-3.807552	23708.451457
HLA A*6801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.540272	0.732703	-3.807568	34695.383350
HLA A*2602	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.474336	0.666703	-3.807633	29808.199437
HLA B*4002	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.591357	0.783681	-3.807676	39026.224883
HLA A*0211	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.523510	0.715416	-3.808094	33381.854846
HLA A*1101	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.509524	0.701295	-3.808229	32323.916793
HLA B*1502	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.601419	0.793168	-3.808252	39941.041659
HLA A*0211	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.549223	0.740887	-3.808337	35417.934320
HLA A*3101	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.338923	0.530534	-3.808389	21823.438305
HLA A*2603	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.584137	0.775707	-3.808430	38382.793135
HLA A*6801	1:490-498	9	YEVLERIST	1.211490	-0.403834	-4.616108	0.807656	-3.808453	41315.058048
HLA B*3901	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.509787	0.701295	-3.808493	32343.508034
HLA A*3301	1:5-13	9	ADIDVPETP	0.888251	-0.059843	-4.637033	0.828408	-3.808625	43354.370101
HLA A*6802	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.416350	0.607629	-3.808722	26082.574313
HLA A*2603	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.563287	0.754547	-3.808740	36583.667859
HLA A*1101	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.482972	0.674222	-3.808751	30406.921306
HLA B*1517	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.140450	0.331684	-3.808766	13818.166763
HLA A*2501	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.454795	0.645964	-3.808831	28496.733211
HLA A*0202	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.527267	0.718317	-3.808951	33671.874254
HLA A*0206	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.545036	0.736037	-3.809000	35078.131026

HLA A*2603	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.622391	0.813260	-3.809130	41917.067325
HLA A*2402	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.537394	0.728232	-3.809162	34466.213289
HLA A*2601	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.366732	0.557541	-3.809190	23266.533363
HLA B*4501	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.591002	0.781791	-3.809211	38994.357641
HLA B*5701	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.415859	0.606435	-3.809425	26053.100277
HLA A*2403	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.367209	0.557541	-3.809667	23292.098880
HLA B*1503	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.405437	0.595350	-3.810087	25435.313544
HLA A*3201	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.564772	0.754590	-3.810182	36708.963320
HLA B*5401	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.552146	0.741770	-3.810376	35657.097420
HLA B*5401	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.546458	0.736037	-3.810421	35193.129241
HLA B*4403	1:52-60	9	EIRARQPVA	1.173199	-0.316033	-4.667701	0.857166	-3.810535	46526.534806
HLA B*0802	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.445822	0.635184	-3.810639	27914.020512
HLA B*0803	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.458622	0.647881	-3.810742	28748.976481
HLA A*0301	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.365829	0.554890	-3.810940	23218.249696
HLA B*4403	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.624853	0.813884	-3.810970	42155.393779
HLA B*4501	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.618817	0.807776	-3.811041	41573.570354
HLA B*0801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.343465	0.532233	-3.811231	22052.850315
HLA B*5701	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.418557	0.607235	-3.811322	26215.407919
HLA A*0211	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.323043	0.511716	-3.811327	21039.867769
HLA B*4001	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.406828	0.595477	-3.811351	25516.904646
HLA B*4801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.418597	0.607235	-3.811362	26217.819011
HLA B*3901	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.343744	0.532233	-3.811511	22067.052000
HLA A*3001	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.201048	0.389429	-3.811619	15887.235996
HLA A*0203	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.004613	0.192958	-3.811655	10106.775170
HLA A*2301	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.523929	0.712255	-3.811674	33414.015729
HLA B*5401	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.552856	0.740887	-3.811969	35715.401120
HLA A*0211	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.457943	0.645964	-3.811979	28704.063784
HLA B*7301	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-3.947638	0.135619	-3.812018	8864.160140
HLA B*3901	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.463925	0.651841	-3.812084	29102.156727
HLA A*0203	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.425852	0.613596	-3.812256	26659.485932
HLA A*2403	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.342830	0.530534	-3.812296	22020.661891
HLA B*3501	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.468342	0.656026	-3.812316	29399.653170
HLA A*6801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.298646	0.486297	-3.812349	19890.511605
HLA B*7301	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.588044	0.775634	-3.812410	38729.667537
HLA B*5301	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.598734	0.786323	-3.812411	39694.828112
HLA B*5101	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.486633	0.674222	-3.812411	30664.292420
HLA B*4601	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.389691	0.577199	-3.812492	24529.621509
HLA A*3301	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.621959	0.809432	-3.812526	41875.363015
HLA B*5701	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.407960	0.595350	-3.812611	25583.528499
HLA B*1502	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.538864	0.726094	-3.812770	34583.134113
HLA B*1517	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.253284	0.440475	-3.812809	17917.790189
HLA B*1503	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.380164	0.567351	-3.812813	23997.372086
HLA B*1509	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.386298	0.573435	-3.812863	24338.745571
HLA B*4801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.408231	0.595350	-3.812881	25599.449917
HLA A*2601	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.386611	0.573435	-3.813176	24356.263972
HLA A*2601	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.390377	0.577199	-3.813178	24568.401270
HLA B*3901	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.504280	0.690895	-3.813385	31935.956616
HLA B*3901	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.457988	0.644580	-3.813408	28707.014366
HLA A*0101	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.308354	0.494882	-3.813472	20340.144121
HLA B*0702	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.409004	0.595477	-3.813526	25645.053760
HLA B*7301	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.576966	0.763388	-3.813578	37754.258680
HLA A*6901	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.197783	0.384129	-3.813654	15768.216079
HLA A*1101	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.465652	0.651841	-3.813811	29218.105085
HLA B*0803	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.515203	0.701295	-3.813908	32749.350057
HLA B*4501	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.600245	0.786323	-3.813922	39833.149342
HLA A*0301	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.293031	0.479051	-3.813980	19634.990009
HLA B*7301	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.588251	0.774258	-3.813992	38748.109968
HLA A*0250	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.568757	0.754547	-3.814210	37047.324258
HLA B*5101	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.506662	0.692424	-3.814238	32111.626771
HLA A*0201	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.391573	0.577199	-3.814374	24636.146875
HLA A*0211	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.488722	0.674222	-3.814500	30812.124212
HLA B*5301	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.604807	0.790294	-3.814513	40253.842630
HLA B*2705	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.448024	0.633434	-3.814589	28055.877766
HLA A*0212	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.410493	0.595477	-3.815016	25733.163970
HLA A*6802	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.272802	0.457680	-3.815122	18741.382255

HLA B*1503	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.372681	0.557541	-3.815139	23587.427358
HLA A*2301	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.533681	0.718317	-3.815365	34172.864532
HLA A*3001	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.101722	0.286262	-3.815459	12639.256249
HLA B*4801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.429190	0.613596	-3.815595	26865.219233
HLA A*3301	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.634073	0.818458	-3.815614	43059.851685
HLA A*1101	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.468587	0.652880	-3.815707	29416.198906
HLA B*5101	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.442972	0.627189	-3.815784	27731.442961
HLA A*2301	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.543061	0.727191	-3.815870	34918.897973
HLA B*4001	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.364154	0.548275	-3.815880	23128.863584
HLA A*3002	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.348168	0.532233	-3.815935	22292.993976
HLA A*1101	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.282620	0.466612	-3.816008	19169.911883
HLA A*0202	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.373703	0.557541	-3.816161	23643.001058
HLA A*2501	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.443360	0.627189	-3.816172	27756.207978
HLA A*2402	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.582135	0.765882	-3.816253	38206.285279
HLA B*5301	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.566548	0.750232	-3.816317	36859.405871
HLA B*4002	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.489337	0.673013	-3.816324	30855.828003
HLA B*3801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.547964	0.731526	-3.816438	35315.381673
HLA B*5801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.348702	0.532233	-3.816468	22320.387589
HLA B*3501	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.331327	0.514746	-3.816581	21445.061210
HLA A*0203	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.153255	0.336669	-3.816586	14231.645685
HLA B*4501	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.641267	0.824605	-3.816662	43779.082206
HLA A*2603	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.626105	0.809432	-3.816673	42277.123048
HLA A*0201	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.384273	0.567351	-3.816922	24225.510336
HLA B*4002	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.630311	0.813260	-3.817051	42688.510754
HLA B*4403	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.598327	0.781170	-3.817158	39657.694672
HLA A*1101	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.452342	0.635184	-3.817158	28336.239475
HLA B*3901	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-3.836582	0.019419	-3.817163	6864.076836
HLA B*1801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.374706	0.557541	-3.817164	23697.680057
HLA A*6801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.365447	0.548275	-3.817172	23197.784591
HLA B*1503	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.332100	0.514746	-3.817354	21483.264265
HLA A*0201	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.374948	0.557541	-3.817406	23710.888525
HLA B*1517	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.462128	0.644580	-3.817547	28981.964437
HLA A*2902	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.413153	0.595477	-3.817676	25891.237251
HLA B*1501	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.154594	0.336669	-3.817925	14275.598644
HLA B*1517	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-3.931567	0.113627	-3.817941	8542.148479
HLA B*4601	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.373209	0.555251	-3.817958	23616.156047
HLA A*2501	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.427240	0.609194	-3.818047	26744.859233
HLA B*3901	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.470938	0.652880	-3.818059	29575.928521
HLA B*5701	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.425720	0.607629	-3.818092	26651.410563
HLA A*2403	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.332913	0.514746	-3.818167	21523.514764
HLA A*0202	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.554270	0.736037	-3.818233	35831.906981
HLA A*0202	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.560031	0.741770	-3.818261	36310.385458
HLA B*3801	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.551112	0.732703	-3.818409	35572.321942
HLA B*2705	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.419207	0.600770	-3.818437	26254.722187
HLA B*4002	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.643055	0.824605	-3.818450	43959.688949
HLA A*0216	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.297624	0.479051	-3.818573	19843.758263
HLA B*0801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.366913	0.548275	-3.818638	23276.227324
HLA B*1501	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.150497	0.331684	-3.818813	14141.543947
HLA A*6801	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.609166	0.790294	-3.818872	40659.837545
HLA A*2602	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.609175	0.790294	-3.818881	40660.717416
HLA A*3201	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.446086	0.627189	-3.818897	27930.938954
HLA A*6901	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.373811	0.554890	-3.818921	23648.885467
HLA A*3101	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.414328	0.595350	-3.818978	25961.366418
HLA A*0202	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.155764	0.336669	-3.819095	14314.110743
HLA A*3201	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.458998	0.639875	-3.819123	28773.871858
HLA A*0301	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.367420	0.548275	-3.819146	23303.442332
HLA A*1101	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.223716	0.404390	-3.819327	16738.486181
HLA A*0101	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.367808	0.548275	-3.819533	23324.253010
HLA B*5301	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.595052	0.775312	-3.819740	39359.745597
HLA A*2501	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.471617	0.651841	-3.819776	29622.205409
HLA B*4801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.393227	0.573435	-3.819792	24730.154069
HLA B*5401	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.535519	0.715584	-3.819935	34317.740208
HLA B*2705	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.447140	0.627189	-3.819952	27998.866794
HLA B*4403	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.027544	0.207166	-3.820377	10654.757712
HLA B*5401	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.547572	0.727191	-3.820381	35283.490347

HLA A*2501	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.421160	0.600770	-3.820390	26373.019095
HLA B*0803	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.487194	0.666703	-3.820492	30703.965874
HLA A*2602	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.536177	0.715584	-3.820593	34369.763047
HLA A*2601	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.368900	0.548275	-3.820626	23383.001328
HLA A*1101	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.427074	0.606435	-3.820639	26734.588449
HLA A*0203	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.299908	0.479051	-3.820857	19948.379755
HLA A*8001	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.428584	0.607629	-3.820956	26827.748221
HLA A*6802	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.427417	0.606435	-3.820982	26755.712940
HLA B*0702	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.421867	0.600770	-3.821097	26415.999288
HLA A*0101	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.376038	0.554890	-3.821148	23770.482090
HLA A*3001	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.205649	0.384476	-3.821172	16056.416992
HLA A*3201	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.607695	0.786323	-3.821372	40522.372222
HLA B*4402	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.369706	0.548275	-3.821432	23426.430919
HLA B*5301	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.603341	0.781791	-3.821551	40118.183988
HLA B*1509	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.456738	0.635184	-3.821554	28624.512606
HLA B*2705	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.449018	0.627429	-3.821589	28120.153879
HLA B*7301	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.562524	0.740887	-3.821637	36519.402456
HLA B*4402	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.416999	0.595350	-3.821649	26121.548061
HLA B*3901	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.288301	0.466612	-3.821689	19422.322956
HLA A*6802	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.311103	0.489404	-3.821699	20469.296803
HLA A*1101	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.353941	0.532233	-3.821708	22591.292744
HLA B*5701	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.395252	0.573435	-3.821817	24845.748118
HLA B*1502	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.473690	0.651841	-3.821848	29763.886168
HLA B*3901	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.422621	0.600770	-3.821851	26461.912491
HLA B*2705	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.467931	0.645964	-3.821967	29371.832790
HLA B*5101	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.467999	0.645964	-3.822035	29376.441204
HLA B*3501	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.422859	0.600770	-3.822088	26476.375199
HLA B*5101	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.488792	0.666703	-3.822089	30817.125323
HLA A*3201	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.548253	0.726094	-3.822159	35338.888926
HLA B*7301	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.570721	0.748391	-3.822330	37215.256446
HLA B*1517	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.475212	0.652880	-3.822332	29868.409792
HLA A*0219	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.379992	0.557541	-3.822451	23987.896869
HLA A*6802	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.418033	0.595477	-3.822555	26183.800582
HLA B*4501	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.613021	0.790294	-3.822727	41022.407460
HLA B*4001	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.390130	0.567351	-3.822779	24554.449439
HLA A*0216	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.289575	0.466612	-3.822962	19479.355886
HLA B*7301	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.598290	0.775312	-3.822978	39654.262121
HLA A*2402	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.555687	0.732703	-3.822983	35948.987372
HLA A*2301	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.515452	0.692424	-3.823028	32768.135500
HLA B*4403	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.616200	0.793168	-3.823032	41323.775853
HLA B*0803	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.497434	0.674222	-3.823212	31436.452421
HLA A*2603	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.524596	0.701295	-3.823301	33465.392765
HLA A*3201	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.503768	0.680376	-3.823392	31898.314960
HLA B*4002	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.609715	0.786323	-3.823393	40711.341998
HLA B*4002	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.624656	0.801202	-3.823454	42136.241426
HLA B*1517	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.471335	0.647881	-3.823455	29602.981308
HLA A*2403	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.318393	0.494882	-3.823512	20815.812880
HLA A*3101	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.390985	0.567351	-3.823634	24602.849691
HLA A*0201	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.397089	0.573435	-3.823654	24951.081534
HLA A*3101	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.397298	0.573435	-3.823863	24963.097877
HLA B*7301	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.551244	0.727191	-3.824053	35583.100344
HLA A*0250	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.319178	0.494882	-3.824296	20853.459036
HLA B*4001	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.381848	0.557541	-3.824307	24090.636029
HLA A*2402	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.542774	0.718317	-3.824457	34895.858878
HLA B*5101	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.425232	0.600770	-3.824461	26621.437745
HLA A*6801	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.329854	0.505350	-3.824504	21372.442782
HLA A*0219	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.420020	0.595477	-3.824543	26303.912368
HLA A*2403	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.431829	0.607235	-3.824594	27028.930441
HLA A*1101	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.458047	0.633434	-3.824612	28710.897172
HLA B*5101	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.505065	0.680376	-3.824688	31993.713956
HLA A*6901	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.340854	0.516095	-3.824760	21920.701684
HLA A*3001	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.306425	0.481648	-3.824777	20250.003314
HLA A*0202	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.526179	0.701295	-3.824885	33587.639201
HLA B*7301	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.537161	0.712255	-3.824906	34447.758850
HLA A*6801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.199883	0.374749	-3.825134	15844.662840

HLA B*5301	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.588655	0.763388	-3.825267	38784.181901
HLA A*0216	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.320170	0.494882	-3.825288	20901.121309
HLA B*4001	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.398767	0.573435	-3.825332	25047.645477
HLA A*2402	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.575711	0.750232	-3.825480	37645.348517
HLA B*5801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.342407	0.516757	-3.825651	21999.229047
HLA B*1503	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.103986	0.278063	-3.825923	12705.343831
HLA B*1801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.426860	0.600770	-3.826089	26721.430252
HLA A*0211	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.435304	0.609194	-3.826110	27246.062526
HLA B*0802	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.477954	0.651841	-3.826113	30057.575744
HLA B*1517	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.426897	0.600770	-3.826127	26723.743312
HLA A*3001	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.290082	0.463883	-3.826199	19502.131521
HLA B*5701	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.393932	0.567351	-3.826581	24770.322874
HLA A*6901	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.290583	0.463883	-3.826700	19524.616904
HLA A*0202	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.332074	0.505350	-3.826724	21481.985861
HLA A*3201	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.558280	0.731526	-3.826755	36164.335778
HLA B*1502	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.575237	0.748391	-3.826846	37604.232240
HLA B*3901	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.483144	0.656026	-3.827118	30418.932037
HLA B*5101	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.475019	0.647881	-3.827139	29855.162778
HLA B*3901	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.341952	0.514746	-3.827206	21976.152561
HLA A*2602	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.620406	0.793168	-3.827238	41725.886785
HLA B*3501	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.440856	0.613596	-3.827260	27596.600208
HLA A*0211	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-3.878694	0.051389	-3.827305	7563.003572
HLA A*0216	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.231709	0.404390	-3.827320	17049.401025
HLA A*2602	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.519751	0.692424	-3.827327	33094.154370
HLA A*0203	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.170604	0.343210	-3.827394	14811.659517
HLA A*3301	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.603104	0.775707	-3.827397	40096.269448
HLA B*3801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.542943	0.715416	-3.827527	34909.453882
HLA A*0301	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.204436	0.376904	-3.827533	16011.657960
HLA B*0803	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.479422	0.651841	-3.827581	30159.377848
HLA A*2602	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.614064	0.786323	-3.827742	41121.061340
HLA B*5401	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.560494	0.732703	-3.827790	36349.103813
HLA B*2705	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.437047	0.609194	-3.827854	27355.651780
HLA A*2902	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.333449	0.505350	-3.828098	21550.079424
HLA A*2402	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.555327	0.727191	-3.828136	35919.244237
HLA A*0212	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.435435	0.607235	-3.828201	27254.318075
HLA B*4402	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.441835	0.613596	-3.828239	27658.926309
HLA B*1509	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.514547	0.686294	-3.828253	32699.956813
HLA A*8001	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.205193	0.376904	-3.828289	16039.574325
HLA B*4501	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.623371	0.794851	-3.828520	42011.735776
HLA A*0219	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.442181	0.613596	-3.828585	27680.930922
HLA B*0801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.292573	0.463883	-3.828690	19614.287423
HLA A*3001	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.247796	0.419078	-3.828718	17692.778882
HLA A*0212	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.386277	0.557541	-3.828736	24337.560571
HLA B*4002	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.604488	0.775707	-3.828781	40224.236963
HLA A*6802	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.442493	0.613596	-3.828897	27700.854941
HLA A*2602	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.603452	0.774258	-3.829194	40128.385927
HLA A*6801	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.592700	0.763388	-3.829313	39147.176886
HLA A*8001	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.386911	0.557541	-3.829370	24373.135693
HLA A*0203	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.213552	0.384129	-3.829424	16351.300726
HLA A*3002	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.530803	0.701295	-3.829509	33947.145814
HLA B*4403	1:397-405	9	VARQPFPGP	0.713125	0.118777	-4.661453	0.831902	-3.829552	45862.046235
HLA B*2705	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.397078	0.567351	-3.829727	24950.406630
HLA B*1801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.475795	0.645964	-3.829831	29908.509713
HLA A*2602	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.504341	0.674222	-3.830119	31940.448951
HLA A*2603	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.583108	0.752770	-3.830338	38291.951568
HLA A*6801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.164420	0.334057	-3.830362	14602.253229
HLA B*1801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.478407	0.647881	-3.830527	30088.975507
HLA A*2301	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.531955	0.701295	-3.830660	34037.253837
HLA A*2902	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.439892	0.609194	-3.830699	27535.457278
HLA A*0301	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.327744	0.496961	-3.830783	21268.865533
HLA A*0301	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.297427	0.466612	-3.830814	19834.742699
HLA B*1501	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.398440	0.567535	-3.830905	25028.817364
HLA B*5401	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.476951	0.645964	-3.830987	29988.222197
HLA A*6802	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.277721	0.446544	-3.831177	18954.897503
HLA A*6901	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.361725	0.530534	-3.831191	22999.845947

HLA A*0301	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.361882	0.530534	-3.831348	23008.184041
HLA A*3201	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.174659	0.343210	-3.831449	14950.610639
HLA B*4001	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.398985	0.567535	-3.831450	25060.250611
HLA B*4801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.432224	0.600770	-3.831453	27053.507159
HLA B*2705	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.439117	0.607629	-3.831488	27486.343087
HLA A*2603	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.579966	0.748391	-3.831575	38015.984290
HLA B*3501	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.399082	0.567351	-3.831731	25065.809728
HLA B*0801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.405221	0.573435	-3.831786	25422.657289
HLA A*1101	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.440990	0.609194	-3.831796	27605.111309
HLA A*0202	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.310870	0.479051	-3.831819	20458.336812
HLA B*5101	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.465260	0.633434	-3.831825	29191.719865
HLA A*3101	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.364072	0.532233	-3.831839	23124.484638
HLA A*3201	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.573733	0.741770	-3.831963	37474.259149
HLA B*1801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.459158	0.627189	-3.831970	28784.458921
HLA B*0802	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.479956	0.647881	-3.832075	30196.437667
HLA A*6802	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-3.971917	0.139834	-3.832083	9373.832123
HLA A*2402	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.524523	0.692424	-3.832099	33459.780870
HLA B*5701	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.387365	0.555251	-3.832114	24398.597183
HLA A*2601	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.399561	0.567351	-3.832210	25093.488062
HLA A*0212	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.445898	0.613596	-3.832302	27918.853306
HLA A*3001	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.066991	0.234640	-3.832351	11667.865966
HLA B*1503	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.460074	0.627429	-3.832646	28845.254118
HLA A*8001	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.446295	0.613596	-3.832699	27944.390384
HLA B*1801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.477291	0.644580	-3.832711	30011.755205
HLA B*5301	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.587306	0.754547	-3.832759	38663.933097
HLA A*6801	1:281-289	9	ANLVTVDAA	1.058291	-0.239833	-4.651236	0.818458	-3.832777	44795.616459
HLA B*4801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.439216	0.606435	-3.832781	27492.589115
HLA B*5401	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.513168	0.680376	-3.832792	32596.279376
HLA A*2301	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.548225	0.715416	-3.832809	35336.594847
HLA A*1101	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.388065	0.555251	-3.832814	24437.963031
HLA B*7301	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.587405	0.754547	-3.832858	38672.719134
HLA B*5101	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.485834	0.652880	-3.832954	30607.941518
HLA A*2603	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.619395	0.786323	-3.833073	41628.934655
HLA B*1509	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.479159	0.645964	-3.833195	30141.109587
HLA B*4002	1:237-245	9	DSAVAAALV	0.764846	0.042930	-4.641011	0.807776	-3.833234	43753.274258
HLA A*2602	1:444-452	9	WQCPVVLLA	0.981042	-0.203019	-4.611377	0.778023	-3.833354	40867.352562
HLA B*2705	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.348267	0.514746	-3.833521	22298.059861
HLA B*1502	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.124234	0.290570	-3.833664	13311.723374
HLA B*4601	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.407387	0.573435	-3.833952	25549.780189
HLA B*1517	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.443325	0.609194	-3.834131	27753.955699
HLA A*3101	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.389033	0.554890	-3.834143	24492.492927
HLA A*2603	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.624454	0.790294	-3.834160	42116.642080
HLA A*6901	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.133270	0.299099	-3.834172	13591.594325
HLA A*0250	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.467816	0.633434	-3.834381	29364.047802
HLA A*2602	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.507438	0.673013	-3.834425	32169.005686
HLA A*0211	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.525343	0.690895	-3.834448	33523.014328
HLA B*1503	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.411720	0.577199	-3.834521	25805.936156
HLA A*6801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.193911	0.359286	-3.834625	15628.259410
HLA B*5301	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.600522	0.765882	-3.834640	39858.585625
HLA A*0201	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.402181	0.567535	-3.834645	25245.310081
HLA A*3201	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.340154	0.505350	-3.834804	21885.390762
HLA A*2902	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.448449	0.613596	-3.834853	28083.363254
HLA B*0802	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.462158	0.627189	-3.834970	28984.002769
HLA A*2501	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.488029	0.652880	-3.835149	30762.989827
HLA A*3001	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.281868	0.446544	-3.835324	19136.754320
HLA A*0250	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.577159	0.741770	-3.835389	37771.010597
HLA A*2602	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.601340	0.765882	-3.835458	39933.695730
HLA A*3101	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.383742	0.548275	-3.835467	24195.909480
HLA B*4501	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.583991	0.748391	-3.835600	38369.921201
HLA B*4403	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.622074	0.786323	-3.835751	41886.464999
HLA B*1501	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.347680	0.511716	-3.835964	22267.922738
HLA A*2603	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.610242	0.774258	-3.835984	40760.706524
HLA A*0211	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.537304	0.701295	-3.836010	34459.128598
HLA A*3301	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.584463	0.748391	-3.836072	38411.666874
HLA A*2603	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.384388	0.548275	-3.836113	24231.932996

HLA B*1501	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.409600	0.573435	-3.836165	25680.317155
HLA A*3201	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.599556	0.763388	-3.836168	39770.059931
HLA B*1501	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.315318	0.479051	-3.836267	20668.925476
HLA B*3801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.437066	0.600770	-3.836296	27356.835734
HLA B*4403	1:220-228	9	RTQIGDGHA	0.947448	-0.128400	-4.655378	0.819048	-3.836330	45224.904621
HLA B*5701	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.413538	0.577199	-3.836339	25914.218715
HLA B*1517	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.353121	0.516757	-3.836364	22548.679465
HLA A*0202	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.469815	0.633434	-3.836381	29499.546131
HLA B*4403	1:475-483	9	VSSEDAMTA	1.027674	-0.251967	-4.612185	0.775707	-3.836478	40943.477594
HLA A*0250	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.572530	0.736037	-3.836493	37370.604198
HLA A*3001	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.269877	0.433361	-3.836515	18615.577342
HLA B*4501	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.492702	0.656026	-3.836675	31095.795215
HLA A*2601	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.270283	0.433361	-3.836922	18633.008018
HLA A*1101	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.432459	0.595477	-3.836981	27068.146766
HLA B*4403	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.631859	0.794851	-3.837008	42840.971896
HLA A*3001	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.205602	0.368545	-3.837057	16054.679817
HLA B*5801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.367812	0.530534	-3.837278	23324.505375
HLA B*4801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.445049	0.607629	-3.837421	27864.381832
HLA B*5401	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.549677	0.712255	-3.837422	35454.933802
HLA A*0206	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.332354	0.494882	-3.837472	21495.819918
HLA B*3801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.565738	0.728232	-3.837506	36790.675203
HLA A*2601	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.368296	0.530534	-3.837762	23350.513560
HLA B*4002	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.613536	0.775634	-3.837901	41071.038204
HLA B*0702	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.451581	0.613596	-3.837985	28286.615103
HLA B*3901	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.447220	0.609194	-3.838027	28004.017274
HLA B*5101	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.489910	0.651841	-3.838069	30896.584990
HLA B*5801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.335049	0.496961	-3.838087	21629.619243
HLA B*4402	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.445808	0.607629	-3.838180	27913.114456
HLA A*8001	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.433734	0.595477	-3.838257	27147.778241
HLA A*6901	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.327686	0.489404	-3.838282	21265.989172
HLA B*1801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.478290	0.639875	-3.838415	30080.837706
HLA A*3002	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.465652	0.627189	-3.838464	29218.105085
HLA B*4403	1:19-27	9	VVDFGAQYA	1.013002	-0.199742	-4.651729	0.813260	-3.838468	44846.536635
HLA A*3201	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.612779	0.774258	-3.838521	40999.555380
HLA A*6802	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.415751	0.577199	-3.838552	26046.617642
HLA A*3301	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.604579	0.765882	-3.838698	40232.724596
HLA B*5301	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.551103	0.712255	-3.838848	35571.552181
HLA A*6802	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.412288	0.573435	-3.838853	25839.743236
HLA B*5301	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.593476	0.754590	-3.838886	39217.127330
HLA B*0802	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.466369	0.627429	-3.838940	29266.355227
HLA B*1501	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.387217	0.548275	-3.838942	24390.282997
HLA B*3901	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.181317	0.342132	-3.839186	15181.593958
HLA B*3501	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.412720	0.573435	-3.839286	25865.477429
HLA A*0202	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.448639	0.609194	-3.839446	28095.672109
HLA A*3201	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.491315	0.651841	-3.839474	30996.700811
HLA A*3001	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.292563	0.452913	-3.839650	19613.862983
HLA B*1503	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.487789	0.647881	-3.839908	30746.019225
HLA A*3002	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.555654	0.715584	-3.840070	35946.264755
HLA B*5301	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.581865	0.741770	-3.840095	38182.523118
HLA B*0802	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.484718	0.644580	-3.840138	30529.389342
HLA B*5301	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.566527	0.726094	-3.840433	36857.611267
HLA A*0212	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.447021	0.606435	-3.840586	27991.142851
HLA B*5301	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.572124	0.731526	-3.840598	37335.645007
HLA A*0301	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.352329	0.511716	-3.840613	22507.607682
HLA B*4002	1:252-260	9	RLTCVFVDH	0.987377	-0.192526	-4.635506	0.794851	-3.840655	43202.185313
HLA B*1503	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.371292	0.530534	-3.840758	23512.133018
HLA A*0203	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.299680	0.458831	-3.840848	19937.914404
HLA A*2402	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.542189	0.701295	-3.840894	34848.883625
HLA B*4403	1:182-190	9	VMHTPHGQQ	0.852122	-0.027517	-4.665673	0.824605	-3.841068	46309.821059
HLA A*3001	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.281598	0.440475	-3.841123	19124.852335
HLA B*1517	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.373390	0.532233	-3.841157	23625.995677
HLA A*6801	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.627550	0.786323	-3.841228	42418.016748
HLA B*0802	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.487227	0.645964	-3.841263	30706.291433
HLA B*1501	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.140427	0.299099	-3.841328	13817.419236
HLA B*1801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.493280	0.651841	-3.841438	31137.206067

HLA A*1101	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.442291	0.600770	-3.841521	27687.970102
HLA B*5301	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.569882	0.728232	-3.841650	37143.450851
HLA B*0803	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.487660	0.645964	-3.841696	30736.872295
HLA A*3001	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.295126	0.453330	-3.841796	19729.970016
HLA B*4002	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.560247	0.718317	-3.841930	36328.461990
HLA B*0702	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.336872	0.494882	-3.841990	21720.612850
HLA B*0803	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.482019	0.639875	-3.842143	30340.208379
HLA B*5101	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.486819	0.644580	-3.842238	30677.400565
HLA B*4601	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.409906	0.567535	-3.842370	25698.384104
HLA B*5801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.354131	0.511716	-3.842415	22601.194441
HLA A*2402	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.583317	0.740887	-3.842430	38310.392821
HLA B*1501	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.397331	0.554890	-3.842442	24964.988615
HLA A*0203	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.347795	0.505350	-3.842444	22273.826403
HLA B*0803	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.498531	0.656026	-3.842505	31515.974458
HLA B*1801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.498613	0.656026	-3.842587	31521.942450
HLA A*3301	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.624418	0.781791	-3.842628	42113.224523
HLA B*4403	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.516937	0.674222	-3.842715	32880.363138
HLA A*2602	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.449161	0.606435	-3.842726	28129.435152
HLA A*0216	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.449196	0.606435	-3.842762	28131.717901
HLA B*1501	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.359538	0.516757	-3.842781	22884.296001
HLA A*0201	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.397677	0.554890	-3.842787	24984.850011
HLA A*0219	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.450207	0.607235	-3.842972	28197.235552
HLA B*5401	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.398297	0.555251	-3.843046	25020.559136
HLA B*1517	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.470285	0.627189	-3.843097	29531.481259
HLA A*0203	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.420385	0.577199	-3.843185	26325.978312
HLA A*0202	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.558659	0.715416	-3.843243	36195.848352
HLA A*1101	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.470624	0.627189	-3.843435	29554.495956
HLA B*1509	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.483438	0.639875	-3.843563	30439.509375
HLA A*2603	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.569673	0.726094	-3.843579	37125.571322
HLA B*0801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.121645	0.278063	-3.843582	13232.598994
HLA A*2902	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.401168	0.557541	-3.843627	25186.515117
HLA A*0211	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.536263	0.692424	-3.843839	34376.643390
HLA B*4002	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.610082	0.765882	-3.844200	40745.714541
HLA B*5401	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-3.946284	0.101982	-3.844302	8836.581556
HLA B*1509	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.511082	0.666703	-3.844379	32440.062982
HLA B*1501	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.203713	0.359286	-3.844427	15985.000816
HLA B*4001	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.376677	0.532233	-3.844444	23805.485860
HLA B*4501	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-3.935876	0.091322	-3.844554	8627.323269
HLA B*5801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.353161	0.508560	-3.844601	22550.753320
HLA B*4601	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.330991	0.486297	-3.844694	21428.477423
HLA A*0101	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.375265	0.530534	-3.844731	23728.211742
HLA B*0702	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.418225	0.573435	-3.844790	26195.418578
HLA A*2402	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.586580	0.741770	-3.844810	38599.354303
HLA B*0801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.412490	0.567535	-3.844955	25851.767986
HLA A*6802	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-3.957369	0.112320	-3.845050	9065.028218
HLA B*5401	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.563651	0.718317	-3.845335	36614.357331
HLA B*1502	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.531687	0.686294	-3.845393	34016.268603
HLA A*2601	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.377690	0.532233	-3.845456	23861.056974
HLA B*7301	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.577121	0.731526	-3.845595	37767.741346
HLA B*7301	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-3.991737	0.146138	-3.845599	9811.545607
HLA B*5101	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.501801	0.656026	-3.845775	31754.203447
HLA A*3201	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.594796	0.748391	-3.846405	39336.542866
HLA B*3501	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.423693	0.577199	-3.846494	26527.272218
HLA B*4402	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.313217	0.466612	-3.846605	20569.202785
HLA B*4001	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.361365	0.514746	-3.846619	22980.816551
HLA B*1509	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.494565	0.647881	-3.846684	31229.484046
HLA B*4402	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.453240	0.606435	-3.846805	28394.859065
HLA A*2601	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.401744	0.554890	-3.846854	25219.920032
HLA B*1509	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.498951	0.651841	-3.847110	31546.508369
HLA B*4002	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.637851	0.790294	-3.847557	43436.067714
HLA B*5301	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.563221	0.715584	-3.847638	36578.126699
HLA A*6901	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.353088	0.505350	-3.847738	22546.971728
HLA B*3901	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.455108	0.607235	-3.847873	28517.244424
HLA A*2301	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.538792	0.690895	-3.847896	34577.334781
HLA A*0216	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.415538	0.567535	-3.848002	26033.798050

HLA A*0101	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.364897	0.516757	-3.848140	23168.436769
HLA B*7301	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.150793	0.302627	-3.848166	14151.186760
HLA A*0211	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.475644	0.627429	-3.848216	29898.156196
HLA B*0702	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.456087	0.607629	-3.848459	28581.649773
HLA A*8001	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.281821	0.433361	-3.848460	19134.683878
HLA B*4501	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.637954	0.789472	-3.848482	43446.408254
HLA B*4001	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.425737	0.577199	-3.848538	26652.419851
HLA B*4402	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.406172	0.557541	-3.848631	25478.419526
HLA B*1503	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.488534	0.639875	-3.848659	30798.791883
HLA A*2301	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.535006	0.686294	-3.848713	34277.291237
HLA B*4501	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.649962	0.801202	-3.848760	44664.460926
HLA B*1517	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.135042	0.286262	-3.848780	13647.148432
HLA A*0216	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.462391	0.613596	-3.848795	28999.530150
HLA A*3002	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.564363	0.715416	-3.848947	36674.424671
HLA A*0201	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.397367	0.548275	-3.849092	24967.014564
HLA A*0216	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.426477	0.577199	-3.849278	26697.877363
HLA A*3002	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.493867	0.644580	-3.849287	31179.346766
HLA B*7301	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.483109	0.633434	-3.849674	30416.463691
HLA A*0219	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.417224	0.567535	-3.849689	26135.117794
HLA A*2501	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.477157	0.627429	-3.849729	30002.502097
HLA A*0219	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.456188	0.606435	-3.849754	28588.299359
HLA B*5101	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.426977	0.577199	-3.849778	26728.659229
HLA B*0801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.405040	0.555251	-3.849789	25412.069395
HLA B*4601	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.364594	0.514746	-3.849848	23152.273721
HLA B*5401	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-3.970681	0.120764	-3.849918	9347.195847
HLA A*3301	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.582706	0.732703	-3.850003	38256.544406
HLA B*5801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.339433	0.489404	-3.850029	21849.072886
HLA A*3301	1:356-364	9	SHHNVGGLP	0.660012	0.126311	-4.636380	0.786323	-3.850057	43289.216338
HLA A*3201	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.524314	0.674222	-3.850092	33443.674527
HLA A*2601	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.336548	0.486297	-3.850251	21704.403059
HLA B*0803	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.494922	0.644580	-3.850342	31255.174710
HLA A*6802	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.398654	0.548275	-3.850380	25041.142082
HLA A*0202	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.477827	0.627429	-3.850398	30048.796186
HLA A*2603	1:23-31	9	GAQYAQLIA	1.160023	-0.346139	-4.664388	0.813884	-3.850504	46172.983169
HLA B*4801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.417986	0.567351	-3.850635	26180.967706
HLA A*0216	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.417997	0.567351	-3.850646	26181.675896
HLA B*4001	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.405900	0.555251	-3.850649	25462.435632
HLA B*4002	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.640289	0.789472	-3.850817	43680.667557
HLA A*0250	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.569217	0.718317	-3.850901	37086.627788
HLA A*2602	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.601196	0.750232	-3.850964	39920.519655
HLA A*0301	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.367726	0.516757	-3.850969	23319.837072
HLA A*3001	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-3.675812	-0.175217	-3.851028	4740.362749
HLA B*4403	1:231-239	9	GLSGGVDSA	1.114995	-0.305563	-4.660568	0.809432	-3.851135	45768.604619
HLA B*0803	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.484615	0.633434	-3.851180	30522.123140
HLA A*2402	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.587228	0.736037	-3.851192	38657.031182
HLA A*0203	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.418759	0.567535	-3.851223	26227.607487
HLA B*4402	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.424740	0.573435	-3.851305	26591.354779
HLA B*0702	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.400061	0.548275	-3.851787	25122.420114
HLA B*5801	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.357155	0.505350	-3.851805	22759.104965
HLA B*0802	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.459088	0.607235	-3.851853	28779.787678
HLA A*0206	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.228791	0.376904	-3.851887	16935.228692
HLA B*1801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.360513	0.508560	-3.851953	22935.731343
HLA A*2501	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.459616	0.607629	-3.851988	28814.840486
HLA B*0801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.366755	0.514746	-3.852009	23267.792091
HLA A*0212	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.256463	0.404390	-3.852074	18049.422045
HLA A*1101	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.479540	0.627429	-3.852111	30167.536896
HLA B*1801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.316037	0.463883	-3.852154	20703.169691
HLA B*0802	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.447725	0.595477	-3.852248	28036.608429
HLA B*3501	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.447770	0.595477	-3.852293	28039.490401
HLA A*0301	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.368407	0.516095	-3.852312	23356.451529
HLA B*1517	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.236706	0.384129	-3.852578	17246.718730
HLA A*8001	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.426080	0.573435	-3.852645	26673.479415
HLA A*2501	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.459908	0.607235	-3.852673	28834.176722
HLA A*0202	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.459257	0.606435	-3.852822	28790.999934
HLA A*0212	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.430161	0.577199	-3.852962	26925.310874

HLA B*5801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.369206	0.516095	-3.853111	23399.452040
HLA A*0219	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.420490	0.567351	-3.853139	26332.388020
HLA A*0212	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.420516	0.567351	-3.853165	26333.955075
HLA A*6801	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.579285	0.726094	-3.853191	37956.388995
HLA B*4601	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.370014	0.516757	-3.853257	23443.039009
HLA A*0206	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.420713	0.567351	-3.853362	26345.924752
HLA B*4403	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.571788	0.718317	-3.853471	37306.772793
HLA B*5301	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.342891	0.489404	-3.853488	22023.759472
HLA B*5301	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.594474	0.740887	-3.853588	39307.399199
HLA A*2601	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.358962	0.505350	-3.853612	22853.984724
HLA A*2501	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.501512	0.647881	-3.853631	31733.080709
HLA A*0301	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.287098	0.433361	-3.853737	19368.600214
HLA A*0202	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.348718	0.494882	-3.853836	22321.232860
HLA B*4501	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.619748	0.765882	-3.853866	41662.729553
HLA A*0203	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.427362	0.573435	-3.853928	26752.384001
HLA B*1502	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.586716	0.732703	-3.854013	38611.467660
HLA B*4801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.431256	0.577199	-3.854057	26993.275441
HLA A*0203	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.362676	0.508560	-3.854117	23050.293973
HLA A*3301	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.449669	0.595350	-3.854319	28162.324624
HLA B*1502	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.590360	0.736037	-3.854324	38936.809391
HLA A*0202	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.545227	0.690895	-3.854331	35093.505667
HLA A*2602	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.489523	0.635184	-3.854339	30869.018024
HLA B*3801	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.527418	0.673013	-3.854405	33683.534583
HLA B*1517	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.341139	0.486297	-3.854842	21935.055598
HLA B*4002	1:181-189	9	EVMHTPHGQ	0.891954	-0.110784	-4.636020	0.781170	-3.854851	43253.400114
HLA B*1501	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.314047	0.458831	-3.855216	20608.521135
HLA A*0219	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.432679	0.577199	-3.855480	27081.915220
HLA A*2603	1:280-288	9	GANLVTVDA	1.116366	-0.323198	-4.648672	0.793168	-3.855505	44532.002975
HLA B*5101	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.469259	0.613596	-3.855663	29461.747710
HLA B*4001	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.386305	0.530534	-3.855771	24339.140584
HLA B*5701	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.423317	0.567535	-3.855781	26504.320616
HLA B*5401	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.548253	0.692424	-3.855829	35338.888926
HLA B*7301	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.536268	0.680376	-3.855892	34377.015340
HLA B*0803	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.451426	0.595477	-3.855949	28276.517094
HLA B*0801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.372105	0.516095	-3.856010	23556.184753
HLA B*3801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.546956	0.690895	-3.856061	35233.515273
HLA A*6901	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.372892	0.516757	-3.856135	23598.914638
HLA B*7301	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.557538	0.701295	-3.856243	36102.564758
HLA A*0211	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.364805	0.508560	-3.856245	23163.549077
HLA A*0202	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.597233	0.740887	-3.856346	39557.843210
HLA A*2602	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.592386	0.736037	-3.856349	39118.808397
HLA B*4402	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.411649	0.555251	-3.856398	25801.748278
HLA A*2403	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.451771	0.595350	-3.856421	28299.013043
HLA A*2602	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.588039	0.731526	-3.856513	38729.248492
HLA A*0216	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.463796	0.607235	-3.856561	29093.498846
HLA B*5401	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.557945	0.701295	-3.856650	36136.369355
HLA B*2705	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.463096	0.606435	-3.856661	29046.633637
HLA A*6802	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.387271	0.530534	-3.856737	24393.318006
HLA A*0201	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.297347	0.440475	-3.856872	19831.094706
HLA B*4002	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.605378	0.748391	-3.856987	40306.795253
HLA A*0202	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.537405	0.680376	-3.857029	34467.145594
HLA A*2602	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-3.938188	0.081144	-3.857044	8673.371823
HLA B*4001	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.365959	0.508560	-3.857399	23225.159173
HLA A*0203	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.092328	0.234640	-3.857688	12368.820239
HLA B*4601	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.388420	0.530534	-3.857886	24457.934395
HLA A*0101	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.374003	0.516095	-3.857909	23659.378698
HLA A*0250	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.598952	0.740887	-3.858066	39714.804387
HLA A*3101	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.370042	0.511716	-3.858326	23444.560949
HLA A*3201	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.591103	0.732703	-3.858400	39003.429768
HLA B*0702	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.388963	0.530534	-3.858428	24488.518199
HLA A*0211	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.511385	0.652880	-3.858505	32462.710015
HLA A*0206	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.337603	0.479051	-3.858552	21757.188010
HLA B*5801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.353464	0.494882	-3.858582	22566.496435
HLA A*0212	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.367213	0.508560	-3.858653	23292.350897
HLA A*0202	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.316399	0.457680	-3.858719	20720.425163

HLA A*0206	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.466044	0.607235	-3.858810	29244.514153
HLA B*4501	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.634545	0.775634	-3.858911	43106.699905
HLA A*6801	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.574410	0.715416	-3.858994	37532.691355
HLA A*0201	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.367587	0.508560	-3.859027	23312.394953
HLA B*4601	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.391270	0.532233	-3.859036	24618.959905
HLA A*2403	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.407392	0.548275	-3.859117	25550.056633
HLA A*3101	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.263204	0.403979	-3.859224	18331.751968
HLA A*2301	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.533566	0.674222	-3.859345	34163.807033
HLA A*6801	1:271-279	9	VQRDFVAAT	1.020270	-0.247629	-4.632059	0.772641	-3.859418	42860.676443
HLA B*3501	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.317129	0.457680	-3.859449	20755.316114
HLA B*5701	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.407852	0.548275	-3.859578	25577.162704
HLA A*0301	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.368144	0.508560	-3.859584	23342.303964
HLA B*0702	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.323562	0.463883	-3.859680	21065.037774
HLA B*7301	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.592390	0.732703	-3.859687	39119.231656
HLA B*3801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.467139	0.607235	-3.859905	29318.332827
HLA A*2602	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.207411	0.347374	-3.860037	16121.696913
HLA B*5301	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.587233	0.727191	-3.860042	38657.449445
HLA A*0216	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.417737	0.557541	-3.860195	26165.958580
HLA B*3501	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-3.916220	0.055954	-3.860267	8245.562349
HLA B*0803	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.513227	0.652880	-3.860347	32600.688230
HLA B*4501	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.644161	0.783681	-3.860481	44071.843604
HLA A*0101	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.372387	0.511716	-3.860671	23571.482080
HLA B*3501	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.468366	0.607629	-3.860737	29401.243702
HLA B*0802	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.461510	0.600770	-3.860740	28940.758195
HLA B*3501	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.467200	0.606435	-3.860766	29322.456949
HLA A*3101	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.428469	0.567535	-3.860934	26820.637542
HLA B*4501	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.592602	0.731526	-3.861076	39138.283057
HLA B*4601	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.409387	0.548275	-3.861112	25667.677848
HLA A*2403	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.434618	0.573435	-3.861183	27203.056236
HLA B*4001	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.377633	0.516095	-3.861539	23857.959119
HLA B*5301	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.563017	0.701295	-3.861722	36560.914875
HLA B*4501	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.536071	0.674222	-3.861849	34361.396918
HLA A*2603	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.429435	0.567535	-3.861899	26880.338623
HLA A*0211	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.542332	0.680376	-3.861956	34860.385767
HLA A*0212	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.292577	0.430602	-3.861975	19614.499646
HLA B*3801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.514977	0.652880	-3.862097	32732.346118
HLA A*0201	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.089796	0.227657	-3.862138	12296.896932
HLA B*4002	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.554676	0.692424	-3.862252	35865.458149
HLA B*4501	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.636521	0.774258	-3.862263	43303.270010
HLA B*4403	1:205-213	9	QWTPANIAN	1.195876	-0.405582	-4.652605	0.790294	-3.862311	44937.123318
HLA B*7301	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.578007	0.715416	-3.862591	37844.848324
HLA B*0801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.090951	0.228245	-3.862707	12329.670755
HLA B*4403	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.644500	0.781791	-3.862709	44106.190006
HLA B*7301	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.578347	0.715584	-3.862764	37874.546754
HLA A*3301	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.613061	0.750232	-3.862829	41026.180387
HLA B*0702	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.469378	0.606435	-3.862944	29469.877455
HLA A*2301	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.543364	0.680376	-3.862987	34943.275528
HLA B*1509	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.393525	0.530534	-3.862991	24747.150906
HLA A*0211	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.293837	0.430602	-3.863234	19671.458364
HLA A*8001	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.440510	0.577199	-3.863311	27574.662634
HLA A*6801	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.629197	0.765882	-3.863316	42579.185372
HLA B*3901	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.202566	0.339229	-3.863337	15942.855657
HLA B*5301	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.000196	0.136752	-3.863443	10004.504247
HLA A*6802	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.372046	0.508560	-3.863486	23552.999060
HLA B*0702	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.418836	0.555251	-3.863585	26232.290224
HLA B*1502	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.511526	0.647881	-3.863645	32473.248905
HLA B*2705	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.195377	0.331684	-3.863692	15681.105981
HLA A*3201	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.556185	0.692424	-3.863761	35990.240792
HLA A*2402	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.511678	0.647881	-3.863798	32484.669897
HLA A*3301	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.627236	0.763388	-3.863848	42387.278004
HLA A*0212	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.437477	0.573435	-3.864042	27382.747552
HLA A*1101	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.471671	0.607629	-3.864043	29625.891453
HLA B*5801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.330970	0.466612	-3.864358	21427.434117
HLA A*0201	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.359371	0.494882	-3.864489	22875.507782
HLA B*4601	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.419421	0.554890	-3.864532	26267.650567

HLA A*6802	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.369946	0.505350	-3.864595	23439.361394
HLA B*4801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.361612	0.496961	-3.864651	22993.874245
HLA B*4801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.432249	0.567535	-3.864714	27055.117128
HLA A*0206	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.471392	0.606435	-3.864957	29606.825129
HLA A*0201	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.379776	0.514746	-3.865030	23975.960829
HLA A*3301	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.551328	0.686294	-3.865034	35590.031042
HLA A*0216	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.460582	0.595477	-3.865105	28878.980539
HLA B*0801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.422668	0.557541	-3.865127	26464.775766
HLA B*3901	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.492589	0.627429	-3.865160	31087.721473
HLA B*1517	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.472444	0.607235	-3.865210	29678.668154
HLA A*0206	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.505170	0.639875	-3.865295	32001.503614
HLA A*6801	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.640940	0.775634	-3.865306	43746.173823
HLA B*0802	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.474775	0.609194	-3.865582	29838.370138
HLA A*3201	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.616050	0.750232	-3.865818	41309.470679
HLA A*3002	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.594087	0.728232	-3.865855	39272.327823
HLA B*1502	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.606748	0.740887	-3.865861	40434.122177
HLA B*2705	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.461298	0.595350	-3.865949	28926.670658
HLA B*0803	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.546331	0.680376	-3.865955	35182.849633
HLA A*2603	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.607798	0.741770	-3.866028	40532.019118
HLA B*4801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.421287	0.555251	-3.866036	26380.724677
HLA B*3901	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.461418	0.595350	-3.866068	28934.652754
HLA A*2501	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.461562	0.595477	-3.866084	28944.202858
HLA A*2601	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.374729	0.508560	-3.866169	23698.962110
HLA B*1509	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.546653	0.680376	-3.866277	35208.935237
HLA A*2301	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.522456	0.656026	-3.866429	33300.867379
HLA A*3201	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.593925	0.727191	-3.866734	39257.670892
HLA B*2705	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.094396	0.227657	-3.866739	12427.844900
HLA A*0219	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.378531	0.511716	-3.866815	23907.314425
HLA A*3002	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.518687	0.651841	-3.866846	33013.150493
HLA B*4601	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.375429	0.508560	-3.866870	23737.199133
HLA B*3501	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.300267	0.433361	-3.866906	19964.898124
HLA B*4002	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.641187	0.774258	-3.866929	43771.030387
HLA B*1509	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.383230	0.516095	-3.867135	24167.390713
HLA B*4601	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.300500	0.433361	-3.867139	19975.593769
HLA B*4501	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.642460	0.775312	-3.867148	43899.562394
HLA A*2402	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.582616	0.715416	-3.867200	38248.680595
HLA A*3002	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.378928	0.511716	-3.867212	23929.182190
HLA A*3201	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.399507	0.532233	-3.867274	25090.365937
HLA A*0211	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.067433	0.200115	-3.867318	11679.738913
HLA B*5301	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.603367	0.736037	-3.867330	40120.571443
HLA A*2603	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.633274	0.765882	-3.867392	42980.721813
HLA A*2602	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.630948	0.763388	-3.867560	42751.141423
HLA A*0212	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.383662	0.516095	-3.867567	24191.459385
HLA B*7301	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.494931	0.627189	-3.867743	31255.851066
HLA B*0803	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.503007	0.635184	-3.867823	31842.452436
HLA B*3801	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.554141	0.686294	-3.867847	35821.247002
HLA A*2603	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.649659	0.781791	-3.867868	44633.301558
HLA B*5701	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.422781	0.554890	-3.867891	26471.648890
HLA B*1503	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.364854	0.496961	-3.867893	23166.180783
HLA B*1502	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.595104	0.727191	-3.867913	39364.430377
HLA B*5401	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.512578	0.644580	-3.867998	32552.047507
HLA B*4403	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.616390	0.748391	-3.867999	41341.887942
HLA A*6802	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.382765	0.514746	-3.868019	24141.517477
HLA B*0803	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.495481	0.627189	-3.868293	31295.443342
HLA B*0802	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.463878	0.595350	-3.868528	29099.008108
HLA B*4002	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.632031	0.763388	-3.868643	42857.894076
HLA A*3002	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.464242	0.595477	-3.868765	29123.418815
HLA A*0203	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.385647	0.516757	-3.868891	24302.300319
HLA A*2602	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.623742	0.754590	-3.869152	42047.661184
HLA A*2403	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.335775	0.466612	-3.869162	21665.806759
HLA A*3001	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.299793	0.430602	-3.869190	19943.092448
HLA B*3501	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.399791	0.530534	-3.869257	25106.795382
HLA A*2902	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.228561	0.359286	-3.869275	16926.252536
HLA B*1801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.522176	0.652880	-3.869296	33279.435952
HLA B*1801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.208571	0.339229	-3.869343	16164.839533

HLA B*4501	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.587661	0.718317	-3.869344	38695.530307
HLA A*0212	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.437068	0.567535	-3.869533	27356.983732
HLA A*3002	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.065572	0.195916	-3.869656	11629.802583
HLA B*0801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.359075	0.489404	-3.869671	22859.920096
HLA A*6801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.105105	0.235291	-3.869814	12738.103616
HLA A*0201	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.400428	0.530534	-3.869894	25143.630947
HLA A*0101	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.375293	0.505350	-3.869943	23729.752196
HLA A*0201	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.386167	0.516095	-3.870072	24331.373173
HLA B*3501	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.381860	0.511716	-3.870144	24091.287676
HLA B*5301	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.585560	0.715416	-3.870144	38508.833500
HLA B*4402	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.437510	0.567351	-3.870159	27384.821557
HLA A*2301	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.518158	0.647881	-3.870278	32972.990506
HLA B*1503	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.497664	0.627189	-3.870475	31453.123476
HLA B*5801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.349653	0.479051	-3.870602	22369.345285
HLA A*0203	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.385363	0.514746	-3.870617	24286.397322
HLA B*0803	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.466075	0.595350	-3.870725	29246.570950
HLA B*4403	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.634277	0.763388	-3.870889	43080.123020
HLA B*1509	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.527147	0.656026	-3.871121	33662.585319
HLA B*1501	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.366243	0.494882	-3.871361	23240.367260
HLA B*4403	1:462-470	9	DGRTYGHPI	0.789562	-0.013928	-4.647133	0.775634	-3.871499	44374.484077
HLA B*4403	1:17-25	9	VLVVDFGAQ	0.830280	-0.040808	-4.661021	0.789472	-3.871549	45816.416969
HLA A*2501	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.429141	0.557541	-3.871600	26862.167311
HLA B*4403	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.626159	0.754547	-3.871613	42282.383810
HLA B*3901	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.099349	0.227657	-3.871691	12570.383834
HLA B*5401	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.312181	0.440475	-3.871706	20520.188073
HLA A*0216	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.386465	0.514746	-3.871719	24348.095931
HLA A*2403	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.439319	0.567535	-3.871784	27499.134096
HLA A*2403	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.387997	0.516095	-3.871902	24434.129338
HLA A*2403	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.361502	0.489404	-3.872098	22988.028456
HLA B*5101	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.467550	0.595350	-3.872201	29346.102533
HLA B*5101	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.427456	0.555251	-3.872206	26758.173725
HLA A*2403	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.291304	0.419078	-3.872226	19557.071033
HLA B*0801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.427123	0.554890	-3.872233	26737.625876
HLA A*6802	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.383951	0.511716	-3.872235	24207.562134
HLA A*0201	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.329953	0.457680	-3.872273	21377.299481
HLA A*3101	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.361713	0.489404	-3.872310	22999.223822
HLA B*3501	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.420594	0.548275	-3.872319	26338.656799
HLA A*3002	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.507522	0.635184	-3.872338	32175.271403
HLA B*4403	1:326-334	9	DGKTAEFLV	0.872140	-0.097882	-4.646612	0.774258	-3.872354	44321.222516
HLA A*2501	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.276892	0.404390	-3.872503	18918.734050
HLA B*0702	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.377941	0.505350	-3.872591	23874.873139
HLA B*4001	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.367514	0.494882	-3.872632	23308.485639
HLA B*4403	1:262-270	9	LLRAGERAQ	0.829674	-0.028472	-4.673835	0.801202	-3.872633	47188.395834
HLA B*4403	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.449920	0.577199	-3.872721	28178.631334
HLA A*1101	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.486351	0.613596	-3.872755	30644.392030
HLA A*3201	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.613674	0.740887	-3.872788	41084.149493
HLA B*3801	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.547080	0.674222	-3.872859	35243.619020
HLA A*0211	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.512914	0.639875	-3.873039	32577.239975
HLA A*2902	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.440663	0.567535	-3.873127	27584.360770
HLA A*0219	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.359437	0.486297	-3.873140	22878.973155
HLA B*4002	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.648496	0.775312	-3.873184	44513.938150
HLA A*2403	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.428096	0.554890	-3.873206	26797.577090
HLA B*0801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.285134	0.411911	-3.873223	19281.200268
HLA B*2705	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.486842	0.613596	-3.873246	30679.060223
HLA A*2601	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.389400	0.516095	-3.873305	24513.171913
HLA A*0202	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.513278	0.639875	-3.873403	32604.568516
HLA A*0201	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.390292	0.516757	-3.873535	24563.616892
HLA B*4801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.431300	0.557541	-3.873759	26996.050165
HLA A*1101	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.441215	0.567351	-3.873864	27619.451730
HLA B*1801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.451085	0.577199	-3.873886	28254.344732
HLA A*2403	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.451182	0.577199	-3.873982	28260.612395
HLA A*3002	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.614971	0.740887	-3.874084	41207.020768
HLA B*4501	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.628678	0.754590	-3.874088	42528.308735
HLA B*5401	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.451619	0.577199	-3.874419	28289.063648
HLA A*0219	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.332107	0.457680	-3.874427	21483.612935

HLA B*1501	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.363872	0.489404	-3.874469	23113.853506
HLA A*0219	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.315001	0.440475	-3.874526	20653.835746
HLA B*1503	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.390635	0.516095	-3.874541	24583.025977
HLA B*1509	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.327460	0.452913	-3.874547	21254.947562
HLA A*6901	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.369455	0.494882	-3.874573	23412.874263
HLA A*2601	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.389329	0.514746	-3.874583	24509.193829
HLA B*1503	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.482300	0.607629	-3.874672	30359.911234
HLA A*2902	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.452034	0.577199	-3.874835	28316.164825
HLA A*2403	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.407077	0.532233	-3.874844	25531.541467
HLA A*0206	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.432466	0.557541	-3.874924	27068.586076
HLA B*3801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.526769	0.651841	-3.874928	33633.278236
HLA B*4002	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.610968	0.736037	-3.874931	40828.901377
HLA A*2501	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.488583	0.613596	-3.874987	30802.291061
HLA B*0702	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.391864	0.516757	-3.875107	24652.678994
HLA A*8001	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.386921	0.511716	-3.875205	24373.663122
HLA A*3301	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.502393	0.627189	-3.875205	31797.523223
HLA A*3201	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.519789	0.644580	-3.875208	33097.019066
HLA B*5101	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.432917	0.557541	-3.875375	27096.716789
HLA B*7301	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.603727	0.728232	-3.875495	40153.793511
HLA A*6901	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.342144	0.466612	-3.875532	21985.903585
HLA B*4403	1:206-214	9	WTPANIANA	1.064045	-0.280364	-4.659254	0.783681	-3.875574	45630.403573
HLA A*0101	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.365031	0.489404	-3.875627	23175.582176
HLA B*1502	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.531776	0.656026	-3.875750	34023.262243
HLA A*0101	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.390600	0.514746	-3.875854	24581.031186
HLA A*6802	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.309388	0.433361	-3.876027	20388.618478
HLA B*4002	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.588290	0.712255	-3.876036	38751.673723
HLA A*2301	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.542842	0.666703	-3.876139	34901.334006
HLA A*2301	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.503345	0.627189	-3.876156	31867.268136
HLA B*5701	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.408576	0.532233	-3.876343	25619.816071
HLA A*3301	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.612403	0.736037	-3.876366	40964.082246
HLA B*5101	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.484086	0.607629	-3.876457	30484.993449
HLA B*0702	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.434242	0.557541	-3.876700	27179.519940
HLA A*2601	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.388474	0.511716	-3.876758	24460.977822
HLA A*0101	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.385326	0.508560	-3.876766	24284.295225
HLA B*5801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.358537	0.481648	-3.876889	22831.617285
HLA A*6802	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.208576	0.331684	-3.876892	16165.014434
HLA B*0803	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.477693	0.600770	-3.876923	30039.531657
HLA A*0301	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.366353	0.489404	-3.876950	23246.277218
HLA A*6901	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.373940	0.496961	-3.876978	23655.923096
HLA B*7301	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.618784	0.741770	-3.877014	41570.421756
HLA A*6802	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.330434	0.453330	-3.877104	21401.020640
HLA A*0212	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.425452	0.548275	-3.877178	26634.978976
HLA B*4501	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.063726	0.186500	-3.877226	11580.455642
HLA B*4002	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.619031	0.741770	-3.877261	41594.042058
HLA B*4001	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.363687	0.486297	-3.877390	23103.977189
HLA B*1517	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.450923	0.573435	-3.877488	28243.799852
HLA A*0301	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.363879	0.486297	-3.877583	23114.228639
HLA A*0250	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.593112	0.715416	-3.877695	39184.256265
HLA A*0211	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.473189	0.595477	-3.877712	29729.608804
HLA B*1501	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.331168	0.453330	-3.877838	21437.173613
HLA A*1101	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.485240	0.607235	-3.878005	30566.077025
HLA B*3901	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.505323	0.627189	-3.878135	32012.758691
HLA A*3301	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.552421	0.674222	-3.878199	35679.673974
HLA A*6801	1:261-269	9	GLLRAGERA	1.084571	-0.302780	-4.660072	0.781791	-3.878281	45716.390176
HLA A*3301	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.633109	0.754590	-3.878520	42964.448429
HLA B*5101	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.518433	0.639875	-3.878558	32993.867599
HLA B*2705	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.436107	0.557541	-3.878566	27296.519366
HLA B*1801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.506113	0.627429	-3.878684	32071.001930
HLA B*7301	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.565179	0.686294	-3.878885	36743.335719
HLA B*5301	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.597230	0.718317	-3.878914	39557.629207
HLA B*3501	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.446497	0.567535	-3.878961	27957.394549
HLA A*0211	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.485449	0.606435	-3.879014	30580.797527
HLA A*1101	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.452518	0.573435	-3.879083	28347.739002
HLA A*3001	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.263350	0.384129	-3.879221	18337.901710
HLA A*3101	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.395365	0.516095	-3.879270	24852.200768

HLA A*3101	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.387875	0.508560	-3.879315	24427.256637
HLA A*2603	1:64-72	9	SGGPASVYA	1.137612	-0.374224	-4.642799	0.763388	-3.879411	43933.774532
HLA A*0212	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.394157	0.514746	-3.879411	24783.190667
HLA B*4801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.427741	0.548275	-3.879466	26775.695268
HLA A*2603	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.552505	0.673013	-3.879492	35686.623482
HLA B*0802	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.446859	0.567351	-3.879507	27980.696201
HLA A*0212	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.434465	0.554890	-3.879575	27193.492159
HLA B*3801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.559998	0.680376	-3.879622	36307.635470
HLA A*3301	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.605818	0.726094	-3.879724	40347.592226
HLA B*4002	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.634418	0.754547	-3.879871	43094.108811
HLA A*0101	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.366173	0.486297	-3.879876	23236.595732
HLA A*2603	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.634582	0.754590	-3.879993	43110.431306
HLA B*0802	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.493700	0.613596	-3.880104	31167.373012
HLA B*0801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.359317	0.479051	-3.880266	22872.661618
HLA B*0803	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.507736	0.627429	-3.880307	32191.115186
HLA A*0206	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.337997	0.457680	-3.880317	21776.971266
HLA B*2705	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.457556	0.577199	-3.880357	28678.453058
HLA A*1101	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.377363	0.496961	-3.880402	23843.120810
HLA B*4403	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.635073	0.754590	-3.880484	43159.202407
HLA B*3801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.528365	0.647881	-3.880484	33757.051042
HLA B*4801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.435379	0.554890	-3.880489	27250.779676
HLA B*4402	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.412725	0.532233	-3.880492	25865.757289
HLA A*8001	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.435520	0.554890	-3.880630	27259.626534
HLA A*2301	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.515877	0.635184	-3.880693	32800.237443
HLA B*4403	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.616778	0.736037	-3.880741	41378.807497
HLA A*3001	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.135136	0.254355	-3.880781	13650.101934
HLA B*3801	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.582116	0.701295	-3.880821	38204.631780
HLA A*2501	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.487458	0.606435	-3.881023	30722.575277
HLA B*0802	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.487686	0.606435	-3.881251	30738.701463
HLA A*0212	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.378373	0.496961	-3.881412	23898.650488
HLA A*0212	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.215714	0.334057	-3.881656	16432.885612
HLA A*3201	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.609946	0.728232	-3.881714	40732.931618
HLA A*2601	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.398685	0.516757	-3.881928	25042.903251
HLA A*6801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.455493	0.573435	-3.882058	28542.556773
HLA B*4001	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.437014	0.554890	-3.882125	27353.579984
HLA B*5301	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.509686	0.627189	-3.882498	32335.984993
HLA B*4801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.414859	0.532233	-3.882625	25993.127104
HLA A*0101	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.340403	0.457680	-3.882723	21897.944500
HLA A*2402	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.569379	0.686294	-3.883085	37100.474156
HLA A*2602	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.598520	0.715416	-3.883104	39675.291161
HLA A*3001	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.290763	0.407463	-3.883300	19532.751801
HLA A*6802	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.323792	0.440475	-3.883317	21076.208767
HLA A*3201	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.619445	0.736037	-3.883408	41633.664290
HLA A*2402	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.556495	0.673013	-3.883482	36015.950795
HLA B*0802	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.456940	0.573435	-3.883505	28637.833272
HLA A*0203	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.431784	0.548275	-3.883510	27026.152337
HLA B*4501	1:350-358	9	GTANIKSHH	1.042779	-0.288232	-4.638060	0.754547	-3.883513	43456.986353
HLA A*0216	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.342365	0.458831	-3.883534	21997.086910
HLA B*5401	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.531424	0.647881	-3.883543	33995.664131
HLA A*3301	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.598967	0.715416	-3.883550	39716.093524
HLA B*5801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.342412	0.458831	-3.883581	21999.467075
HLA A*2501	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.431965	0.548275	-3.883691	27037.412736
HLA A*2603	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.611940	0.728232	-3.883708	40920.448107
HLA A*0206	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.479326	0.595477	-3.883849	30152.689075
HLA B*5801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.370178	0.486297	-3.883882	23451.918387
HLA B*4402	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.398673	0.514746	-3.883927	25042.225864
HLA B*0803	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.461129	0.577199	-3.883930	28915.405566
HLA B*3501	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.183159	0.299099	-3.884061	15246.121203
HLA B*0702	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.451438	0.567351	-3.884087	28277.281968
HLA B*4002	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.636904	0.752770	-3.884134	43341.472192
HLA A*2902	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.379207	0.494882	-3.884326	23944.592203
HLA A*1101	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.461594	0.577199	-3.884395	28946.395130
HLA B*5101	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.451865	0.567351	-3.884514	28305.137486
HLA B*4001	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.401351	0.516757	-3.884594	25197.145347
HLA B*1801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.416858	0.532233	-3.884624	26113.070556

HLA B*4402	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-3.976132	0.091322	-3.884811	9465.251271
HLA A*2403	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.119507	0.234640	-3.884867	13167.615010
HLA A*2602	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.492868	0.607629	-3.885240	31107.741471
HLA A*2301	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.529861	0.644580	-3.885281	33873.581868
HLA B*1801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.498895	0.613596	-3.885299	31542.412720
HLA B*0802	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.493160	0.607629	-3.885531	31128.616361
HLA B*5101	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.492899	0.607235	-3.885664	31109.929310
HLA B*5101	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.326203	0.440475	-3.885728	21193.518505
HLA B*1509	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.441006	0.555251	-3.885755	27606.156713
HLA B*5701	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.382837	0.496961	-3.885876	24145.566508
HLA B*4501	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.614121	0.728232	-3.885889	41126.400736
HLA A*2603	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.576806	0.690895	-3.885911	37740.372482
HLA A*2603	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.601706	0.715584	-3.886123	39967.411706
HLA A*3201	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.552905	0.666703	-3.886202	35719.458894
HLA B*1517	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.493883	0.607629	-3.886255	31180.527526
HLA A*0219	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.394848	0.508560	-3.886288	24822.639879
HLA A*0212	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.416928	0.530534	-3.886394	26117.308965
HLA B*5701	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.416947	0.530534	-3.886413	26118.439323
HLA B*0803	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.495862	0.609194	-3.886668	31322.882755
HLA A*3002	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.494311	0.607629	-3.886682	31211.242986
HLA B*7301	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.482169	0.595477	-3.886692	30350.714977
HLA A*2603	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.622985	0.736037	-3.886949	41974.478578
HLA A*0206	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.500603	0.613596	-3.887007	31666.712970
HLA A*6802	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.441948	0.554890	-3.887059	27666.109565
HLA A*2902	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.441997	0.554890	-3.887108	27669.252826
HLA B*1509	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.496428	0.609194	-3.887234	31363.747639
HLA B*5701	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.403341	0.516095	-3.887247	25312.868033
HLA A*3201	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.573543	0.686294	-3.887249	37457.841488
HLA A*3201	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.588565	0.701295	-3.887271	38776.209632
HLA B*1503	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.392668	0.505350	-3.887317	24698.333160
HLA B*4403	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-3.677912	-0.209501	-3.887413	4763.344764
HLA A*3101	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.373837	0.486297	-3.887540	23650.292825
HLA B*4002	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.554298	0.666703	-3.887595	35834.233217
HLA A*0203	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.442627	0.554890	-3.887738	27709.398195
HLA A*0301	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.224473	0.336669	-3.887803	16767.669773
HLA A*6801	1:446-454	9	CPVVLLADV	0.750859	-0.002468	-4.636213	0.748391	-3.887822	43272.592051
HLA A*2402	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.543878	0.656026	-3.887852	34984.699657
HLA B*5301	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.580286	0.692424	-3.887862	38043.964649
HLA B*3901	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.495622	0.607629	-3.887993	31305.603284
HLA A*2301	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.539987	0.651841	-3.888146	34672.679302
HLA A*0201	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.393556	0.505350	-3.888205	24748.891399
HLA A*0301	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.369899	0.481648	-3.888251	23436.825444
HLA A*2403	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.374570	0.486297	-3.888273	23690.245518
HLA B*4501	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.536266	0.647881	-3.888385	34376.829364
HLA B*1501	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.009246	0.120764	-3.888482	10215.174484
HLA A*0206	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.319129	0.430602	-3.888527	20851.090057
HLA A*0250	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.589935	0.701295	-3.888640	38898.701520
HLA A*3002	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.579574	0.690895	-3.888679	37981.654202
HLA B*1501	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.404941	0.516095	-3.888847	25406.296038
HLA A*2501	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.462344	0.573435	-3.888909	28996.392635
HLA B*1517	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.502525	0.613596	-3.888929	31807.157862
HLA B*1517	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.495469	0.606435	-3.889035	31294.596829
HLA A*3101	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.352952	0.463883	-3.889069	22539.898194
HLA A*2501	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.375425	0.486297	-3.889128	23736.942304
HLA A*6802	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.405376	0.516095	-3.889281	25431.736137
HLA B*4403	1:49-57	9	SIEEIRARQ	0.739557	0.035755	-4.664621	0.775312	-3.889309	46197.719074
HLA A*6802	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.406156	0.516757	-3.889399	25477.454696
HLA B*4402	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.457015	0.567535	-3.889480	28642.791382
HLA B*1503	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.421717	0.532233	-3.889483	26406.854783
HLA A*2301	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.542379	0.652880	-3.889499	34864.157787
HLA B*0702	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.404248	0.514746	-3.889502	25365.782028
HLA A*2902	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.437818	0.548275	-3.889543	27404.235935
HLA B*1502	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.570089	0.680376	-3.889713	37161.137953
HLA B*5701	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.401457	0.511716	-3.889741	25203.280213
HLA A*0212	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.379273	0.489404	-3.889870	23948.219530

HLA B*5401	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.485221	0.595350	-3.889871	30564.754181
HLA A*0203	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.384797	0.494882	-3.889915	24254.753756
HLA A*2501	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.323360	0.433361	-3.889999	21055.239534
HLA B*4501	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.626089	0.736037	-3.890052	42275.522076
HLA B*0702	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-3.909642	0.019419	-3.890223	8121.602354
HLA B*1503	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.309423	0.419078	-3.890345	20390.273048
HLA B*0801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.124427	0.233980	-3.890447	13317.629910
HLA A*2603	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.523912	0.633434	-3.890478	33412.750390
HLA A*6801	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.622050	0.731526	-3.890524	41884.199049
HLA A*2902	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.036331	0.145582	-3.890748	10872.530941
HLA A*6901	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.126057	0.235291	-3.890767	13367.724440
HLA A*0206	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.349806	0.458831	-3.890975	22377.212688
HLA A*0206	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.402796	0.511716	-3.891080	25281.117926
HLA A*1101	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.405916	0.514746	-3.891170	25463.399893
HLA B*5801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.344515	0.453330	-3.891185	22106.243501
HLA A*1101	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.486720	0.595350	-3.891370	30670.430980
HLA A*3301	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.619853	0.728232	-3.891622	41672.873371
HLA B*5801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.325040	0.433361	-3.891679	21136.840408
HLA A*2601	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.370768	0.479051	-3.891717	23483.784959
HLA A*8001	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.408672	0.516757	-3.891915	25625.499317
HLA A*2601	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.388951	0.496961	-3.891989	24487.855808
HLA B*3901	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.505629	0.613596	-3.892033	32035.280722
HLA B*4601	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.408252	0.516095	-3.892157	25600.696359
HLA A*8001	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.387043	0.494882	-3.892161	24380.520745
HLA A*2301	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.538268	0.645964	-3.892303	34535.645653
HLA A*0250	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.404171	0.511716	-3.892455	25361.253972
HLA B*1517	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.401041	0.508560	-3.892481	25179.158354
HLA B*2705	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.424762	0.532233	-3.892528	26592.649517
HLA B*4601	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.389510	0.496961	-3.892548	24519.405541
HLA A*0219	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.323238	0.430602	-3.892636	21049.317229
HLA A*3301	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.634467	0.741770	-3.892697	43099.004910
HLA A*6901	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.351542	0.458831	-3.892711	22466.853796
HLA A*2402	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.528014	0.635184	-3.892831	33729.851342
HLA B*1501	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.401549	0.508560	-3.892989	25208.598305
HLA B*4403	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.621254	0.728232	-3.893022	41807.455814
HLA A*2501	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.470302	0.577199	-3.893103	29532.599615
HLA A*0219	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.441499	0.548275	-3.893225	27637.537247
HLA B*3901	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.499708	0.606435	-3.893273	31601.509783
HLA A*0211	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.460850	0.567535	-3.893314	28896.796490
HLA A*0250	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.584233	0.690895	-3.893338	38391.307592
HLA B*4002	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.619510	0.726094	-3.893416	41639.971306
HLA B*5801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.351192	0.457680	-3.893512	22448.751158
HLA B*1517	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.196913	0.303325	-3.893588	15736.685055
HLA A*0201	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.390675	0.496961	-3.893714	24585.286936
HLA A*0206	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.410658	0.516757	-3.893901	25742.910765
HLA B*7301	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.560818	0.666703	-3.894115	36376.250903
HLA B*5301	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.567173	0.673013	-3.894160	36912.485864
HLA A*0219	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.467612	0.573435	-3.894177	29350.230561
HLA B*1502	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.609638	0.715416	-3.894222	40704.074600
HLA B*2705	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.389153	0.494882	-3.894271	24499.251445
HLA A*3002	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.489636	0.595350	-3.894286	30877.034967
HLA B*4002	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.360940	0.466612	-3.894328	22958.324981
HLA A*0203	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.410470	0.516095	-3.894375	25731.771872
HLA A*2301	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.489943	0.595477	-3.894466	30898.925138
HLA B*4402	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-3.690552	-0.203931	-3.894483	4904.020145
HLA B*4501	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.621679	0.727191	-3.894488	41848.413303
HLA B*1503	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.508086	0.613596	-3.894490	32217.074052
HLA B*4001	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.399841	0.505350	-3.894490	25109.647868
HLA B*4403	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.636335	0.741770	-3.894565	43284.766959
HLA B*1501	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.129257	0.234640	-3.894617	13466.585199
HLA B*1502	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.622959	0.728232	-3.894728	41971.980802
HLA B*5401	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.381085	0.486297	-3.894788	24048.316750
HLA B*5301	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.585739	0.690895	-3.894844	38524.669723
HLA A*0216	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.468424	0.573435	-3.894989	29405.220407
HLA A*0301	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.299487	0.404390	-3.895098	19929.071689

HLA A*3001	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.254586	0.359286	-3.895300	17971.571768
HLA B*0702	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.472588	0.577199	-3.895389	29688.463827
HLA B*5401	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.328769	0.433361	-3.895408	21319.091865
HLA B*7301	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.539994	0.644580	-3.895414	34673.242033
HLA B*4601	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.407314	0.511716	-3.895598	25545.495682
HLA B*1801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.502842	0.607235	-3.895607	31830.396229
HLA A*3201	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.541576	0.645964	-3.895612	34799.712383
HLA B*7301	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.530803	0.635184	-3.895619	33947.145814
HLA A*6901	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.272656	0.376904	-3.895752	18735.097204
HLA A*0216	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.401152	0.505350	-3.895801	25185.561341
HLA B*5701	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.412643	0.516757	-3.895886	25860.860172
HLA B*3801	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.541956	0.645964	-3.895992	34830.224291
HLA B*5401	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.547889	0.651841	-3.896047	35309.268529
HLA A*8001	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.463587	0.567535	-3.896051	29079.494276
HLA B*5101	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.491576	0.595477	-3.896099	31015.319848
HLA A*0201	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.385544	0.489404	-3.896140	24296.516206
HLA B*4501	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.576534	0.680376	-3.896157	37716.696049
HLA B*1509	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.540772	0.644580	-3.896192	34735.386105
HLA A*0250	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.570441	0.674222	-3.896220	37191.305837
HLA A*2403	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.393246	0.496961	-3.896284	24731.224392
HLA A*2603	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-3.738284	-0.158117	-3.896401	5473.742748
HLA B*0702	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.464022	0.567535	-3.896486	29108.612460
HLA B*1801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.445141	0.548275	-3.896866	27870.261438
HLA A*0212	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.402409	0.505350	-3.897058	25258.561267
HLA B*4001	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.408790	0.511716	-3.897074	25632.431810
HLA A*0212	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.383411	0.486297	-3.897114	24177.460014
HLA B*3901	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.241300	0.344171	-3.897129	17430.093783
HLA B*3901	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.464585	0.567351	-3.897234	29146.430854
HLA A*2402	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.492800	0.595477	-3.897323	31102.861460
HLA B*4501	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.650164	0.752770	-3.897395	44685.245922
HLA B*1801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.465095	0.567535	-3.897560	29180.667280
HLA A*6801	1:304-312	9	GKRKIIGRQ	0.891389	-0.155352	-4.633605	0.736037	-3.897568	43013.519773
HLA B*4601	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.402947	0.505350	-3.897596	25289.872596
HLA B*5701	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.403022	0.505350	-3.897671	25294.251068
HLA A*0219	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.412455	0.514746	-3.897709	25849.670243
HLA A*0101	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.331081	0.433361	-3.897719	21432.883052
HLA A*2402	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.588791	0.690895	-3.897896	38796.353261
HLA A*3301	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.639115	0.740887	-3.898228	43562.673428
HLA A*6901	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.377377	0.479051	-3.898326	23843.894754
HLA A*0212	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.410075	0.511716	-3.898359	25708.395883
HLA B*5101	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.387849	0.489404	-3.898445	24425.803044
HLA A*2902	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.429073	0.530534	-3.898539	26857.953322
HLA B*1503	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.235236	0.336669	-3.898566	17188.409944
HLA A*0203	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.310511	0.411911	-3.898600	20441.410186
HLA B*4801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.410333	0.511716	-3.898617	25723.699189
HLA A*6801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.395630	0.496961	-3.898669	24867.397997
HLA A*0201	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.302649	0.403979	-3.898670	20074.719063
HLA A*2602	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.639690	0.740887	-3.898803	43620.450671
HLA B*0801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.415606	0.516757	-3.898849	26037.882730
HLA B*5801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.339525	0.440475	-3.899049	21853.683213
HLA A*2501	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.202547	0.303325	-3.899222	15942.165679
HLA A*0250	1:189-197	9	QQVLSRFLH	0.865161	-0.172737	-4.591819	0.692424	-3.899395	39067.839182
HLA B*5101	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.506141	0.606435	-3.899706	32073.084004
HLA B*1501	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.276671	0.376904	-3.899768	18909.115760
HLA A*0101	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.378907	0.479051	-3.899856	23928.017131
HLA A*0301	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.358718	0.458831	-3.899886	22841.130038
HLA B*0803	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.507414	0.607235	-3.900180	32167.265426
HLA B*5401	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.556279	0.656026	-3.900253	35998.029763
HLA B*3901	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.178324	0.278063	-3.900261	15077.319149
HLA B*5401	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.533963	0.633434	-3.900529	34195.056303
HLA A*2603	1:166-174	9	FEAFDRRLA	1.007268	-0.257036	-4.650930	0.750232	-3.900698	44764.123423
HLA A*0219	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.455589	0.554890	-3.900700	28548.888370
HLA A*1101	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.455808	0.554890	-3.900918	28563.255491
HLA B*4501	1:349-357	9	SGTANIKSH	1.095056	-0.353286	-4.642712	0.741770	-3.900942	43924.981369
HLA A*0301	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.364843	0.463883	-3.900960	23165.554159

HLA A*0212	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.380037	0.479051	-3.900986	23990.362661
HLA A*3002	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.508330	0.607235	-3.901096	32235.205395
HLA B*1517	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.380359	0.479051	-3.901308	24008.149825
HLA A*6901	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.354735	0.453330	-3.901405	22632.639674
HLA A*3201	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.574431	0.673013	-3.901418	37534.518828
HLA A*2603	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.616954	0.715416	-3.901538	41395.600011
HLA A*3002	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.276382	0.374749	-3.901633	18896.537510
HLA B*3501	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.286013	0.384129	-3.901884	19320.251385
HLA B*7301	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.129577	0.227657	-3.901920	13476.496816
HLA A*0201	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.332523	0.430602	-3.901921	21504.194429
HLA B*2705	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.469510	0.567535	-3.901974	29478.806819
HLA A*2603	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.633831	0.731526	-3.902305	43035.864619
HLA B*4001	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.399303	0.496961	-3.902341	25078.559675
HLA A*2902	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.419123	0.516757	-3.902366	26249.609420
HLA B*3801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.569276	0.666703	-3.902573	37091.643991
HLA B*3901	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.172493	0.269777	-3.902716	14876.223894
HLA A*0202	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.271347	0.368545	-3.902802	18678.727553
HLA A*2501	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.435158	0.532233	-3.902925	27236.925372
HLA B*0702	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.419076	0.516095	-3.902981	26246.769424
HLA B*1501	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.349533	0.446544	-3.902989	22363.174337
HLA B*4403	1:510-518	9	VVLDITSKP	0.556336	0.196434	-4.655850	0.752770	-3.903080	45274.108373
HLA A*2501	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.433669	0.530534	-3.903134	27143.666291
HLA A*2402	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.530456	0.627189	-3.903267	33919.976448
HLA A*3301	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.576346	0.673013	-3.903333	37700.376130
HLA A*8001	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.451722	0.548275	-3.903447	28295.798240
HLA B*0802	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.408957	0.505350	-3.903606	25642.279172
HLA A*8001	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.412342	0.508560	-3.903782	25842.958610
HLA A*0101	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.249457	0.345470	-3.903987	17760.579654
HLA B*0803	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.471352	0.567351	-3.904001	29604.102371
HLA A*3301	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.622349	0.718317	-3.904032	41912.985724
HLA A*0201	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.383143	0.479051	-3.904092	24162.553709
HLA A*2601	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.398981	0.494882	-3.904099	25059.979466
HLA A*2301	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.544141	0.639875	-3.904266	35005.903575
HLA B*0801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.337701	0.433361	-3.904340	21762.132138
HLA A*0206	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.393831	0.489404	-3.904427	24764.561343
HLA B*5801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.368517	0.463883	-3.904635	23362.391007
HLA A*0250	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.550619	0.645964	-3.904655	35531.932003
HLA B*5301	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.390964	0.486297	-3.904667	24601.651832
HLA B*0801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.249034	0.344171	-3.904863	17743.293174
HLA A*3301	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.410261	0.505350	-3.904910	25719.385518
HLA B*4801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.421035	0.516095	-3.904941	26365.458399
HLA B*1503	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.511451	0.606435	-3.905016	32467.627738
HLA B*4403	1:408-416	9	GIRIVGEVT	1.053088	-0.287206	-4.671176	0.765882	-3.905294	46900.297414
HLA B*0801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.252697	0.347374	-3.905323	17893.573254
HLA B*3801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.538864	0.633434	-3.905430	34583.134113
HLA B*0802	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.460728	0.555251	-3.905477	28888.668553
HLA B*4801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.414196	0.508560	-3.905636	25953.502515
HLA B*2705	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.414436	0.508560	-3.905876	25967.827835
HLA B*0803	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.513544	0.607629	-3.905915	32624.506352
HLA B*1801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.473325	0.567351	-3.905974	29738.938633
HLA A*0203	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.395466	0.489404	-3.906062	24857.982689
HLA A*2603	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.638903	0.732703	-3.906200	43541.468360
HLA B*5701	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.414812	0.508560	-3.906252	25990.314857
HLA A*0216	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.423061	0.516757	-3.906304	26488.696211
HLA B*4403	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.618634	0.712255	-3.906380	41556.031199
HLA A*0202	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.501921	0.595477	-3.906444	31762.965779
HLA A*0101	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.403412	0.496961	-3.906450	25316.976561
HLA B*3801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.562484	0.656026	-3.906458	36516.043990
HLA B*5701	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.395929	0.489404	-3.906525	24884.489160
HLA B*4402	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.415096	0.508560	-3.906536	26007.333598
HLA B*3901	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.396023	0.489404	-3.906619	24889.874636
HLA A*0101	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.347377	0.440475	-3.906901	22252.387917
HLA A*3002	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.092732	0.185815	-3.906917	12380.334794
HLA B*1801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.393335	0.486297	-3.907038	24736.309055
HLA A*0301	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.206142	0.299099	-3.907043	16074.668679

HLA B*5801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.360003	0.452913	-3.907090	22908.821832
HLA B*4501	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.484427	0.577199	-3.907228	30508.916294
HLA B*0802	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.464792	0.557541	-3.907251	29160.309906
HLA A*6901	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.389033	0.481648	-3.907385	24492.492927
HLA A*0101	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.338063	0.430602	-3.907461	21780.270224
HLA A*0301	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.365214	0.457680	-3.907534	23185.363671
HLA A*0219	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.311648	0.403979	-3.907669	20495.003829
HLA A*0203	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.338298	0.430602	-3.907696	21792.056296
HLA A*3101	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.142410	0.234640	-3.907770	13880.653083
HLA A*3001	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.100735	0.192958	-3.907777	12610.570521
HLA B*1502	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.609095	0.701295	-3.907801	40653.239124
HLA A*2601	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.397291	0.489404	-3.907888	24962.692737
HLA A*0216	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.416529	0.508560	-3.907969	26093.300409
HLA B*4402	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.394528	0.486297	-3.908232	24804.383465
HLA B*5401	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.561147	0.652880	-3.908267	36403.812146
HLA B*1509	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.503751	0.595350	-3.908401	31897.107018
HLA B*4001	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.367274	0.458831	-3.908443	23295.627362
HLA A*6801	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.588897	0.680376	-3.908520	38805.799190
HLA A*2602	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.636772	0.728232	-3.908540	43328.343717
HLA A*1101	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.413909	0.505350	-3.908559	25936.378687
HLA B*1501	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.242728	0.334057	-3.908671	17487.519458
HLA A*0301	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.361666	0.452913	-3.908753	22996.735492
HLA B*0702	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.405851	0.496961	-3.908889	25459.543069
HLA B*3501	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.405867	0.496961	-3.908906	25460.507220
HLA A*0301	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.362430	0.453330	-3.909100	23037.204240
HLA A*0250	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.518349	0.609194	-3.909155	32987.442470
HLA B*3501	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-3.782192	-0.127048	-3.909240	6056.079373
HLA A*2601	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.391054	0.481648	-3.909405	24606.709856
HLA B*1509	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.536644	0.627189	-3.909456	34406.784356
HLA A*6802	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.321483	0.411911	-3.909572	20964.424647
HLA B*4801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.440139	0.530534	-3.909605	27551.102917
HLA A*2501	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.477362	0.567351	-3.910011	30016.626408
HLA B*1501	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.368097	0.457680	-3.910417	23339.778515
HLA B*1509	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.477806	0.567351	-3.910455	30047.333176
HLA B*0702	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.465349	0.554890	-3.910459	29197.721592
HLA A*0101	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.363922	0.453330	-3.910592	23116.479566
HLA B*4601	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.351552	0.440475	-3.911076	22467.339974
HLA A*0201	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.397400	0.486297	-3.911103	24968.905599
HLA A*0216	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.408249	0.496961	-3.911288	25600.557862
HLA A*3201	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.466606	0.555251	-3.911355	29282.350698
HLA A*8001	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.416863	0.505350	-3.911512	26113.353095
HLA A*2603	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.652434	0.740887	-3.911547	44919.380167
HLA B*0702	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.400985	0.489404	-3.911581	25175.889371
HLA A*0216	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.466608	0.554890	-3.911719	29282.509112
HLA A*2902	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.426585	0.514746	-3.911839	26704.522087
HLA B*4002	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.639199	0.727191	-3.912008	43571.158347
HLA B*0802	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.489382	0.577199	-3.912183	30858.999772
HLA A*2301	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.545767	0.633434	-3.912333	35137.198799
HLA A*2402	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.592851	0.680376	-3.912475	39160.733273
HLA A*0203	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.244232	0.331684	-3.912548	17548.171944
HLA B*4601	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.365966	0.453330	-3.912636	23225.536113
HLA A*0206	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.399004	0.486297	-3.912707	25061.335220
HLA A*0203	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-3.615651	-0.297084	-3.912735	4127.153898
HLA A*6901	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.287669	0.374749	-3.912920	19394.078979
HLA A*2403	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.429700	0.516757	-3.912943	26896.776067
HLA B*1801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.443550	0.530534	-3.913016	27768.373442
HLA A*3101	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.429869	0.516757	-3.913113	26907.254725
HLA B*1517	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.418723	0.505350	-3.913373	26225.479247
HLA A*0219	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.430410	0.516757	-3.913653	26940.755574
HLA B*0802	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.462055	0.548275	-3.913780	28977.104379
HLA A*2601	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.377718	0.463883	-3.913835	23862.606052
HLA A*0206	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.248017	0.334057	-3.913959	17701.778471
HLA B*4001	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.403480	0.489404	-3.914076	25320.948771
HLA A*2402	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.558729	0.644580	-3.914149	36201.723295
HLA A*3001	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.256409	0.342132	-3.914278	18047.176341

HLA B*0803	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.422917	0.508560	-3.914357	26479.956297
HLA B*4402	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.430469	0.516095	-3.914374	26944.399483
HLA B*0801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.367289	0.452913	-3.914376	23296.383535
HLA A*2902	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.430504	0.516095	-3.914409	26946.586065
HLA A*2403	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.419788	0.505350	-3.914437	26289.828316
HLA B*7301	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.491698	0.577199	-3.914499	31024.046127
HLA B*5301	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.594991	0.680376	-3.914615	39354.209758
HLA A*3301	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.570756	0.656026	-3.914730	37218.276524
HLA B*5101	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.482317	0.567535	-3.914782	30361.060962
HLA B*4001	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.345568	0.430602	-3.914965	22159.885842
HLA A*8001	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.447343	0.532233	-3.915109	28011.896311
HLA A*3001	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.265565	0.350403	-3.915162	18431.692015
HLA A*2301	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.542858	0.627429	-3.915430	34902.655718
HLA B*4601	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.410350	0.494882	-3.915468	25724.673344
HLA A*0203	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.401887	0.486297	-3.915590	25228.244061
HLA A*3301	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.631209	0.715584	-3.915625	42776.821095
HLA B*0803	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.489105	0.573435	-3.915670	30839.306694
HLA B*7301	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.561668	0.645964	-3.915704	36447.559222
HLA A*2402	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.582513	0.666703	-3.915810	38239.577150
HLA B*4002	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.648921	0.732703	-3.916218	44557.547098
HLA B*0801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.413230	0.496961	-3.916269	25895.859932
HLA B*1502	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.252958	0.336669	-3.916289	17904.321531
HLA B*4402	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.395419	0.479051	-3.916368	24855.293256
HLA B*1801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.398121	0.481648	-3.916473	25010.409311
HLA B*1517	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.484046	0.567535	-3.916511	30482.189931
HLA B*5801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.363259	0.446544	-3.916715	23081.240212
HLA A*2603	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.583587	0.666703	-3.916884	38334.234559
HLA A*2402	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.591138	0.674222	-3.916916	39006.594959
HLA B*4501	1:38-46	9	RVFSEVIPH	0.661746	0.050509	-4.629181	0.712255	-3.916926	42577.572962
HLA B*1801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.472212	0.555251	-3.916961	29662.777138
HLA A*0301	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.320985	0.403979	-3.917005	20940.394404
HLA B*3901	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.484591	0.567535	-3.917056	30520.471972
HLA B*0702	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.375951	0.458831	-3.917120	23765.724526
HLA B*4002	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.632548	0.715416	-3.917132	42908.932862
HLA B*4001	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.178470	0.261282	-3.917188	15082.377128
HLA B*4402	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.414182	0.496961	-3.917220	25952.660095
HLA A*0201	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.398985	0.481648	-3.917337	25060.250611
HLA A*3301	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.474956	0.557541	-3.917415	29850.802243
HLA A*0206	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.494706	0.577199	-3.917507	31239.622574
HLA B*3501	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.472792	0.554890	-3.917903	29702.440299
HLA B*3901	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.381867	0.463883	-3.917984	24091.678672
HLA A*6802	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.414960	0.496961	-3.917998	25999.174464
HLA B*3901	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.475621	0.557541	-3.918080	29896.538782
HLA B*4801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.434972	0.516757	-3.918216	27225.287308
HLA A*3002	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.518995	0.600770	-3.918225	33036.555056
HLA B*3801	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.553549	0.635184	-3.918365	35772.445453
HLA B*4601	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.407810	0.489404	-3.918406	25574.672173
HLA B*5701	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.413411	0.494882	-3.918530	25906.649396
HLA A*2402	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.570430	0.651841	-3.918588	37190.299846
HLA B*4001	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.397886	0.479051	-3.918835	24996.882616
HLA B*1801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.525273	0.606435	-3.918838	33517.574096
HLA B*3801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.546047	0.627189	-3.918858	35159.826596
HLA B*0802	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.449408	0.530534	-3.918874	28145.418289
HLA A*0250	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.349510	0.430602	-3.918908	22361.964547
HLA A*0101	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.377906	0.458831	-3.919075	23872.935812
HLA A*0202	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.571971	0.652880	-3.919091	37322.518504
HLA B*5401	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.559056	0.639875	-3.919181	36228.956309
HLA B*1503	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.189010	0.269777	-3.919232	15452.885464
HLA B*4501	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-3.709766	-0.209501	-3.919268	5125.855203
HLA A*1101	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.414205	0.494882	-3.919324	25954.064143
HLA B*5301	1:197-205	9	HDFAGLGAQ	0.824970	-0.150748	-4.593565	0.674222	-3.919344	39225.190250
HLA A*3001	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.210028	0.290570	-3.919458	16219.149558
HLA A*0250	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.599836	0.680376	-3.919460	39795.671216
HLA B*4801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.405757	0.486297	-3.919460	25454.034332
HLA B*1502	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.526760	0.607235	-3.919525	33632.550435

HLA B*5401	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.105598	0.185815	-3.919783	12752.583302
HLA A*2301	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.528978	0.609194	-3.919784	33804.749025
HLA B*0803	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.533399	0.613596	-3.919804	34150.687162
HLA B*3501	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.435910	0.516095	-3.919815	27284.117808
HLA B*1502	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.436664	0.516757	-3.919907	27331.539873
HLA B*5701	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.386615	0.466612	-3.920003	24356.527503
HLA A*2402	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.566020	0.645964	-3.920056	36814.566974
HLA B*3501	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.386754	0.466612	-3.920142	24364.302944
HLA B*5801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.351218	0.430602	-3.920616	22450.087095
HLA B*5101	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.494100	0.573435	-3.920665	31196.050242
HLA A*0206	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.494558	0.573435	-3.921123	31228.977206
HLA B*2705	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.476535	0.555251	-3.921284	29959.520708
HLA B*4403	1:440-448	9	DNQIWQCPV	0.792685	-0.061159	-4.652918	0.731526	-3.921392	44969.467899
HLA B*4501	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.654243	0.732703	-3.921540	45106.887265
HLA A*0201	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.380392	0.458831	-3.921560	24009.968234
HLA B*3901	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.476814	0.555251	-3.921564	29978.814162
HLA B*4402	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.452276	0.530534	-3.921742	28331.947515
HLA B*5801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.290289	0.368545	-3.921744	19511.418115
HLA A*3201	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.569647	0.647881	-3.921767	37123.362090
HLA B*0803	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.479634	0.557541	-3.922092	30174.065723
HLA A*0301	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.368644	0.446544	-3.922100	23369.216953
HLA A*2301	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.495563	0.573435	-3.922128	31301.369574
HLA B*4801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.417032	0.494882	-3.922150	26123.526541
HLA B*0802	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.489737	0.567535	-3.922201	30884.218580
HLA A*2402	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.489631	0.567351	-3.922280	30876.700886
HLA A*8001	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.437089	0.514746	-3.922343	27358.315749
HLA A*2601	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.212937	0.290570	-3.922367	16328.140958
HLA A*0301	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.362888	0.440475	-3.922413	23061.519663
HLA B*0803	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.529013	0.606435	-3.922578	33807.492336
HLA A*0212	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.115560	0.192958	-3.922602	13048.481841
HLA A*0211	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.536233	0.613596	-3.922637	34374.225815
HLA A*2403	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.327042	0.404390	-3.922652	21234.489743
HLA B*4402	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.434862	0.511716	-3.923146	27218.365756
HLA A*6901	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.265502	0.342132	-3.923370	18428.999950
HLA B*1502	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-3.974793	0.051389	-3.923404	9436.108829
HLA B*4801	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.428793	0.505350	-3.923443	26840.668359
HLA B*1503	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.267607	0.344156	-3.923451	18518.546970
HLA B*1801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.518931	0.595477	-3.923454	33031.729858
HLA A*3101	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.402533	0.479051	-3.923482	25265.804544
HLA A*2602	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.614649	0.690895	-3.923754	41176.491301
HLA A*1101	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.432353	0.508560	-3.923793	27061.557963
HLA A*0101	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.376837	0.452913	-3.923924	23814.244854
HLA A*2601	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.382762	0.458831	-3.923931	24141.386875
HLA B*4002	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.571823	0.647881	-3.923942	37309.800298
HLA A*3101	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.377326	0.453330	-3.923995	23841.057081
HLA B*3901	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.501209	0.577199	-3.924010	31710.942689
HLA B*3901	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.454600	0.530534	-3.924066	28483.940458
HLA B*0803	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.479382	0.555251	-3.924132	30156.604274
HLA B*4601	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.403363	0.479051	-3.924311	25314.100521
HLA A*0211	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.531658	0.607235	-3.924424	34014.060384
HLA A*6802	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.403736	0.479051	-3.924685	25335.884379
HLA A*0301	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.284234	0.359286	-3.924948	19241.291221
HLA B*4601	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.391624	0.466612	-3.925012	24639.079184
HLA A*0212	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.441817	0.516757	-3.925060	27657.729282
HLA A*6802	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.419959	0.494882	-3.925078	26300.212796
HLA A*2601	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.259146	0.334057	-3.925089	18161.278234
HLA B*4601	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.371748	0.446544	-3.925203	23536.822390
HLA B*4601	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.389125	0.463883	-3.925242	24497.661037
HLA B*3801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.433835	0.508560	-3.925275	27154.094234
HLA A*3001	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-3.891396	-0.034103	-3.925499	7787.456280
HLA A*6901	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.337662	0.411911	-3.925750	21760.130808
HLA B*5401	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.458073	0.532233	-3.925839	28712.605774
HLA B*1517	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.480797	0.554890	-3.925907	30254.976994
HLA A*0219	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.442145	0.516095	-3.926051	27678.684751
HLA B*5301	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.579102	0.652880	-3.926222	37940.375865

HLA B*0801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.379637	0.453330	-3.926307	23968.309320
HLA A*2601	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.379656	0.453330	-3.926326	23969.346669
HLA A*6801	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.582440	0.656026	-3.926414	38233.164659
HLA A*0203	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.260521	0.334057	-3.926463	18218.845824
HLA A*6802	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.301277	0.374749	-3.926528	20011.395576
HLA A*3101	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.385427	0.458831	-3.926595	24289.945022
HLA A*2601	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.379558	0.452913	-3.926645	23963.901085
HLA A*2403	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.435243	0.508560	-3.926683	27242.230443
HLA B*5401	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.494271	0.567351	-3.926920	31208.372679
HLA A*0219	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.331337	0.404390	-3.926947	21445.525276
HLA A*3201	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.617849	0.690895	-3.926954	41481.011280
HLA A*3201	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.226070	0.299099	-3.926972	16829.467010
HLA A*0250	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.533465	0.606435	-3.927031	34155.860594
HLA A*6801	1:467-475	9	GHPIVLRPV	0.723155	0.031435	-4.681664	0.754590	-3.927074	48046.714770
HLA A*0202	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.339055	0.411911	-3.927143	21830.050800
HLA A*0206	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.432632	0.505350	-3.927282	27078.985175
HLA B*1501	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.339306	0.411911	-3.927395	21842.690960
HLA B*1502	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.535194	0.607629	-3.927566	34292.129356
HLA A*6801	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.554860	0.627189	-3.927671	35880.595538
HLA A*0202	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.534962	0.607235	-3.927727	34273.768128
HLA A*0219	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.422692	0.494882	-3.927810	26466.207520
HLA B*4002	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.608278	0.680376	-3.927901	40576.775652
HLA A*2601	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.331915	0.403979	-3.927935	21474.084683
HLA A*6901	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.380859	0.452913	-3.927946	24035.830515
HLA A*0101	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.391913	0.463883	-3.928031	24655.479886
HLA B*4403	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.654309	0.726094	-3.928215	45113.720434
HLA B*4001	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.361605	0.433361	-3.928244	22993.501065
HLA B*0802	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.436819	0.508560	-3.928259	27341.300415
HLA B*5301	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.584503	0.656026	-3.928477	38415.199686
HLA B*5301	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.556016	0.627429	-3.928587	35976.224890
HLA B*4501	1:178-186	9	YHPEVMHTP	0.715400	0.010694	-4.654729	0.726094	-3.928635	45157.428374
HLA B*1517	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.440376	0.511716	-3.928660	27566.160920
HLA B*4403	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.537889	0.609194	-3.928696	34505.578473
HLA B*7301	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.584726	0.656026	-3.928700	38434.947847
HLA B*0802	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.460974	0.532233	-3.928741	28905.083086
HLA B*1509	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.496412	0.567535	-3.928876	31362.559941
HLA B*0803	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.434232	0.505350	-3.928882	27178.931794
HLA B*1801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.443682	0.514746	-3.928936	27776.787250
HLA B*4402	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.434392	0.505350	-3.929042	27188.932014
HLA B*0802	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.484126	0.554890	-3.929236	30487.797226
HLA B*4501	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.644746	0.715416	-3.929330	44131.251131
HLA A*2301	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.542931	0.613596	-3.929335	34908.509613
HLA A*2301	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.535958	0.606435	-3.929523	34352.475292
HLA B*3801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.574245	0.644580	-3.929665	37518.480707
HLA A*6801	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.569605	0.639875	-3.929730	37119.747268
HLA B*4501	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.396359	0.466612	-3.929746	24909.137245
HLA B*1509	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.557214	0.627429	-3.929785	36075.621916
HLA B*4403	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.610183	0.680376	-3.929807	40755.194125
HLA A*1101	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.478130	0.548275	-3.929856	30069.773830
HLA B*2705	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.435212	0.505350	-3.929862	27240.314604
HLA A*2902	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.396674	0.466612	-3.930061	24927.201052
HLA A*2301	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.537762	0.607629	-3.930134	34495.499692
HLA B*4402	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.447051	0.516757	-3.930294	27993.111497
HLA A*2902	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.409358	0.479051	-3.930307	25666.011591
HLA A*0250	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.497854	0.567351	-3.930503	31466.909287
HLA A*2403	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.363884	0.433361	-3.930523	23114.478731
HLA B*1502	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.461103	0.530534	-3.930569	28913.684897
HLA A*2601	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.388269	0.457680	-3.930589	24449.467719
HLA A*6801	1:171-179	9	RRLAGVQYH	0.806427	-0.088110	-4.648907	0.718317	-3.930590	44556.100813
HLA A*0101	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.397209	0.466612	-3.930597	24957.966596
HLA A*0301	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.361589	0.430602	-3.930986	22992.630335
HLA A*0201	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.394998	0.463883	-3.931116	24831.235782
HLA B*5101	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.417556	0.486297	-3.931259	26155.061120
HLA B*1517	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.508777	0.577199	-3.931578	32268.356318
HLA B*1801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.539341	0.607629	-3.931713	34621.134432

HLA B*5401	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.389649	0.457680	-3.931968	24527.232979
HLA A*2601	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.398602	0.466612	-3.931990	25038.161924
HLA B*3501	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.069035	0.136752	-3.932283	11722.911422
HLA B*1502	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.567615	0.635184	-3.932431	36950.047143
HLA B*3501	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.391364	0.458831	-3.932532	24624.287915
HLA B*1801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.427522	0.494882	-3.932641	26762.227277
HLA B*4801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.385589	0.452913	-3.932676	24299.013723
HLA B*0801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.390532	0.457680	-3.932852	24577.175050
HLA A*2301	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.500286	0.567351	-3.932935	31643.594104
HLA B*4403	1:395-403	9	EIVARQPFP	0.755227	-0.028036	-4.660166	0.727191	-3.932975	45726.284071
HLA A*0203	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.379588	0.446544	-3.933044	23965.586490
HLA A*2403	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.412096	0.479051	-3.933044	25828.282986
HLA A*3301	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.624007	0.690895	-3.933112	42073.373512
HLA B*4001	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.373743	0.440475	-3.933267	23645.175561
HLA A*0202	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.463819	0.530534	-3.933285	29095.072814
HLA B*5301	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.579374	0.645964	-3.933410	37964.192712
HLA A*6901	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.380255	0.446544	-3.933711	24002.435722
HLA B*5801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.352994	0.419078	-3.933916	22542.093191
HLA B*5301	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.543272	0.609194	-3.934078	34935.903775
HLA B*4402	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.423589	0.489404	-3.934186	26520.958547
HLA A*0212	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.391874	0.457680	-3.934193	24653.212473
HLA A*6801	1:50-58	9	IEEIRARQP	0.785296	-0.044409	-4.675080	0.740887	-3.934194	47323.890504
HLA B*2705	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.423648	0.489404	-3.934244	26524.545675
HLA B*3801	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.482519	0.548275	-3.934244	30375.189746
HLA A*3101	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.387168	0.452913	-3.934255	24387.512231
HLA B*2705	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.413416	0.479051	-3.934365	25906.929702
HLA A*6802	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.393241	0.458831	-3.934410	24730.956807
HLA A*2301	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.535248	0.600770	-3.934478	34296.396503
HLA B*4402	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.278769	0.344156	-3.934613	19000.687299
HLA B*2705	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-3.993194	0.058419	-3.934775	9844.510072
HLA A*2501	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.446551	0.511716	-3.934835	27960.873433
HLA A*0250	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.587729	0.652880	-3.934849	38701.601601
HLA A*2902	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.055841	0.120764	-3.935077	11372.102769
HLA A*3101	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.381651	0.446544	-3.935107	24079.690991
HLA A*8001	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.432235	0.496961	-3.935274	27054.238951
HLA A*8001	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.465915	0.530534	-3.935381	29235.813920
HLA B*1501	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.417041	0.481648	-3.935393	26124.091849
HLA B*7301	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.562841	0.627429	-3.935412	36546.083597
HLA B*5701	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.394395	0.458831	-3.935563	24796.735873
HLA A*2602	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.388490	0.452913	-3.935577	24461.904158
HLA B*1502	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.562768	0.627189	-3.935580	36539.955093
HLA A*3002	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.432555	0.496961	-3.935593	27074.151294
HLA A*2501	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.440959	0.505350	-3.935609	27603.169950
HLA A*3002	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.221898	0.286262	-3.935635	16668.544419
HLA B*1517	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.484039	0.548275	-3.935765	30481.695219
HLA B*1517	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.394766	0.458831	-3.935934	24817.940253
HLA A*3001	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.283330	0.347374	-3.935956	19201.257025
HLA B*3501	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.339938	0.403979	-3.935959	21874.500899
HLA A*2602	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.466521	0.530534	-3.935987	29276.648339
HLA A*6802	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.400193	0.463883	-3.936310	25130.032200
HLA A*2402	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.542764	0.606435	-3.936330	34895.103755
HLA B*1509	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.549968	0.613596	-3.936372	35478.725882
HLA A*2603	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.592454	0.656026	-3.936428	39124.946102
HLA B*1503	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.057269	0.120764	-3.936506	11409.569617
HLA B*0801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.367263	0.430602	-3.936660	23294.997237
HLA B*0702	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.415747	0.479051	-3.936696	26046.335825
HLA A*3201	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.532302	0.595477	-3.936825	34064.517140
HLA B*5101	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.485118	0.548275	-3.936843	30557.479562
HLA B*3801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.510414	0.573435	-3.936979	32390.260061
HLA A*3301	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.581592	0.644580	-3.937012	38158.569301
HLA B*1502	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.589928	0.652880	-3.937048	38898.070212
HLA B*4403	1:474-482	9	PVSSEDAMT	1.132463	-0.399760	-4.669806	0.732703	-3.937103	46752.608525
HLA A*2902	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.445764	0.508560	-3.937204	27910.245473
HLA B*4002	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.638555	0.701295	-3.937261	43506.620244
HLA B*4801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.426763	0.489404	-3.937360	26715.503951

HLA A*0216	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.137490	0.200115	-3.937375	13724.296074
HLA A*0203	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.401349	0.463883	-3.937466	25197.009034
HLA B*0702	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.404140	0.466612	-3.937528	25359.470414
HLA B*4501	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.610566	0.673013	-3.937553	40791.148391
HLA A*0206	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.384111	0.446544	-3.937566	24216.469068
HLA A*0101	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.419233	0.481648	-3.937585	26256.284620
HLA A*0211	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.514801	0.577199	-3.937602	32719.067935
HLA B*5801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.341595	0.403979	-3.937615	21958.088929
HLA A*0219	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.442970	0.505350	-3.937620	27731.292938
HLA B*0702	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.390640	0.452913	-3.937727	24583.291962
HLA A*0201	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.391084	0.453330	-3.937754	24608.440471
HLA A*0202	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.551469	0.613596	-3.937873	35601.585204
HLA B*0801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.378380	0.440475	-3.937905	23899.038359
HLA B*1501	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.401805	0.463883	-3.937922	25223.467643
HLA B*7301	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.495483	0.557541	-3.937942	31295.612647
HLA B*2705	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.468547	0.530534	-3.938013	29413.493678
HLA A*2301	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.545250	0.607235	-3.938016	35095.404238
HLA A*0212	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.396880	0.458831	-3.938049	24939.070976
HLA B*0803	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.449795	0.511716	-3.938079	28170.552998
HLA A*2402	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.565707	0.627429	-3.938279	36788.087859
HLA A*0219	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.404939	0.466612	-3.938327	25406.158594
HLA B*4601	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.343197	0.404390	-3.938807	22039.253912
HLA B*5701	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.425163	0.486297	-3.938867	26617.261521
HLA A*3001	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.283067	0.344171	-3.938895	19189.626362
HLA B*3501	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.444272	0.505350	-3.938921	27814.530474
HLA A*2902	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.402888	0.463883	-3.939005	25286.452442
HLA B*3801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.566544	0.627429	-3.939115	36859.007063
HLA A*2601	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.379691	0.440475	-3.939216	23971.291821
HLA B*1501	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.392158	0.452913	-3.939245	24669.355664
HLA B*5701	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.420955	0.481648	-3.939307	26360.609281
HLA B*0801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.314157	0.374749	-3.939408	20613.761822
HLA A*0250	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.540232	0.600770	-3.939462	34692.192628
HLA B*1502	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.566908	0.627429	-3.939479	36889.927512
HLA B*0802	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.454417	0.514746	-3.939671	28471.923587
HLA B*5301	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.587816	0.647881	-3.939935	38709.349117
HLA B*1501	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.380490	0.440475	-3.940015	24015.424287
HLA A*8001	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.398924	0.458831	-3.940093	25056.725956
HLA B*1517	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.435055	0.494882	-3.940173	27230.442798
HLA B*5301	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.606950	0.666703	-3.940247	40452.938548
HLA B*4501	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.641563	0.701295	-3.940268	43808.934217
HLA B*4001	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.393234	0.452913	-3.940321	24730.555435
HLA A*3002	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.407143	0.466612	-3.940530	25535.409198
HLA A*2601	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.371184	0.430602	-3.940582	23506.282636
HLA B*5701	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.419708	0.479051	-3.940657	26284.993109
HLA A*2301	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.536090	0.595350	-3.940740	34362.884081
HLA A*8001	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.456858	0.516095	-3.940763	28632.411323
HLA B*1517	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.404678	0.463883	-3.940796	25390.906834
HLA A*3301	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.352712	0.411911	-3.940801	22527.463913
HLA A*0203	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.437858	0.496961	-3.940896	27406.756367
HLA B*5301	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.574412	0.633434	-3.940978	37532.894403
HLA A*2603	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.627297	0.686294	-3.941003	42393.240496
HLA A*8001	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.430457	0.489404	-3.941053	26943.670662
HLA A*2602	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.498940	0.557541	-3.941398	31545.655064
HLA A*0219	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.472068	0.530534	-3.941534	29652.989940
HLA B*3501	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.394538	0.452913	-3.941625	24804.920226
HLA B*4601	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.346033	0.403979	-3.942053	22183.635299
HLA A*2601	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.388829	0.446544	-3.942284	24480.967994
HLA B*1517	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.458528	0.516095	-3.942434	28742.756003
HLA B*5401	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.549681	0.607235	-3.942447	35455.317419
HLA A*2403	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.346474	0.403979	-3.942495	22206.208846
HLA B*5701	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.406414	0.463883	-3.942532	25492.620531
HLA A*0212	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.389167	0.446544	-3.942623	24500.046687
HLA A*8001	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.409318	0.466612	-3.942706	25663.651245
HLA A*2403	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.401720	0.458831	-3.942889	25218.555699
HLA B*3501	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.290263	0.347374	-3.942889	19510.257049

HLA A*8001	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.422151	0.479051	-3.943100	26433.296772
HLA A*3101	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.376616	0.433361	-3.943255	23802.137685
HLA A*3301	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.473805	0.530534	-3.943271	29771.777160
HLA A*0201	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.396359	0.452913	-3.943446	24909.137245
HLA B*5801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.350969	0.407463	-3.943506	22437.216823
HLA A*0219	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.440649	0.496961	-3.943687	27583.465415
HLA B*4402	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.396662	0.452913	-3.943749	24926.526794
HLA B*5401	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.539409	0.595477	-3.943932	34626.566457
HLA A*0201	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.390494	0.446544	-3.943950	24575.047785
HLA A*3002	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.557594	0.613596	-3.943999	36107.252523
HLA A*1101	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.474552	0.530534	-3.944018	29823.038962
HLA A*1101	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.460133	0.516095	-3.944038	28849.155623
HLA B*1503	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.499001	0.554890	-3.944111	31550.092497
HLA B*1801	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.517705	0.573435	-3.944270	32938.581090
HLA A*2403	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.384752	0.440475	-3.944277	24252.260789
HLA B*4402	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.439199	0.494882	-3.944317	27491.548012
HLA A*2402	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.597200	0.652880	-3.944320	39554.847273
HLA B*3801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.553530	0.609194	-3.944336	35770.897287
HLA A*0203	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.303704	0.359286	-3.944418	20123.540634
HLA B*4402	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.402171	0.457680	-3.944491	25244.763789
HLA B*0702	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.303937	0.359286	-3.944651	20134.321267
HLA B*4403	1:427-435	9	DSIVREELT	1.031041	-0.329746	-4.645989	0.701295	-3.944695	44257.728221
HLA A*2603	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.625297	0.680376	-3.944921	42198.518407
HLA A*1101	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.288231	0.343210	-3.945021	19419.171033
HLA B*4601	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.402742	0.457680	-3.945062	25277.972456
HLA A*6801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.378540	0.433361	-3.945179	23907.831774
HLA B*1501	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.180481	0.235291	-3.945190	15152.383552
HLA A*0101	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.248663	0.303325	-3.945338	17728.133352
HLA A*3002	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.554568	0.609194	-3.945375	35856.533964
HLA B*4801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.349902	0.404390	-3.945513	22382.176626
HLA B*2705	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.378886	0.433361	-3.945524	23926.852128
HLA A*2902	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.386000	0.440475	-3.945525	24322.029235
HLA B*7301	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.546369	0.600770	-3.945598	35185.895130
HLA A*0212	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.386101	0.440475	-3.945626	24327.687811
HLA B*5701	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.231951	0.286262	-3.945689	17058.903915
HLA A*0216	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.431998	0.486297	-3.945701	27039.460585
HLA A*6801	1:129-137	9	SDLPEVQPV	0.693212	0.022372	-4.661303	0.715584	-3.945720	45846.170034
HLA A*3301	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.593659	0.647881	-3.945778	39233.679326
HLA B*4001	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.409683	0.463883	-3.945800	25685.180083
HLA A*3001	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.249149	0.303325	-3.945824	17747.997270
HLA A*2602	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.573106	0.627189	-3.945917	37420.168890
HLA B*5101	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.462685	0.516757	-3.945928	29019.147313
HLA A*0301	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.357961	0.411911	-3.946050	22801.375784
HLA A*2402	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.559700	0.613596	-3.946104	36282.698661
HLA B*4601	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.399025	0.452913	-3.946112	25062.555461
HLA B*4001	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.365207	0.419078	-3.946129	23184.987383
HLA B*2705	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.501115	0.554890	-3.946226	31704.081324
HLA B*0803	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.494988	0.548275	-3.946713	31259.909506
HLA B*3501	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.441723	0.494882	-3.946841	27651.744919
HLA B*0702	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.351063	0.403979	-3.947083	22442.072663
HLA B*5301	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.560684	0.613596	-3.947088	36365.035517
HLA B*1502	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.502374	0.555251	-3.947124	31796.147084
HLA A*0219	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.426199	0.479051	-3.947148	26680.839760
HLA B*5801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.322002	0.374749	-3.947253	20989.504398
HLA A*2403	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.458982	0.511716	-3.947266	28772.782235
HLA A*2402	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.587146	0.639875	-3.947271	38649.712316
HLA B*5401	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.553708	0.606435	-3.947274	35785.607572
HLA B*4601	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.428967	0.481648	-3.947319	26851.415683
HLA A*0203	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.331809	0.384476	-3.947332	21468.857561
HLA A*0211	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.433694	0.486297	-3.947398	27145.281625
HLA A*3001	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.291583	0.344156	-3.947427	19569.665475
HLA B*7301	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.595398	0.647881	-3.947517	39391.059030
HLA B*0803	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.479770	0.532233	-3.947537	30183.535033
HLA A*6901	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.351528	0.403979	-3.947549	22466.124549
HLA A*3101	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.359498	0.411911	-3.947586	22882.191472

HLA A*0202	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.459341	0.511716	-3.947625	28796.607701
HLA A*2301	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.524977	0.577199	-3.947777	33494.734759
HLA A*0301	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.366882	0.419078	-3.947804	23274.590398
HLA A*0250	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.543427	0.595477	-3.947950	34948.379961
HLA B*3901	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.502943	0.554890	-3.948054	31837.801644
HLA B*1509	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.525367	0.577199	-3.948167	33524.827935
HLA A*0202	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.332410	0.384129	-3.948282	21498.611059
HLA A*1101	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.465065	0.516757	-3.948308	29178.615118
HLA A*3201	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.427414	0.479051	-3.948363	26755.568194
HLA B*1503	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.360327	0.411911	-3.948416	22925.931136
HLA B*5701	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.280113	0.331684	-3.948429	19059.575167
HLA B*1517	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.437844	0.489404	-3.948440	27405.866776
HLA A*0250	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.588328	0.639875	-3.948453	38755.028144
HLA A*0211	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.454031	0.505350	-3.948681	28446.673877
HLA B*4801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.430356	0.481648	-3.948708	26937.403613
HLA A*3101	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.367862	0.419078	-3.948784	23327.155368
HLA B*4402	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.389287	0.440475	-3.948812	24506.807289
HLA A*0101	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.395405	0.446544	-3.948860	24854.486483
HLA A*0212	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.401828	0.452913	-3.948915	25224.832241
HLA A*0216	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.497241	0.548275	-3.948966	31422.509960
HLA A*2603	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.435388	0.486297	-3.949091	27251.369377
HLA A*2601	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.361114	0.411911	-3.949203	22967.517768
HLA A*3301	1:68-76	9	ASVYADGAP	0.585654	0.094722	-4.629731	0.680376	-3.949355	42631.506640
HLA B*1502	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.454720	0.505350	-3.949370	28491.800385
HLA A*1101	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.517038	0.567535	-3.949502	32888.012830
HLA B*5101	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.464350	0.514746	-3.949604	29130.667222
HLA A*0219	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.439037	0.489404	-3.949633	27481.287818
HLA B*1501	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.235959	0.286262	-3.949697	17217.073935
HLA A*3201	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.585220	0.635184	-3.950036	38478.637709
HLA B*4601	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.409034	0.458831	-3.950203	25646.857403
HLA A*6802	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.416982	0.466612	-3.950370	26120.558877
HLA A*0203	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.403713	0.453330	-3.950383	25334.513773
HLA A*3301	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.617194	0.666703	-3.950491	41418.448766
HLA B*1501	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.369748	0.419078	-3.950670	23428.712249
HLA B*5701	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.391150	0.440475	-3.950675	24612.168364
HLA B*4002	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.505798	0.554890	-3.950908	32047.761279
HLA B*3501	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.404619	0.453330	-3.951289	25387.473016
HLA B*1501	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.319998	0.368545	-3.951453	20892.868628
HLA A*2902	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.437872	0.486297	-3.951575	27407.645986
HLA B*5301	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.596180	0.644580	-3.951600	39462.085708
HLA A*3101	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.433513	0.481648	-3.951865	27133.976302
HLA B*1501	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.295122	0.343210	-3.951912	19729.756544
HLA B*4403	1:94-102	9	YGFQAMAQA	0.983188	-0.310175	-4.624966	0.673013	-3.951953	42166.341889
HLA B*4001	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.409661	0.457680	-3.951981	25683.929528
HLA B*3801	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.547696	0.595350	-3.952346	35293.608426
HLA B*2705	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.297838	0.345470	-3.952368	19853.529748
HLA B*2705	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.469195	0.516757	-3.952438	29457.444634
HLA B*5101	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.507334	0.554890	-3.952445	32161.349244
HLA B*5101	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.410232	0.457680	-3.952552	25717.715904
HLA B*7301	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.604483	0.651841	-3.952642	40223.801748
HLA A*6802	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.405642	0.452913	-3.952729	25447.287755
HLA A*6801	1:364-372	9	PDDLKFTLV	0.990529	-0.262297	-4.681048	0.728232	-3.952816	47978.662031
HLA A*3301	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.520560	0.567535	-3.953024	33155.799997
HLA B*5301	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.604866	0.651841	-3.953025	40259.287219
HLA B*1509	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.510663	0.557541	-3.953122	32408.839526
HLA A*2402	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.586648	0.633434	-3.953214	38605.410506
HLA B*5101	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.485609	0.532233	-3.953375	30592.049430
HLA A*0216	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.469627	0.516095	-3.953533	29486.781751
HLA B*0803	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.521208	0.567535	-3.953673	33205.342874
HLA B*5701	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.411590	0.457680	-3.953910	25798.258899
HLA A*2602	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.563118	0.609194	-3.953925	36569.420856
HLA A*2601	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.235471	0.281539	-3.953932	17197.711199
HLA B*4002	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.640381	0.686294	-3.954087	43689.884524
HLA B*1509	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.560595	0.606435	-3.954160	36357.560515
HLA B*4403	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.436053	0.481648	-3.954405	27293.123141

HLA A*0216	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.412110	0.457680	-3.954430	25829.121369
HLA B*0802	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.470562	0.516095	-3.954468	29550.339198
HLA B*4402	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.418392	0.463883	-3.954510	26205.482227
HLA B*3901	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.459875	0.505350	-3.954524	28831.992949
HLA B*4801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.433612	0.479051	-3.954561	27140.142258
HLA B*5401	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.010608	0.055954	-3.954655	10247.277341
HLA B*0802	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.449537	0.494882	-3.954655	28153.794033
HLA B*4501	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.641013	0.686294	-3.954719	43753.510959
HLA A*0101	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.358826	0.403979	-3.954846	22846.814873
HLA A*3201	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.582431	0.627429	-3.955002	38232.337319
HLA A*3101	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.323574	0.368545	-3.955029	21065.607579
HLA B*3901	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.183296	0.228245	-3.955051	15250.905784
HLA B*1501	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.329842	0.374749	-3.955093	21371.864677
HLA A*2402	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.562794	0.607629	-3.955165	36542.129606
HLA A*3301	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.441664	0.486297	-3.955367	27648.005350
HLA A*2501	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.472252	0.516757	-3.955495	29665.505293
HLA B*5401	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.328639	0.373125	-3.955515	21312.749443
HLA A*0250	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.583108	0.627429	-3.955679	38291.951568
HLA B*5801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.367827	0.411911	-3.955915	23325.262485
HLA B*5401	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.563762	0.607629	-3.956133	36623.668256
HLA B*4403	1:128-136	9	HSDLPEVQP	0.749144	-0.033728	-4.671584	0.715416	-3.956168	46944.466420
HLA B*4001	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.034597	0.078424	-3.956173	10829.208920
HLA B*1509	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.464959	0.508560	-3.956399	29171.512594
HLA B*0803	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.423756	0.466612	-3.957144	26531.147260
HLA B*5301	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.597127	0.639875	-3.957252	39548.214222
HLA A*0101	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.361692	0.404390	-3.957303	22998.104040
HLA B*4801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.416137	0.458831	-3.957305	26069.737024
HLA B*1501	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.302899	0.345470	-3.957429	20086.234177
HLA B*1501	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.388107	0.430602	-3.957505	24440.342867
HLA A*6801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.421768	0.463883	-3.957886	26409.997849
HLA A*0301	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.365369	0.407463	-3.957906	23193.643545
HLA A*2301	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.506300	0.548275	-3.958026	32084.884979
HLA A*0216	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.488677	0.530534	-3.958143	30808.957261
HLA A*2602	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.591930	0.633434	-3.958495	39077.774021
HLA B*1509	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.470278	0.511716	-3.958562	29531.001977
HLA A*0216	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.448104	0.489404	-3.958700	28061.038733
HLA A*2403	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.416522	0.457680	-3.958842	26092.876927
HLA B*0801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.417690	0.458831	-3.958858	26163.127634
HLA A*6801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.473772	0.514746	-3.959026	29769.522378
HLA A*3201	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.554535	0.595350	-3.959186	35853.818349
HLA A*2501	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.514178	0.554890	-3.959289	32672.194812
HLA B*5801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.318976	0.359286	-3.959690	20843.759211
HLA B*1501	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.145582	0.185815	-3.959767	13982.399448
HLA A*2403	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.413118	0.453330	-3.959788	25889.136306
HLA A*3001	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.230734	0.270903	-3.959831	17011.166283
HLA A*3002	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.490458	0.530534	-3.959924	30935.554820
HLA A*3001	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.151235	0.191274	-3.959961	14165.586676
HLA A*2301	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.515287	0.555251	-3.960037	32755.728810
HLA B*0803	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.514930	0.554890	-3.960041	32728.804743
HLA A*0202	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.449539	0.489404	-3.960136	28153.946342
HLA B*3901	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.393518	0.433361	-3.960157	24746.749272
HLA A*0212	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.441927	0.481648	-3.960279	27664.762562
HLA B*5401	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.472052	0.511716	-3.960336	29651.867026
HLA A*3201	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.613296	0.652880	-3.960416	41048.381100
HLA B*0802	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.424320	0.463883	-3.960437	26565.616968
HLA B*5401	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.517996	0.557541	-3.960455	32960.684568
HLA B*1517	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.491151	0.530534	-3.960617	30984.964823
HLA B*0802	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.477414	0.516757	-3.960657	30020.199127
HLA B*3501	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.098399	0.137730	-3.960669	12542.940065
HLA A*2402	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.518391	0.557541	-3.960850	32990.654878
HLA A*0212	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.058608	0.097746	-3.960862	11444.806887
HLA A*3002	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.475670	0.514746	-3.960924	29899.935451
HLA B*5701	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.414375	0.453330	-3.961045	25964.175532
HLA B*4801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.424987	0.463883	-3.961105	26606.463979
HLA A*2501	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.407751	0.446544	-3.961207	25571.213503

HLA A*0211	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.478074	0.516757	-3.961317	30065.869904
HLA A*0216	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.308765	0.347374	-3.961391	20359.409876
HLA B*4002	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.617502	0.656026	-3.961475	41447.812237
HLA A*2402	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.529342	0.567535	-3.961806	33833.107305
HLA A*2501	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.476666	0.514746	-3.961920	29968.598433
HLA A*0202	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.539360	0.577199	-3.962161	34622.632837
HLA B*4402	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.381275	0.419078	-3.962197	24058.857056
HLA B*7301	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.557750	0.595350	-3.962400	36120.147016
HLA A*6801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.331045	0.368545	-3.962500	21431.143879
HLA A*2501	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.457455	0.494882	-3.962573	28671.782503
HLA B*1801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.053942	0.091322	-3.962621	11322.501629
HLA A*0101	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.381745	0.419078	-3.962667	24084.902293
HLA A*3001	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.296938	0.334057	-3.962880	19812.436070
HLA B*1509	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.570599	0.607629	-3.962970	37204.788737
HLA B*5401	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.477728	0.514746	-3.962982	30041.969414
HLA B*4001	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.416329	0.453330	-3.962999	26081.304410
HLA A*0101	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.370517	0.407463	-3.963053	23470.195113
HLA B*5701	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.409629	0.446544	-3.963084	25681.984341
HLA A*2501	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.393755	0.430602	-3.963153	24760.274561
HLA B*1801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.416531	0.453330	-3.963201	26093.441572
HLA B*3801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.530644	0.567351	-3.963292	33934.659890
HLA A*0219	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.427177	0.463883	-3.963294	26740.952977
HLA B*2705	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.367864	0.404390	-3.963475	23327.281566
HLA A*6901	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.174490	0.210953	-3.963536	14944.788331
HLA A*3301	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.609628	0.645964	-3.963664	40703.193792
HLA A*6801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.368231	0.404390	-3.963841	23346.976765
HLA B*1517	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.421693	0.457680	-3.964013	26405.426240
HLA A*3001	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.303542	0.339229	-3.964314	20116.030273
HLA A*3002	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.262424	0.298081	-3.964343	18298.856167
HLA B*0802	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.461503	0.496961	-3.964541	28940.288500
HLA B*7301	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.578141	0.613596	-3.964545	37856.520101
HLA B*5801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.341486	0.376904	-3.964583	21952.625231
HLA B*0803	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.480686	0.516095	-3.964592	30247.285197
HLA B*1503	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.532220	0.567535	-3.964685	34058.067766
HLA B*0801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.369086	0.404390	-3.964696	23392.996920
HLA B*2705	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.461916	0.496961	-3.964955	28967.856843
HLA A*6802	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.446678	0.481648	-3.965030	27969.042949
HLA B*3501	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.246687	0.281539	-3.965148	17647.658574
HLA B*1801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.395753	0.430602	-3.965150	24874.394534
HLA B*5801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.354629	0.389429	-3.965200	22627.130542
HLA B*3801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.571727	0.606435	-3.965292	37301.525699
HLA A*1101	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.477118	0.511716	-3.965401	29999.742950
HLA B*4001	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.377422	0.411911	-3.965511	23846.345744
HLA B*4002	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.618545	0.652880	-3.965665	41547.489164
HLA B*4402	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.424599	0.458831	-3.965768	26582.724802
HLA A*0203	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.447530	0.481648	-3.965882	28024.022235
HLA B*1503	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.310071	0.344171	-3.965900	20420.741105
HLA A*0212	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.429865	0.463883	-3.965982	26906.963596
HLA B*4403	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.432602	0.466612	-3.965989	27077.080816
HLA A*2501	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.462988	0.496961	-3.966026	29039.406139
HLA A*0301	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.340944	0.374749	-3.966194	21925.208513
HLA A*2402	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.566967	0.600770	-3.966196	36894.917110
HLA A*0211	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.539701	0.573435	-3.966266	34649.802660
HLA B*3801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.579884	0.613596	-3.966288	38008.786792
HLA A*2603	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.619240	0.652880	-3.966361	41614.073585
HLA A*2602	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.580020	0.613596	-3.966424	38020.714816
HLA A*0202	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.309738	0.343210	-3.966528	20405.059829
HLA A*8001	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.407166	0.440475	-3.966691	25536.790673
HLA B*5701	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.419771	0.452913	-3.966858	26288.832759
HLA A*2602	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.619821	0.652880	-3.966941	41669.717252
HLA A*3002	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.534302	0.567351	-3.966951	34221.705453
HLA A*2403	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.448630	0.481648	-3.966982	28095.064137
HLA A*8001	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.419926	0.452913	-3.967013	26298.220934
HLA B*7301	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.311270	0.344171	-3.967099	20477.160613
HLA A*2501	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.475854	0.508560	-3.967294	29912.555030

HLA A*0101	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.379337	0.411911	-3.967425	23951.717830
HLA B*0802	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.479307	0.511716	-3.967591	30151.384122
HLA A*0301	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.336163	0.368545	-3.967618	21685.154979
HLA B*1501	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.238610	0.270903	-3.967707	17322.459855
HLA B*0801	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.299433	0.331684	-3.967749	19926.592120
HLA A*2602	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.563247	0.595477	-3.967770	36580.303483
HLA A*6901	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.375293	0.407463	-3.967830	23729.752196
HLA B*0702	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.454208	0.486297	-3.967911	28458.218221
HLA B*3801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.575627	0.607629	-3.967998	37638.017573
HLA A*1101	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.454436	0.486297	-3.968139	28473.155853
HLA A*0101	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.352388	0.384129	-3.968259	22510.651980
HLA B*1517	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.305173	0.336669	-3.968504	20191.697121
HLA B*5101	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.480228	0.511716	-3.968512	30215.393302
HLA B*1502	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.577798	0.609194	-3.968604	37826.631168
HLA A*1101	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.300483	0.331684	-3.968799	19974.837323
HLA A*2301	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.536470	0.567535	-3.968935	34393.012983
HLA A*2402	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.546150	0.577199	-3.968951	35168.196865
HLA B*1517	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.402385	0.433361	-3.969024	25257.194844
HLA A*0203	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.421985	0.452913	-3.969072	26423.145636
HLA B*5801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.353622	0.384476	-3.969145	22574.677428
HLA B*3801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.501900	0.532233	-3.969666	31761.419309
HLA B*5701	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.344440	0.374749	-3.969690	22102.416878
HLA A*0206	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.466735	0.496961	-3.969774	29291.064779
HLA A*6901	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.301501	0.331684	-3.969816	20021.682866
HLA A*6801	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.636530	0.666703	-3.969827	43304.207084
HLA A*3001	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.247989	0.278063	-3.969926	17700.629333
HLA A*2902	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.269031	0.299099	-3.969932	18579.357668
HLA A*3101	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.224346	0.254355	-3.969991	16762.772081
HLA A*0206	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.537805	0.567535	-3.970269	34498.858959
HLA A*2403	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.423312	0.452913	-3.970399	26504.033847
HLA A*3001	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.269517	0.299099	-3.970418	18600.175361
HLA B*3501	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.449471	0.479051	-3.970420	28149.529707
HLA A*2902	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.423479	0.452913	-3.970566	26514.216058
HLA B*0802	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.437193	0.466612	-3.970580	27364.828764
HLA B*0702	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.401255	0.430602	-3.970653	25191.557103
HLA B*5301	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.571435	0.600770	-3.970665	37276.511247
HLA A*6901	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.389766	0.419078	-3.970688	24533.868357
HLA A*2602	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.615382	0.644580	-3.970802	41246.051188
HLA B*0801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.452542	0.481648	-3.970894	28349.272624
HLA A*2603	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.598156	0.627189	-3.970967	39642.036072
HLA B*1509	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.503660	0.532233	-3.971426	31890.377896
HLA A*6901	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.262034	0.290570	-3.971464	18282.430410
HLA B*1502	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.572239	0.600770	-3.971469	37345.543422
HLA B*4801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.429402	0.457680	-3.971722	26878.302825
HLA B*0801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.418493	0.446544	-3.971949	26211.578992
HLA A*2902	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.429750	0.457680	-3.972070	26899.831921
HLA A*2603	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.618080	0.645964	-3.972115	41503.009063
HLA A*2602	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.504581	0.532233	-3.972347	31958.078833
HLA B*4402	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.419036	0.446544	-3.972492	26244.355669
HLA B*4403	1:102-110	9	ALGGIVAHT	0.983470	-0.327444	-4.628605	0.656026	-3.972579	42521.177056
HLA B*5701	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.391676	0.419078	-3.972598	24642.011841
HLA A*6801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.540328	0.567535	-3.972793	34699.888399
HLA B*1509	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.200466	0.227657	-3.972809	15865.935139
HLA A*3201	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.606255	0.633434	-3.972820	40388.211995
HLA B*4002	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.608073	0.635184	-3.972889	40557.682265
HLA B*1801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.462344	0.489404	-3.972940	28996.392635
HLA B*1501	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.086826	0.113627	-3.973199	12213.096368
HLA B*0802	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.459760	0.486297	-3.973463	28824.351046
HLA A*3002	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.479009	0.505350	-3.973658	30130.675549
HLA B*4402	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.427029	0.453330	-3.973699	26731.840598
HLA A*3301	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.613583	0.639875	-3.973708	41075.482240
HLA A*2402	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.582929	0.609194	-3.973735	38276.211008
HLA B*0702	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.414652	0.440475	-3.974177	25980.755494
HLA B*1801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-3.895211	-0.079025	-3.974236	7856.175653
HLA B*4501	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.529137	0.554890	-3.974248	33817.187149

HLA A*2602	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.614358	0.639875	-3.974483	41148.878292
HLA A*3001	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.259976	0.285427	-3.974549	18195.993798
HLA B*3801	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.542184	0.567535	-3.974649	34848.506570
HLA A*0219	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.322113	0.347374	-3.974739	20994.841969
HLA A*6801	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.570242	0.595477	-3.974765	37174.207697
HLA A*3201	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-3.677813	-0.297084	-3.974897	4762.262581
HLA B*3801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.491111	0.516095	-3.975016	30982.115326
HLA B*1501	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.364493	0.389429	-3.975063	23146.888544
HLA B*4403	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.622992	0.647881	-3.975112	41975.159815
HLA A*0212	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.387062	0.411911	-3.975150	24381.575935
HLA B*3901	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.428514	0.453330	-3.975184	26823.394520
HLA A*2402	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.530550	0.555251	-3.975299	33927.317375
HLA A*6801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.379327	0.403979	-3.975348	23951.199531
HLA B*4403	1:60-68	9	ALVLSGGPA	0.772685	-0.105982	-4.642448	0.666703	-3.975746	43898.374951
HLA A*0206	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.530723	0.554890	-3.975834	33940.902278
HLA B*4601	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.406490	0.430602	-3.975887	25497.034105
HLA A*0250	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.484619	0.508560	-3.976060	30522.453385
HLA A*1101	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.429526	0.453330	-3.976196	26886.010587
HLA A*0301	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.365656	0.389429	-3.976226	23208.956553
HLA B*5101	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.506862	0.530534	-3.976328	32126.396395
HLA B*4601	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.313058	0.336669	-3.976388	20561.637334
HLA B*0801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.162926	0.186500	-3.976426	14552.097744
HLA A*0202	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.491292	0.514746	-3.976546	30995.023969
HLA B*3801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.553791	0.577199	-3.976592	35792.384079
HLA A*2602	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.481990	0.505350	-3.976640	30338.238797
HLA A*0301	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.360872	0.384129	-3.976743	22954.723405
HLA B*0802	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.466221	0.489404	-3.976817	29256.382279
HLA A*0250	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.544369	0.567535	-3.976834	35024.278068
HLA B*4001	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.068176	0.091322	-3.976854	11699.722795
HLA B*2705	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.463159	0.486297	-3.976862	29050.876701
HLA B*1503	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.471782	0.494882	-3.976900	29633.425232
HLA B*4801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.430358	0.453330	-3.977028	26937.549342
HLA A*2602	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.628904	0.651841	-3.977062	42550.401521
HLA A*3101	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.407695	0.430602	-3.977093	25567.893620
HLA A*8001	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.463495	0.486297	-3.977198	29073.359566
HLA B*0803	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.389125	0.411911	-3.977213	24497.661037
HLA A*0202	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.361739	0.384476	-3.977263	23000.592519
HLA A*2601	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.396483	0.419078	-3.977405	24916.280320
HLA A*6901	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.231862	0.254455	-3.977407	17055.397378
HLA A*2602	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.381989	0.404390	-3.977600	24098.456958
HLA B*4403	1:287-295	9	DAAETFLEA	0.953519	-0.318335	-4.612796	0.635184	-3.977612	41001.108030
HLA B*4002	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.578437	0.600770	-3.977667	37882.333644
HLA A*2301	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.535319	0.557541	-3.977778	34301.963146
HLA A*0301	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.323316	0.345470	-3.977846	21053.075422
HLA B*5401	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.551312	0.573435	-3.977877	35588.683301
HLA A*2602	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.489645	0.511716	-3.977929	30877.703139
HLA A*2902	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.467405	0.489404	-3.978001	29336.261115
HLA A*2902	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.424618	0.446544	-3.978074	26583.875304
HLA A*3301	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.533374	0.555251	-3.978123	34148.654957
HLA A*3301	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.630043	0.651841	-3.978202	42662.191698
HLA B*3801	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.535749	0.557541	-3.978208	34335.939238
HLA B*4501	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.585450	0.607235	-3.978215	38499.043304
HLA A*2601	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.382694	0.404390	-3.978305	24137.599707
HLA A*8001	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.442192	0.463883	-3.978310	27681.679685
HLA A*1101	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.467861	0.489404	-3.978457	29367.066226
HLA A*3001	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.091830	0.113362	-3.978469	12354.642614
HLA A*2402	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.551991	0.573435	-3.978556	35644.368230
HLA A*3101	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.324063	0.345470	-3.978593	21089.325142
HLA A*2902	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.437430	0.458831	-3.978599	27379.784959
HLA A*0250	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.592209	0.613596	-3.978614	39102.939485
HLA B*0803	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.442528	0.463883	-3.978646	27703.102910
HLA A*8001	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.436347	0.457680	-3.978667	27311.585979
HLA B*1801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.494849	0.516095	-3.978754	31249.933452
HLA B*4403	1:283-291	9	LVTVDAAET	0.885383	-0.199089	-4.665072	0.686294	-3.978778	46245.729515
HLA A*3101	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.419318	0.440475	-3.978843	26261.398688

HLA B*5301	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.586129	0.607235	-3.978894	38559.282018
HLA B*4001	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.323360	0.344156	-3.979204	21055.239534
HLA A*0211	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-3.682226	-0.297084	-3.979310	4810.892700
HLA B*1503	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.468744	0.489404	-3.979340	29426.863110
HLA B*5401	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.207025	0.227657	-3.979368	16107.399735
HLA B*1501	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.386907	0.407463	-3.979443	24372.871982
HLA A*0219	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.426007	0.446544	-3.979462	26669.006473
HLA A*3101	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.352607	0.373125	-3.979482	22521.980382
HLA A*0216	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.426275	0.446544	-3.979730	26685.459052
HLA B*5301	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.535023	0.555251	-3.979772	34278.589316
HLA A*3001	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.215117	0.235291	-3.979826	16410.320497
HLA A*0201	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.398913	0.419078	-3.979835	25056.048195
HLA A*6801	1:493-501	9	LERISTRIT	1.013477	-0.322582	-4.670736	0.690895	-3.979841	46852.874754
HLA A*3201	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.586305	0.606435	-3.979871	38574.930301
HLA B*4001	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.426693	0.446544	-3.980148	26711.168465
HLA A*0250	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.587557	0.607235	-3.980323	38686.320508
HLA B*3801	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.535601	0.555251	-3.980350	34324.238754
HLA A*0206	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.191773	0.211398	-3.980374	15551.510575
HLA A*3301	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.607888	0.627429	-3.980459	40540.352376
HLA A*2403	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.444413	0.463883	-3.980530	27823.560351
HLA B*1801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.392451	0.411911	-3.980540	24686.043616
HLA B*0803	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.495399	0.514746	-3.980653	31289.518232
HLA A*6901	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.094184	0.113362	-3.980823	12421.795379
HLA A*0212	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.434225	0.453330	-3.980895	27178.490693
HLA A*3101	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.438619	0.457680	-3.980939	27454.837167
HLA B*1801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.535829	0.554890	-3.980939	34342.255443
HLA A*3002	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.554416	0.573435	-3.980981	35843.927489
HLA B*2705	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.492739	0.511716	-3.981023	31098.486929
HLA A*2402	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.588288	0.607235	-3.981054	38751.464081
HLA A*8001	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.462976	0.481648	-3.981328	29038.620650
HLA B*1503	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.340666	0.359286	-3.981381	21911.216652
HLA B*3901	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.498345	0.516757	-3.981588	31502.507999
HLA B*5301	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.577177	0.595477	-3.981700	37772.645328
HLA B*0702	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.463375	0.481648	-3.981727	29065.339206
HLA B*1503	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.284462	0.302627	-3.981835	19251.390916
HLA B*4001	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.371341	0.389429	-3.981912	23514.804328
HLA A*1101	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.358917	0.376904	-3.982014	22851.635732
HLA B*1517	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.325252	0.343210	-3.982042	21147.134230
HLA A*2601	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.341517	0.359286	-3.982231	21954.169182
HLA B*0803	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.477284	0.494882	-3.982403	30011.268128
HLA B*1501	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.326722	0.344156	-3.982566	21218.872321
HLA A*2402	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.578049	0.595350	-3.982699	37848.533760
HLA B*4403	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-3.979581	-0.003120	-3.982701	9540.720903
HLA B*4501	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.531071	0.548275	-3.982797	33968.088405
HLA B*5301	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.560054	0.577199	-3.982855	36312.349862
HLA B*4501	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.610054	0.627189	-3.982865	40743.069469
HLA A*0219	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.441697	0.458831	-3.982865	27650.099446
HLA A*0301	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.367343	0.384476	-3.982866	23299.282425
HLA A*2501	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.499081	0.516095	-3.982986	31555.896236
HLA A*2602	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.630927	0.647881	-3.983046	42749.059963
HLA B*1509	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.449798	0.466612	-3.983185	28170.705398
HLA A*3301	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.636091	0.652880	-3.983211	43260.420567
HLA A*2403	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.360285	0.376904	-3.983381	22923.698763
HLA A*0202	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.123257	0.139834	-3.983423	13281.798841
HLA B*1517	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.436800	0.453330	-3.983470	27340.117133
HLA B*5301	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.424099	0.440475	-3.983624	26552.111000
HLA B*1503	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.065220	0.081144	-3.984076	11620.369020
HLA A*3001	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.282261	0.298081	-3.984180	19154.051262
HLA A*0202	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.552090	0.567535	-3.984554	35652.468098
HLA A*6801	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.632468	0.647881	-3.984587	42901.041081
HLA A*0202	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.558057	0.573435	-3.984622	36145.754274
HLA A*6901	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.328884	0.344156	-3.984727	21324.743977
HLA A*2501	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.437855	0.452913	-3.984942	27406.608099
HLA A*6802	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.353495	0.368545	-3.984950	22568.083560
HLA A*2602	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.481920	0.496961	-3.984958	30333.315402

HLA B*5801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.369462	0.384129	-3.985333	23413.254249
HLA A*0101	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.360332	0.374749	-3.985582	22926.179190
HLA B*4601	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.393199	0.407463	-3.985735	24728.548673
HLA B*4601	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.370244	0.384476	-3.985768	23455.471080
HLA B*3901	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.482867	0.496961	-3.985905	30399.519793
HLA B*5701	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.419290	0.433361	-3.985929	26259.693888
HLA B*1501	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.370526	0.384476	-3.986050	23470.703003
HLA A*0211	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.540955	0.554890	-3.986066	34750.046536
HLA A*1101	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.285348	0.299099	-3.986249	19290.694738
HLA A*0216	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.322944	0.336669	-3.986275	21035.087732
HLA B*1801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.498042	0.511716	-3.986326	31480.530834
HLA A*3002	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.553936	0.567535	-3.986401	35804.391328
HLA B*5801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.359528	0.373125	-3.986403	22883.800800
HLA A*2603	1:151-159	9	GFDVVASSA	1.020901	-0.373020	-4.634441	0.647881	-3.986561	43096.440218
HLA B*5101	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.502776	0.516095	-3.986682	31825.575025
HLA B*0801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.332171	0.345470	-3.986701	21486.751211
HLA B*5401	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.534995	0.548275	-3.986720	34276.364068
HLA B*4402	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.288752	0.301939	-3.986813	19442.507378
HLA B*7301	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.626744	0.639875	-3.986869	42339.379199
HLA A*0211	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.517484	0.530534	-3.986950	32921.835105
HLA A*2603	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.492373	0.505350	-3.987022	31072.252659
HLA A*0206	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.503199	0.516095	-3.987105	31856.581229
HLA B*5301	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.582553	0.595350	-3.987203	38243.094133
HLA A*0101	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.364159	0.376904	-3.987255	23129.113834
HLA B*1503	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.330679	0.343210	-3.987469	21413.064852
HLA B*4601	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.360893	0.373125	-3.987768	22955.841075
HLA B*5401	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-3.872792	-0.114983	-3.987776	7460.920274
HLA A*2902	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.469580	0.481648	-3.987932	29483.591519
HLA A*3201	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.595651	0.607629	-3.988023	39414.080691
HLA B*5301	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.594733	0.606435	-3.988298	39330.797514
HLA A*0101	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.377781	0.389429	-3.988352	23866.091846
HLA B*4501	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.641307	0.652880	-3.988427	43783.108671
HLA A*3002	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.392708	0.403979	-3.988728	24700.604724
HLA B*4002	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.640712	0.651841	-3.988871	43723.223636
HLA A*0202	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.505027	0.516095	-3.988932	31990.944757
HLA A*3002	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.537213	0.548275	-3.988938	34451.858983
HLA A*0203	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.334530	0.345470	-3.989060	21603.774637
HLA B*0802	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.468234	0.479051	-3.989183	29392.337833
HLA A*3101	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.373378	0.384129	-3.989250	23625.356615
HLA A*0301	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.362402	0.373125	-3.989277	23035.708744
HLA B*1503	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.447093	0.457680	-3.989413	27995.837543
HLA A*6901	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.358149	0.368545	-3.989604	22811.246153
HLA B*1502	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.557012	0.567351	-3.989661	36058.841620
HLA A*3301	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.262227	0.272539	-3.989688	18290.542494
HLA B*7301	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.596194	0.606435	-3.989760	39463.366642
HLA A*2603	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.634394	0.644580	-3.989814	43091.777530
HLA A*0216	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.401793	0.411911	-3.989882	25222.785371
HLA A*0211	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.506068	0.516095	-3.989973	32067.705589
HLA B*7301	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.557406	0.567351	-3.990055	36091.629005
HLA B*0802	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.443071	0.452913	-3.990158	27737.744687
HLA A*0201	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.397630	0.407463	-3.990166	24982.146852
HLA B*4601	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.402096	0.411911	-3.990185	25240.393884
HLA A*2501	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.430711	0.440475	-3.990235	26959.417587
HLA B*4801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.420972	0.430602	-3.990370	26361.607556
HLA A*2301	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.545504	0.554890	-3.990614	35115.915352
HLA A*1101	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.469691	0.479051	-3.990640	29491.089112
HLA A*3201	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.506768	0.516095	-3.990673	32119.445138
HLA B*1503	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.367610	0.376904	-3.990707	23313.656162
HLA A*0211	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.338131	0.347374	-3.990758	21783.687529
HLA A*6901	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.219036	0.228245	-3.990791	16559.072362
HLA B*1517	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.359418	0.368545	-3.990873	22877.982995
HLA A*0201	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.375462	0.384129	-3.991334	23738.997020
HLA B*4501	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.592224	0.600770	-3.991453	39104.208761
HLA A*3001	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.294358	0.302627	-3.991731	19695.097888
HLA B*5701	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.364878	0.373125	-3.991753	23167.434082

HLA A*2601	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.376252	0.384129	-3.992123	23782.187177
HLA A*0211	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.540579	0.548275	-3.992305	34719.980526
HLA A*0202	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.192501	0.200115	-3.992386	15577.613360
HLA B*4501	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.587898	0.595477	-3.992421	38716.679276
HLA B*5701	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.396427	0.403979	-3.992447	24913.045466
HLA A*0203	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.339875	0.347374	-3.992501	21871.305990
HLA A*0216	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.456397	0.463883	-3.992515	28602.067372
HLA A*3002	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.396951	0.404390	-3.992561	24943.118833
HLA B*1801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.489737	0.496961	-3.992775	30884.218580
HLA B*4601	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.412175	0.419078	-3.993097	25833.034180
HLA A*0219	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.474874	0.481648	-3.993226	29845.150644
HLA B*4801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.426615	0.433361	-3.993254	26706.400243
HLA A*6901	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.295260	0.301939	-3.993322	19736.054961
HLA B*5101	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.490310	0.496961	-3.993348	30925.013067
HLA B*2705	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.457253	0.463883	-3.993370	28658.446045
HLA A*0206	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.541757	0.548275	-3.993482	34814.211622
HLA B*1503	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.332751	0.339229	-3.993522	21515.481915
HLA B*5401	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.561065	0.567535	-3.993529	36396.919878
HLA B*4001	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.397576	0.403979	-3.993596	24979.038580
HLA B*4402	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.427008	0.433361	-3.993647	26730.539083
HLA B*5701	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.424416	0.430602	-3.993814	26571.510020
HLA B*4403	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.646967	0.652880	-3.994087	44357.443016
HLA B*3901	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.505873	0.511716	-3.994157	32053.309754
HLA A*3101	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.378655	0.384476	-3.994179	23914.170211
HLA B*4402	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.219393	0.225172	-3.994221	16572.694539
HLA B*5301	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.561598	0.567351	-3.994247	36441.644384
HLA B*1801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.511225	0.516757	-3.994468	32450.770074
HLA B*1509	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.435029	0.440475	-3.994554	27228.822396
HLA B*4801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.435083	0.440475	-3.994608	27232.210620
HLA B*1509	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.480905	0.486297	-3.994608	30262.507031
HLA A*6802	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.345133	0.350403	-3.994730	22137.718669
HLA B*4001	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.402204	0.407463	-3.994741	25246.675861
HLA A*2402	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.461402	0.466612	-3.994789	28933.557041
HLA A*6801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.525327	0.530534	-3.994793	33521.744861
HLA A*2902	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.363496	0.368545	-3.994951	23093.855220
HLA A*3301	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.326694	0.331684	-3.995010	21217.494865
HLA A*3101	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.294377	0.299099	-3.995278	19695.950292
HLA A*0101	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.337532	0.342132	-3.995401	21753.657177
HLA A*8001	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.399951	0.404390	-3.995562	25116.033179
HLA B*5301	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.603254	0.607629	-3.995626	40110.154499
HLA A*6901	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.207044	0.211398	-3.995646	16108.096864
HLA A*3101	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.355045	0.359286	-3.995759	22648.807536
HLA A*0101	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.380382	0.384476	-3.995906	24009.448674
HLA A*2402	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.526525	0.530534	-3.995991	33614.360519
HLA A*6802	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.373266	0.376904	-3.996362	23619.222505
HLA B*0702	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.415509	0.419078	-3.996431	26032.108026
HLA A*2601	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.386007	0.389429	-3.996578	24322.423977
HLA A*2602	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.603835	0.607235	-3.996600	40163.787222
HLA A*3301	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.544957	0.548275	-3.996682	35071.679480
HLA A*3101	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.330909	0.334057	-3.996852	21424.420408
HLA A*6901	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.300260	0.303325	-3.996935	19964.574103
HLA B*3501	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.478741	0.481648	-3.997093	30112.098866
HLA B*1509	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.552010	0.554890	-3.997120	35645.910920
HLA B*4501	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.643163	0.645964	-3.997199	43970.629894
HLA A*2301	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.502555	0.505350	-3.997205	31809.394893
HLA B*4801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.443764	0.446544	-3.997220	27782.047175
HLA B*0702	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.443891	0.446544	-3.997347	27790.164442
HLA A*2601	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.341573	0.344156	-3.997417	21957.019838
HLA A*2501	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.486978	0.489404	-3.997575	30688.688012
HLA A*3201	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.565261	0.567535	-3.997725	36750.293585
HLA A*0219	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.450651	0.452913	-3.997738	28226.081096
HLA B*0803	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.477110	0.479051	-3.998059	29999.256068
HLA A*2501	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.464691	0.466612	-3.998079	29153.527271
HLA A*2603	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.607404	0.609194	-3.998210	40495.197867
HLA B*5801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.341425	0.343210	-3.998216	21949.537655

HLA B*4001	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.402637	0.404390	-3.998247	25271.819409
HLA A*3101	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.335004	0.336669	-3.998335	21627.396095
HLA A*2902	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.451872	0.453330	-3.998542	28305.596873
HLA B*0801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.332666	0.334057	-3.998609	21511.292053
HLA A*2601	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.346021	0.347374	-3.998647	22183.035252
HLA A*0250	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.556246	0.557541	-3.998704	35995.303431
HLA B*5801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.344186	0.345470	-3.998716	22089.506914
HLA B*1503	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.477818	0.479051	-3.998767	30048.145950
HLA A*3101	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.232816	0.233980	-3.998836	17092.899278
HLA B*0801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.417960	0.419078	-3.998882	26179.409755
HLA B*1502	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.333017	0.334057	-3.998959	21528.638726
HLA A*6901	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.388432	0.389429	-3.999002	24458.595977
HLA A*0211	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.456778	0.457680	-3.999098	28627.145270
HLA B*1801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.101144	0.101982	-3.999161	12622.446701
HLA A*2902	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.403240	0.403979	-3.999261	25306.980306
HLA A*2601	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.374144	0.374749	-3.999395	23667.059622
HLA B*2705	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.452756	0.453330	-3.999426	28363.232405
HLA A*2601	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.376451	0.376904	-3.999548	23793.125707
HLA A*8001	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.452915	0.453330	-3.999585	28373.668376
HLA A*3001	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.289530	0.289937	-3.999593	19477.353747
HLA B*7301	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.607237	0.607629	-3.999608	40479.646562
HLA A*2601	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.407408	0.407463	-3.999945	25551.024212
HLA A*2501	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.464047	0.463883	-4.000165	29110.344729
HLA A*2501	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.479488	0.479051	-4.000437	30163.946643
HLA A*3301	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.634011	0.633434	-4.000577	43053.795436
HLA A*2902	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.405024	0.404390	-4.000634	25411.107077
HLA B*1801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.334715	0.334057	-4.000658	21613.009658
HLA A*0206	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.384820	0.384129	-4.000692	24256.065946
HLA B*5801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.337373	0.336669	-4.000703	21745.656077
HLA B*3901	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.480217	0.479051	-4.001165	30214.576003
HLA B*5101	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.447918	0.446544	-4.001374	28049.048534
HLA B*1501	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.114752	0.113362	-4.001390	13024.221173
HLA A*3002	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.333104	0.331684	-4.001419	21532.948457
HLA B*4002	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.628969	0.627429	-4.001541	42556.847412
HLA A*2602	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.628998	0.627429	-4.001569	42559.610236
HLA A*3002	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.338298	0.336669	-4.001629	21792.056296
HLA B*1501	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.385986	0.384129	-4.001857	24321.239771
HLA B*4002	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.647899	0.645964	-4.001935	44452.813027
HLA A*3301	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.609572	0.607629	-4.001943	40697.909340
HLA A*2301	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.513732	0.511716	-4.002016	32638.629005
HLA A*0206	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.532565	0.530534	-4.002031	34085.163343
HLA A*2601	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.370634	0.368545	-4.002089	23476.544529
HLA A*3001	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.304047	0.301939	-4.002109	20139.441367
HLA A*6802	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.361471	0.359286	-4.002185	22986.411797
HLA A*0250	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.575704	0.573435	-4.002269	37644.737551
HLA A*1101	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.461103	0.458831	-4.002272	28913.684897
HLA B*5101	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.435663	0.433361	-4.002302	27268.623783
HLA A*0201	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.386841	0.384476	-4.002364	24369.180335
HLA B*4501	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.642258	0.639875	-4.002383	43879.142852
HLA B*5701	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.414328	0.411911	-4.002416	25961.366418
HLA A*2301	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.533136	0.530534	-4.002602	34130.001269
HLA A*0202	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.344741	0.342132	-4.002609	22117.727346
HLA B*4501	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.654586	0.651841	-4.002745	45142.528735
HLA A*0216	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.456268	0.453330	-4.002938	28593.558267
HLA B*2705	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.443419	0.440475	-4.002944	27759.962182
HLA B*4402	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.377842	0.374749	-4.003093	23869.449018
HLA B*2705	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.462074	0.458831	-4.003243	28978.358510
HLA A*0211	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.500206	0.496961	-4.003244	31637.774236
HLA B*4801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.264534	0.261282	-4.003252	18387.969768
HLA A*2902	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.337321	0.334057	-4.003263	21743.068116
HLA A*0211	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.467182	0.463883	-4.003299	29321.187926
HLA A*6901	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.376510	0.373125	-4.003385	23796.343879
HLA B*1503	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.278760	0.275316	-4.003444	19000.276137
HLA A*6901	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.362775	0.359286	-4.003489	23055.531948
HLA B*0702	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.456837	0.453330	-4.003507	28631.017273

HLA B*4601	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.302736	0.299099	-4.003638	20078.737739
HLA B*1502	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.561394	0.557541	-4.003852	36424.496782
HLA A*0201	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.380793	0.376904	-4.003890	24032.189917
HLA B*0801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.411480	0.407463	-4.004017	25791.700144
HLA A*6802	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.351514	0.347374	-4.004140	22465.395325
HLA B*5701	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.411912	0.407463	-4.004449	25817.386490
HLA B*1517	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.200405	0.195916	-4.004488	15863.703639
HLA A*0202	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.463624	0.458831	-4.004793	29082.011454
HLA B*5101	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.510386	0.505350	-4.005036	32388.157397
HLA A*0250	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.416985	0.411911	-4.005073	26120.700187
HLA B*4501	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.349237	0.344156	-4.005081	22347.935762
HLA B*5801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.355539	0.350403	-4.005135	22674.552941
HLA A*0201	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.394566	0.389429	-4.005137	24806.530581
HLA A*3201	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.291471	0.286262	-4.005208	19564.584388
HLA A*2902	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.424414	0.419078	-4.005336	26571.366272
HLA B*3901	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.445846	0.440475	-4.005371	27915.530670
HLA A*3201	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.619045	0.613596	-4.005449	41595.392195
HLA B*0802	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.464341	0.458831	-4.005510	29130.036854
HLA A*6901	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.390020	0.384476	-4.005543	24548.206900
HLA A*8001	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.413075	0.407463	-4.005612	25886.615396
HLA B*4001	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.389891	0.384129	-4.005762	24540.903818
HLA B*3801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.560703	0.554890	-4.005813	36366.609398
HLA B*1801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.472468	0.466612	-4.005856	29680.273781
HLA B*0802	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.439305	0.433361	-4.005944	27498.241507
HLA B*0702	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.439378	0.433361	-4.006017	27502.853529
HLA A*3001	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.281356	0.275316	-4.006040	19114.198581
HLA B*4002	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.645956	0.639875	-4.006081	44254.376336
HLA A*2403	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.337800	0.331684	-4.006116	21767.077390
HLA A*3002	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.492415	0.486297	-4.006118	31075.278560
HLA A*0201	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.418127	0.411911	-4.006215	26189.467253
HLA B*0801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.390478	0.384129	-4.006349	24574.117165
HLA B*0803	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.523172	0.516757	-4.006415	33355.859706
HLA A*2301	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.538672	0.532233	-4.006438	34567.796060
HLA B*1502	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.538681	0.532233	-4.006448	34568.544099
HLA B*1502	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.492838	0.486297	-4.006541	31105.553785
HLA A*3001	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.146418	0.139834	-4.006584	14009.354387
HLA A*6802	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.425718	0.419078	-4.006640	26651.266382
HLA A*6801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.288184	0.281539	-4.006645	19417.070035
HLA B*4501	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.488296	0.481648	-4.006648	30781.968057
HLA A*6802	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.198003	0.191274	-4.006730	15776.236722
HLA A*1101	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.381515	0.374749	-4.006765	24072.136606
HLA B*4001	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.348972	0.342132	-4.006840	22334.278254
HLA B*5401	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.561786	0.554890	-4.006896	36457.419418
HLA B*0702	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.464651	0.457680	-4.006971	29150.846199
HLA B*1502	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.602495	0.595477	-4.007018	40040.127448
HLA B*7301	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.504193	0.496961	-4.007232	31929.564766
HLA B*0802	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.489140	0.481648	-4.007492	30841.809354
HLA B*5801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.351695	0.344156	-4.007539	22474.755492
HLA A*2301	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.524298	0.516757	-4.007541	33442.408065
HLA A*0203	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.426928	0.419078	-4.007850	26725.622821
HLA B*1502	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.621545	0.613596	-4.007949	41835.510762
HLA B*1502	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.519782	0.511716	-4.008066	33096.481916
HLA A*1101	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.441478	0.433361	-4.008117	27636.191636
HLA A*6801	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.635696	0.627429	-4.008267	43221.120703
HLA B*5301	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.565827	0.557541	-4.008286	36798.239252
HLA B*4601	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.392571	0.384129	-4.008443	24692.855543
HLA B*1503	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.525381	0.516757	-4.008624	33525.916146
HLA B*1501	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.350938	0.342132	-4.008807	22435.638901
HLA A*0219	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.420796	0.411911	-4.008884	26350.913723
HLA B*5701	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.377678	0.368545	-4.009133	23860.411554
HLA A*0101	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.382271	0.373125	-4.009146	24114.106435
HLA B*1502	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.615725	0.606435	-4.009291	41278.641995
HLA A*2902	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.440012	0.430602	-4.009410	27543.055478
HLA B*5301	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.583061	0.573435	-4.009626	38287.808688
HLA A*0250	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.586928	0.577199	-4.009729	38630.271776

HLA A*0301	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.343822	0.334057	-4.009764	22070.991902
HLA B*4403	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.654511	0.644580	-4.009930	45134.714497
HLA A*0203	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.378521	0.368545	-4.009976	23906.797087
HLA A*6801	1:201-209	9	GLGAQWTPA	0.948960	-0.304380	-4.654621	0.644580	-4.010041	45146.192125
HLA A*3001	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.217208	0.207166	-4.010042	16489.523450
HLA B*2705	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.429132	0.419078	-4.010054	26861.586032
HLA B*3501	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.456604	0.446544	-4.010060	28615.687207
HLA A*1101	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.473974	0.463883	-4.010091	29783.375884
HLA A*2301	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.456672	0.446544	-4.010128	28620.176982
HLA B*1801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.221183	0.210953	-4.010230	16641.153755
HLA B*4501	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.605757	0.595350	-4.010407	40341.917449
HLA B*4002	1:16-24 9	PVLVVDFGA	0.941651	-0.314462	-4.637771	0.627189	-4.010582	43428.078982	
HLA A*3201	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.578105	0.567351	-4.010754	37853.448232
HLA B*2705	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.286107	0.275316	-4.010791	19324.432654
HLA B*0803	1:15-23 9	RPVLVVDFG	1.020076	-0.530672	-4.500197	0.489404	-4.010793	31637.089616	
HLA A*3002	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.444281	0.433361	-4.010920	27815.132375
HLA A*0211	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.345105	0.334057	-4.011047	22136.281565
HLA B*2705	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.492742	0.481648	-4.011094	31098.655169
HLA B*0801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.370681	0.359286	-4.011395	23479.084777
HLA A*3201	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.618789	0.607235	-4.011555	41570.871541
HLA A*3201	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.620838	0.609194	-4.011644	41767.442230
HLA B*5701	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.396126	0.384476	-4.011650	24895.800006
HLA B*3501	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.125071	0.113362	-4.011709	13337.385399
HLA A*2601	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.396288	0.384476	-4.011812	24905.094903
HLA A*6801	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.621073	0.609194	-4.011879	41790.044066
HLA A*3201	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.612727	0.600770	-4.011957	40994.676003
HLA A*2403	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.401394	0.389429	-4.011964	25199.599114
HLA B*4501	1:59-67 9	VALVLSGGP	0.588823	0.038606	-4.639458	0.627429	-4.012029	43597.094728	
HLA A*0212	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.431131	0.419078	-4.012053	26985.536927
HLA B*5701	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.396218	0.384129	-4.012089	24901.053217
HLA B*5801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.354225	0.342132	-4.012094	22606.085768
HLA A*0206	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.371426	0.359286	-4.012140	23519.384424
HLA A*0219	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.465549	0.453330	-4.012219	29211.150977
HLA A*6802	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.314190	0.301939	-4.012251	20615.323136
HLA B*1501	1:13-21 9	PARPVLVVD	1.322529	-0.949404	-4.385492	0.373125	-4.012367	24293.624666	
HLA B*1801	1:28-36 9	QLIARRVRE	1.072167	-0.566817	-4.517773	0.505350	-4.012423	32943.749123	
HLA A*3001	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.294025	0.281539	-4.012486	19679.973839
HLA A*2602	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.205573	0.192958	-4.012615	16053.637602
HLA A*0216	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.494349	0.481648	-4.012701	31213.944693
HLA A*0101	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.381270	0.368545	-4.012725	24058.596746
HLA A*0301	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.360106	0.347374	-4.012732	22914.275585
HLA A*6901	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.363327	0.350403	-4.012924	23084.861638
HLA B*5801	1:33-41 9	RVREARVFS	1.063374	-0.731690	-4.344663	0.331684	-4.012979	22113.779102	
HLA A*1101	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.494640	0.481648	-4.012992	31234.890851
HLA B*5701	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.372305	0.359286	-4.013019	23567.019333
HLA A*6801	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.580462	0.567351	-4.013111	38059.403803
HLA A*0101	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.372436	0.359286	-4.013150	23574.160133
HLA A*2902	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.387936	0.374749	-4.013186	24430.692746
HLA A*3002	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.590386	0.577199	-4.013187	38939.126542
HLA A*0203	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.108761	0.095477	-4.013283	12845.782840
HLA A*2603	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.665332	0.651841	-4.013491	46273.508309
HLA B*7301	1:8-16 9	DVPETPARP	0.603076	-0.035541	-4.581482	0.567535	-4.013946	38148.868154	
HLA A*1101	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.418138	0.403979	-4.014159	26190.175673
HLA B*0702	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.421681	0.407463	-4.014218	26404.711997
HLA A*3301	1:6-14 9	DIDVPETPA	0.752912	-0.322310	-4.444859	0.430602	-4.014257	27852.174306	
HLA A*0301	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.364805	0.350403	-4.014402	23163.549077
HLA B*3501	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.382978	0.368545	-4.014433	24153.405270
HLA B*0702	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.418839	0.404390	-4.014449	26232.432138
HLA A*2603	1:59-67 9	VALVLSGGP	0.588823	0.038606	-4.641988	0.627429	-4.014559	43851.852493	
HLA A*2602	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.358826	0.344156	-4.014669	22846.814873
HLA B*2705	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.150511	0.135619	-4.014892	14142.002979
HLA B*3801	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.478859	0.463883	-4.014976	30120.245124
HLA A*6901	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.360487	0.345470	-4.015017	22934.366506
HLA A*8001	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.383596	0.368545	-4.015051	24187.795215
HLA A*0212	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.422598	0.407463	-4.015134	26460.480969

HLA B*5801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.362557	0.347374	-4.015183	23043.935174
HLA B*4601	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.374499	0.359286	-4.015213	23686.400982
HLA A*0301	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.357383	0.342132	-4.015251	22771.051150
HLA B*3901	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.419341	0.403979	-4.015362	26262.819438
HLA A*8001	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.445987	0.430602	-4.015385	27924.593337
HLA B*1502	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.314545	0.299099	-4.015446	20632.170535
HLA B*0802	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.473335	0.457680	-4.015655	29739.582178
HLA A*6802	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.423122	0.407463	-4.015658	26492.422296
HLA A*3301	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.629268	0.613596	-4.015672	42586.096393
HLA A*0203	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.405103	0.389429	-4.015674	25415.781531
HLA A*0301	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.161474	0.145582	-4.015891	14503.526788
HLA B*5801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.350304	0.334057	-4.016247	22402.891757
HLA A*3301	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.611764	0.595477	-4.016287	40903.848343
HLA A*3002	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.375676	0.359286	-4.016390	23750.686603
HLA A*0206	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.384954	0.368545	-4.016409	24263.546790
HLA A*1101	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.469543	0.452913	-4.016630	29481.039582
HLA B*7301	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.572065	0.555251	-4.016814	37330.595806
HLA B*4403	1:460-468	9	QGDGRTYGH	1.037678	-0.397803	-4.656724	0.639875	-4.016849	45365.313298
HLA A*3101	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.424367	0.407463	-4.016904	26568.491464
HLA B*0801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.406335	0.389429	-4.016905	25487.931945
HLA B*1509	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.531760	0.514746	-4.017014	34021.973833
HLA B*1502	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.594540	0.577199	-4.017341	39313.353813
HLA A*0201	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.392233	0.374749	-4.017484	24673.626705
HLA A*3001	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.131146	0.113627	-4.017520	13525.286365
HLA B*0803	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.503967	0.486297	-4.017671	31912.986473
HLA B*3801	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.532572	0.514746	-4.017826	34085.716539
HLA A*0212	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.402044	0.384129	-4.017916	25237.390012
HLA B*4002	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.625184	0.607235	-4.017950	42187.561943
HLA B*2705	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.361177	0.343210	-4.017968	22970.872810
HLA B*4601	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.386552	0.368545	-4.018007	24352.970077
HLA A*2602	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.591507	0.573435	-4.018072	39039.739386
HLA B*5801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.357336	0.339229	-4.018107	22768.587506
HLA B*0803	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.515379	0.496961	-4.018417	32762.640529
HLA B*2705	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.465041	0.446544	-4.018497	29177.036630
HLA A*2601	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.391634	0.373125	-4.018509	24639.612368
HLA B*4801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.408014	0.389429	-4.018585	25586.711990
HLA A*2403	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.317827	0.299099	-4.018728	20788.691256
HLA A*3301	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.592280	0.573435	-4.018845	39109.286277
HLA B*3501	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.423246	0.404390	-4.018857	26500.019402
HLA A*3001	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.100002	0.081144	-4.018858	12589.303276
HLA A*3001	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.241121	0.222188	-4.018933	17422.928846
HLA A*0211	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.164692	0.145582	-4.019110	14611.419707
HLA A*2501	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.290094	0.270903	-4.019191	19502.659050
HLA B*5401	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.549869	0.530534	-4.019335	35470.665487
HLA B*3801	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.524753	0.505350	-4.019403	33477.524916
HLA B*1517	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.472320	0.452913	-4.019407	29670.159784
HLA A*0301	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.363581	0.344156	-4.019425	23098.353326
HLA A*6802	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.403905	0.384476	-4.019429	25345.754932
HLA A*2603	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.626719	0.607235	-4.019484	42336.859709
HLA B*3501	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.210775	0.191274	-4.019502	16247.076101
HLA A*0250	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.534391	0.514746	-4.019645	34228.741330
HLA B*0801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.404215	0.384476	-4.019739	25363.860936
HLA A*0212	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.219896	0.200115	-4.019781	16591.892128
HLA B*2705	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.450467	0.430602	-4.019865	28214.173011
HLA A*2301	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.534624	0.514746	-4.019878	34247.078436
HLA A*2402	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.568162	0.548275	-4.019888	36996.652199
HLA B*1503	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.478898	0.458831	-4.020067	30123.015353
HLA A*0250	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.367664	0.347374	-4.020291	23316.557201
HLA A*3002	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.536825	0.516095	-4.020730	34421.119882
HLA A*1101	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.389287	0.368545	-4.020742	24506.807289
HLA A*6802	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.362935	0.342132	-4.020803	23064.015004
HLA B*7301	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.365035	0.344156	-4.020879	23175.832932
HLA B*3901	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.122928	0.101982	-4.020946	13271.743222
HLA B*4801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.365226	0.344156	-4.021069	23185.990831
HLA A*3201	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.467713	0.446544	-4.021168	29357.058960

HLA A*0219	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.311749	0.290570	-4.021179	20499.772039
HLA B*1502	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.588716	0.567535	-4.021180	38789.637556
HLA B*0803	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.502891	0.481648	-4.021243	31834.012612
HLA B*1509	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.538070	0.516757	-4.021313	34519.955162
HLA B*4403	1:154-162	9	VVASSAGAP	0.567899	0.078065	-4.667313	0.645964	-4.021349	46485.022276
HLA A*0211	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.510776	0.489404	-4.021373	32417.256374
HLA B*7301	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.164655	0.143276	-4.021378	14610.155023
HLA A*0301	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.365691	0.344171	-4.021520	23210.839998
HLA A*6801	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.673530	0.651841	-4.021689	47155.220582
HLA B*1509	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.503338	0.481648	-4.021690	31866.750945
HLA A*3301	1:512-520	9	LDITSKPPA	0.921873	-0.312679	-4.630943	0.609194	-4.021750	42750.678868
HLA A*0201	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.390377	0.368545	-4.021832	24568.401270
HLA A*2601	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.365064	0.343210	-4.021854	23177.337525
HLA B*4403	1:511-519	9	VLDITSKPP	0.628251	0.023590	-4.673842	0.651841	-4.022001	47189.161692
HLA A*2403	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.429578	0.407463	-4.022115	26889.210685
HLA B*4402	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.452775	0.430602	-4.022172	28364.459967
HLA B*1801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.501423	0.479051	-4.022372	31726.557827
HLA B*4403	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.618051	0.595477	-4.022574	41500.314830
HLA A*2403	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.453216	0.430602	-4.022614	28393.322976
HLA B*0801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.231378	0.208642	-4.022735	17036.400797
HLA A*3301	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.629221	0.606435	-4.022786	42581.488921
HLA A*0216	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.399700	0.376904	-4.022796	25101.498766
HLA B*5401	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.426911	0.403979	-4.022932	26724.610761
HLA A*2501	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.481863	0.458831	-4.023032	30329.377260
HLA A*2902	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.435116	0.411911	-4.023204	27234.273223
HLA B*0801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.362601	0.339229	-4.023373	23046.303933
HLA A*2501	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.476706	0.453330	-4.023376	29971.354715
HLA B*4001	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.407855	0.384476	-4.023378	25577.301074
HLA A*2403	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.435313	0.411911	-4.023402	27246.652125
HLA A*0211	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.482315	0.458831	-4.023483	30360.896712
HLA A*0212	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.400404	0.376904	-4.023501	25142.270741
HLA B*4002	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.619015	0.595477	-4.023537	41592.466954
HLA A*6901	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.296151	0.272539	-4.023612	19776.562254
HLA B*3501	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.398375	0.374749	-4.023625	25025.026363
HLA B*0802	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.464271	0.440475	-4.023795	29125.309530
HLA A*0250	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.554347	0.530534	-4.023813	35838.304492
HLA A*3001	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.251487	0.227657	-4.023830	17843.789480
HLA A*6901	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.357914	0.334057	-4.023857	22798.908859
HLA B*4403	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.624785	0.600770	-4.024015	42148.780674
HLA B*1509	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.457631	0.433361	-4.024270	28683.418200
HLA B*3501	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.383573	0.359286	-4.024287	24186.486717
HLA B*3501	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.302466	0.278063	-4.024403	20066.249894
HLA B*4403	1:59-67	9	VALVLSGGP	0.588823	0.038606	-4.651860	0.627429	-4.024432	44860.125121
HLA A*0216	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.383756	0.359286	-4.024470	24196.694875
HLA A*0216	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.477463	0.452913	-4.024550	30023.609845
HLA B*0702	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.397839	0.373125	-4.024714	24994.178155
HLA B*4403	1:16-24	9	PVLVVDFGA	0.941651	-0.314462	-4.651929	0.627189	-4.024740	44867.163634
HLA A*2602	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.625654	0.600770	-4.024884	42233.232653
HLA B*5101	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.483762	0.458831	-4.024931	30462.242923
HLA A*0201	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.259649	0.234640	-4.025009	18182.316017
HLA B*4801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.444345	0.419078	-4.025267	27819.195545
HLA A*2301	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.541430	0.516095	-4.025335	34788.042060
HLA B*2705	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.483017	0.457680	-4.025337	30410.046930
HLA A*0216	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.170937	0.145582	-4.025355	14823.042268
HLA B*5101	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.507010	0.481648	-4.025362	32137.347677
HLA B*4601	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.400301	0.374749	-4.025552	25136.286710
HLA A*6801	1:321-329	9	VRDVLDGKT	0.852657	-0.199777	-4.678461	0.652880	-4.025582	47693.736696
HLA A*3101	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.415016	0.389429	-4.025587	26002.550347
HLA B*4601	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.415079	0.389429	-4.025650	26006.348739
HLA B*5301	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.573977	0.548275	-4.025703	37495.349167
HLA A*0216	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.359798	0.334057	-4.025741	22898.042095
HLA A*6801	1:343-351	9	VESGGGSGT	0.953925	-0.320491	-4.659214	0.633434	-4.025780	45626.207224
HLA B*4001	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.394329	0.368545	-4.025784	24792.980025
HLA B*4801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.437712	0.411911	-4.025801	27397.565322
HLA A*0212	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.400557	0.374749	-4.025808	25151.113394

HLA A*8001	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.472414	0.446544	-4.025869	29676.580970
HLA A*3001	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.251184	0.225172	-4.026012	17831.341077
HLA B*4402	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.410153	0.384129	-4.026024	25712.985919
HLA A*0201	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.373552	0.347374	-4.026178	23634.816490
HLA A*2603	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.632762	0.606435	-4.026327	42930.062127
HLA A*0101	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.373886	0.347374	-4.026512	23652.979833
HLA A*0101	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.365764	0.339229	-4.026535	23214.732934
HLA B*3901	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.485381	0.458831	-4.026549	30576.000180
HLA A*2603	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.634275	0.607629	-4.026646	43079.889962
HLA A*2501	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.374097	0.347374	-4.026724	23664.499037
HLA A*2601	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.297723	0.270903	-4.026820	19848.267581
HLA B*1502	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.523790	0.496961	-4.026829	33403.352229
HLA A*3301	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.634073	0.607235	-4.026838	43059.851685
HLA A*0201	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.399975	0.373125	-4.026850	25117.391966
HLA B*5801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.371022	0.344171	-4.026851	23497.509793
HLA B*5301	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.594423	0.567535	-4.026887	39302.721207
HLA A*0202	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.490782	0.463883	-4.026900	30958.658836
HLA B*4501	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.559277	0.532233	-4.027043	36247.384490
HLA B*4001	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.403976	0.376904	-4.027072	25349.868798
HLA A*2602	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.358840	0.331684	-4.027156	22847.556477
HLA A*3002	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.535768	0.508560	-4.027208	34337.425300
HLA B*4002	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.635029	0.607629	-4.027400	43154.766392
HLA B*4001	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.372883	0.345470	-4.027413	23598.403973
HLA A*0219	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.446645	0.419078	-4.027567	27966.924697
HLA A*3201	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.558104	0.530534	-4.027570	36149.665376
HLA B*5101	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.522503	0.494882	-4.027621	33304.470654
HLA B*1509	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.458244	0.430602	-4.027642	28723.947250
HLA B*7301	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.544470	0.516757	-4.027713	35032.426546
HLA B*3901	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.509442	0.481648	-4.027794	32317.796965
HLA A*2501	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.485508	0.457680	-4.027827	30584.933775
HLA B*5101	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.507036	0.479051	-4.027985	32139.260188
HLA B*1502	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.431972	0.403979	-4.027993	27037.851548
HLA B*1501	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.313770	0.285427	-4.028343	20595.369535
HLA B*4402	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.432748	0.404390	-4.028358	27086.164348
HLA A*6801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.318957	0.290570	-4.028387	20842.857131
HLA B*4403	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.372784	0.344156	-4.028628	23593.042663
HLA A*3001	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.298413	0.269777	-4.028636	19879.861517
HLA A*0216	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.149402	0.120764	-4.028638	14105.937897
HLA B*4501	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.602263	0.573435	-4.028828	40018.688538
HLA A*2403	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.379259	0.350403	-4.028856	23947.442199
HLA A*2501	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.440799	0.411911	-4.028888	27593.017371
HLA A*0216	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.413132	0.384129	-4.029003	25889.976663
HLA A*6802	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.374518	0.345470	-4.029048	23687.426130
HLA B*4001	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.388356	0.359286	-4.029070	24454.362158
HLA A*3001	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.290435	0.261282	-4.029153	19517.963599
HLA A*0301	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.368393	0.339229	-4.029164	23355.693406
HLA B*2705	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.441105	0.411911	-4.029193	27612.429968
HLA B*4601	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.319883	0.290570	-4.029313	20887.330985
HLA A*0101	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.379771	0.350403	-4.029368	23975.701415
HLA B*4001	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.404126	0.374749	-4.029377	25358.647276
HLA B*5401	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.546162	0.516757	-4.029405	35169.148159
HLA B*3801	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.560146	0.530534	-4.029612	36320.012056
HLA A*2403	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.366370	0.336669	-4.029701	23247.157553
HLA A*2601	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.222748	0.192958	-4.029790	16701.219746
HLA A*3101	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.374140	0.344171	-4.029968	23666.803551
HLA B*5101	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.496628	0.466612	-4.030015	31378.173280
HLA B*4501	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.636450	0.606435	-4.030016	43296.242604
HLA A*0212	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.375500	0.345470	-4.030030	23741.051915
HLA B*4402	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.434014	0.403979	-4.030034	27165.260978
HLA B*2705	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.374593	0.344156	-4.030437	23691.527169
HLA A*0203	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.437933	0.407463	-4.030470	27411.501338
HLA B*4002	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.644340	0.613596	-4.030744	44089.967538
HLA A*3301	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.527789	0.496961	-4.030827	33712.338314
HLA A*0212	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.378310	0.347374	-4.030936	23895.159939
HLA B*5301	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.545816	0.514746	-4.031071	35141.190881

HLA B*4801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.435189	0.403979	-4.031209	27238.840973
HLA B*0702	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.365291	0.334057	-4.031234	23189.503239
HLA A*2603	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.632007	0.600770	-4.031237	42855.575574
HLA A*3301	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.408200	0.376904	-4.031297	25597.649608
HLA A*0216	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.285872	0.254455	-4.031417	19313.981178
HLA B*1517	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.462034	0.430602	-4.031432	28975.693547
HLA B*3501	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.302396	0.270903	-4.031493	20062.993472
HLA B*4403	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.638776	0.607235	-4.031542	43528.750273
HLA A*6801	1:246-254	9	QRAIGDRLT	0.791483	-0.184248	-4.638835	0.607235	-4.031600	43534.637814
HLA A*3002	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.152475	0.120764	-4.031711	14206.107406
HLA A*6901	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-3.873662	-0.158117	-4.031779	7475.869448
HLA A*2603	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.543540	0.511716	-4.031824	34957.456348
HLA B*1801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.465196	0.433361	-4.031835	29187.456229
HLA A*2301	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.528816	0.496961	-4.031854	33792.132664
HLA A*0211	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.334513	0.302627	-4.031886	21602.956534
HLA A*2602	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.313490	0.281539	-4.031951	20582.114981
HLA A*3101	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.371292	0.339229	-4.032063	23512.133018
HLA A*3201	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.580361	0.548275	-4.032086	38050.551255
HLA A*8001	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.416623	0.384476	-4.032147	26098.947495
HLA B*1517	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.478734	0.446544	-4.032190	30111.610161
HLA B*4601	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.409116	0.376904	-4.032213	25651.713996
HLA B*1503	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.478769	0.446544	-4.032225	30114.053767
HLA A*0203	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.243795	0.211398	-4.032396	17530.523163
HLA A*0203	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.409558	0.376904	-4.032655	25677.816578
HLA B*0801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.405811	0.373125	-4.032686	25457.201710
HLA B*1509	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.310753	0.278063	-4.032690	20452.803693
HLA B*1503	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.486041	0.453330	-4.032711	30622.516517
HLA A*3101	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.374898	0.342132	-4.032767	23708.194939
HLA A*0101	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.377293	0.344156	-4.033136	23839.251465
HLA B*3801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.528195	0.494882	-4.033314	33743.904825
HLA A*0212	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.336003	0.302627	-4.033376	21677.179075
HLA B*3501	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.445327	0.411911	-4.033415	27882.175210
HLA B*1801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.492420	0.458831	-4.033588	31075.614790
HLA B*4601	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.337116	0.303325	-4.033791	21732.836924
HLA B*1801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.474369	0.440475	-4.033893	29810.457149
HLA A*1101	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.452988	0.419078	-4.033910	28378.427226
HLA B*0802	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.464555	0.430602	-4.033953	29144.381099
HLA A*0219	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.373230	0.339229	-4.034002	23617.305922
HLA A*0201	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.379475	0.345470	-4.034006	23959.364042
HLA A*2501	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.515694	0.481648	-4.034046	32786.399602
HLA B*0801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.305100	0.270903	-4.034197	20188.311125
HLA A*2601	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.365888	0.331684	-4.034204	23221.390113
HLA A*0101	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.324845	0.290570	-4.034275	21127.351657
HLA B*1517	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.438555	0.403979	-4.034576	27450.827214
HLA B*0803	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.467952	0.433361	-4.034591	29373.262910
HLA B*7301	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.589648	0.554890	-4.034759	38873.036595
HLA A*8001	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.380244	0.345470	-4.034774	24001.786478
HLA A*3201	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.546662	0.511716	-4.034946	35209.697151
HLA A*1101	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.492857	0.457680	-4.035177	31106.900035
HLA B*1501	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.307884	0.272539	-4.035345	20318.148438
HLA B*7301	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.454440	0.419078	-4.035362	28473.463928
HLA B*0803	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.488308	0.452913	-4.035395	30782.800703
HLA B*4002	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.602770	0.567351	-4.035419	40065.479151
HLA A*2402	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.547142	0.511716	-4.035425	35248.576635
HLA A*6801	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.567695	0.532233	-4.035461	36956.844221
HLA A*2603	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.468923	0.433361	-4.035561	29438.964499
HLA A*8001	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.439592	0.403979	-4.035612	27516.396515
HLA B*3901	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.493308	0.457680	-4.035628	31139.227518
HLA A*0101	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.372312	0.336669	-4.035642	23567.401821
HLA A*2403	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.404204	0.368545	-4.035659	25363.174867
HLA B*2705	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.412631	0.376904	-4.035728	25860.160660
HLA B*0702	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.412742	0.376904	-4.035838	25866.736824
HLA B*1501	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.269834	0.233980	-4.035854	18613.764682
HLA A*8001	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.395172	0.359286	-4.035886	24841.178505
HLA A*2403	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.420166	0.384129	-4.036037	26312.736525

HLA A*0206	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.499964	0.463883	-4.036081	31620.149991
HLA A*2301	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.544663	0.508560	-4.036103	35047.970760
HLA A*2603	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.609546	0.573435	-4.036111	40695.487529
HLA B*3501	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.247533	0.211398	-4.036134	17682.061940
HLA B*1509	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.533118	0.496961	-4.036156	34128.524185
HLA A*0250	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.591310	0.554890	-4.036420	39022.002561
HLA B*1509	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.494389	0.457680	-4.036709	31216.815513
HLA B*1517	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.335850	0.299099	-4.036751	21669.557791
HLA A*8001	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.456000	0.419078	-4.036922	28575.929274
HLA B*3501	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.306723	0.269777	-4.036946	20263.920979
HLA B*1501	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.335195	0.298081	-4.037114	21636.875318
HLA B*1503	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.421630	0.384476	-4.037153	26401.569560
HLA B*5101	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.490587	0.453330	-4.037257	30944.760875
HLA B*5101	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.421782	0.384476	-4.037306	26410.855114
HLA A*6901	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.339952	0.302627	-4.037325	21875.210942
HLA A*6801	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.644976	0.607629	-4.037348	44154.654362
HLA B*4403	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.592310	0.554890	-4.037421	39112.036873
HLA A*0301	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.237538	0.200115	-4.037423	17279.779581
HLA A*6802	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.381609	0.344156	-4.037452	24077.346273
HLA B*0801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.406039	0.368545	-4.037494	25470.564118
HLA A*2603	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.595104	0.557541	-4.037563	39364.430377
HLA A*6901	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.376924	0.339229	-4.037695	23819.012131
HLA B*2705	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.441751	0.403979	-4.037771	27653.540092
HLA A*2403	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.422382	0.384476	-4.037905	26447.314605
HLA A*0202	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.592865	0.554890	-4.037975	39162.004425
HLA A*2601	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.388408	0.350403	-4.038005	24457.272830
HLA A*2902	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.319585	0.281539	-4.038046	20872.985150
HLA B*4002	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.644500	0.606435	-4.038065	44106.190006
HLA A*6801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.491017	0.452913	-4.038104	30975.411659
HLA B*0702	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.381341	0.343210	-4.038131	24062.501693
HLA A*0101	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.372225	0.334057	-4.038167	23562.684903
HLA B*4801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.445641	0.407463	-4.038178	27902.395028
HLA B*5401	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.554289	0.516095	-4.038194	35833.457788
HLA B*5701	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.415169	0.376904	-4.038265	26011.695564
HLA B*3801	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.524641	0.486297	-4.038344	33468.832779
HLA A*6802	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.375265	0.336669	-4.038596	23728.211742
HLA B*1503	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.502534	0.463883	-4.038652	31807.846163
HLA B*1517	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.520329	0.481648	-4.038681	33138.226474
HLA A*6802	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.342057	0.303325	-4.038732	21981.503197
HLA B*1502	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.517841	0.479051	-4.038790	32948.917967
HLA B*5401	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.535770	0.496961	-4.038809	34337.611062
HLA A*6801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.293244	0.254355	-4.038889	19644.658693
HLA A*3301	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.639678	0.600770	-4.038908	43619.270778
HLA A*1101	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.485477	0.446544	-4.038933	30582.782856
HLA A*0101	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.370700	0.331684	-4.039016	23480.100953
HLA B*3801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.505685	0.466612	-4.039073	32039.440368
HLA A*0250	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.485679	0.446544	-4.039135	30597.014821
HLA B*4501	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.652753	0.613596	-4.039157	44952.441534
HLA A*0206	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.492157	0.452913	-4.039244	31056.791542
HLA B*1502	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.479725	0.440475	-4.039250	30180.432691
HLA B*0802	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.492638	0.453330	-4.039308	31091.253477
HLA B*1801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-3.829863	-0.209501	-4.039364	6758.691277
HLA A*0201	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.371092	0.331684	-4.039408	23501.323670
HLA B*2705	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.329986	0.290570	-4.039416	21378.918626
HLA B*5701	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.428887	0.389429	-4.039458	26846.477189
HLA B*0803	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.486013	0.446544	-4.039468	30620.528608
HLA B*3501	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.139125	0.099536	-4.039589	13776.069340
HLA A*6801	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.646050	0.606435	-4.039616	44263.953824
HLA A*0203	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.414544	0.374749	-4.039794	25974.290860
HLA A*3001	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.248520	0.208642	-4.039877	17722.283976
HLA B*0803	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.497567	0.457680	-4.039887	31446.147776
HLA B*1503	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.480451	0.440475	-4.039976	30230.926176
HLA B*0802	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.486532	0.446544	-4.039988	30657.159962
HLA A*2402	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.594885	0.554890	-4.039996	39344.630338
HLA B*1509	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.545396	0.505350	-4.040046	35107.177672

HLA B*1502	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.613700	0.573435	-4.040265	41086.594433
HLA B*4001	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.371980	0.331684	-4.040296	23549.431595
HLA A*0201	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.383761	0.343210	-4.040551	24196.956680
HLA A*2403	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.382687	0.342132	-4.040555	24137.207965
HLA B*1502	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.507193	0.466612	-4.040581	32150.911578
HLA B*1501	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.387959	0.347374	-4.040586	24432.014455
HLA A*8001	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.415404	0.374749	-4.040654	26025.771410
HLA A*3001	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.236629	0.195916	-4.040713	17243.640011
HLA A*0202	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.557547	0.516757	-4.040791	36103.346010
HLA B*4403	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.589103	0.548275	-4.040829	38824.277874
HLA A*8001	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.425034	0.384129	-4.040905	26609.342895
HLA B*5301	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.573155	0.532233	-4.040922	37424.420350
HLA A*0202	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.527328	0.486297	-4.041032	33676.610776
HLA A*0101	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.385269	0.344171	-4.041098	24281.142422
HLA B*3901	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.460211	0.419078	-4.041133	28854.306417
HLA A*0250	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.557968	0.516757	-4.041211	36138.324346
HLA B*1801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.494149	0.452913	-4.041236	31199.594554
HLA B*4402	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.453200	0.411911	-4.041288	28392.247763
HLA A*0212	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.425892	0.384476	-4.041415	26661.937868
HLA A*3201	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.614995	0.573435	-4.041560	41209.250082
HLA A*0212	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.431192	0.389429	-4.041763	26989.332902
HLA A*2603	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.655735	0.613596	-4.042139	45262.108497
HLA A*2603	1:424-432	9	RHADSIVRE	1.136340	-0.540863	-4.637745	0.595477	-4.042268	43425.494707
HLA B*0801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.344910	0.302627	-4.042283	22126.344145
HLA B*3801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.523971	0.481648	-4.042323	33417.269677
HLA A*3002	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.506237	0.463883	-4.042354	32080.198778
HLA A*0212	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.384510	0.342132	-4.042378	24238.750743
HLA B*3501	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.195052	0.152623	-4.042429	15669.403389
HLA B*1517	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.276582	0.233980	-4.042602	18905.228903
HLA A*8001	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.454579	0.411911	-4.042668	28482.553637
HLA A*0250	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.591042	0.548275	-4.042767	38997.944043
HLA B*3801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.559615	0.516757	-4.042858	36275.633076
HLA A*2902	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.427022	0.384129	-4.042893	26731.406753
HLA B*4402	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.450387	0.407463	-4.042924	28208.983880
HLA B*0801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.062391	0.019419	-4.042972	11544.925637
HLA A*2402	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.557721	0.514746	-4.042975	36117.802220
HLA A*3002	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.265351	0.222188	-4.043163	18422.620328
HLA A*3101	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.390671	0.347374	-4.043297	24585.020930
HLA B*7301	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.573937	0.530534	-4.043403	37491.900949
HLA B*1509	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.125691	0.082233	-4.043458	13356.447605
HLA B*0801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.394070	0.350403	-4.043667	24778.230414
HLA A*2301	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.538606	0.494882	-4.043724	34562.560234
HLA B*0702	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.380453	0.336669	-4.043783	24013.345644
HLA B*4402	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.420838	0.376904	-4.043934	26353.479847
HLA A*2601	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.279343	0.235291	-4.044052	19025.785013
HLA A*0201	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.403388	0.359286	-4.044102	25315.606977
HLA A*2403	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.418878	0.374749	-4.044129	26234.844797
HLA A*3301	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.556091	0.511716	-4.044375	35982.453506
HLA B*0702	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.413064	0.368545	-4.044519	25885.915187
HLA A*6802	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.272198	0.227657	-4.044541	18715.343439
HLA B*5301	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.599474	0.554890	-4.044584	39762.530337
HLA A*3201	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.621804	0.577199	-4.044604	41860.413973
HLA A*6901	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.388890	0.344171	-4.044719	24484.411659
HLA A*0201	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.395170	0.350403	-4.044767	24841.044117
HLA B*1517	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.421757	0.376904	-4.044853	26409.283483
HLA B*5701	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.299292	0.254355	-4.044937	19920.125130
HLA A*0206	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.457001	0.411911	-4.045090	28641.861671
HLA A*6802	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.434552	0.389429	-4.045123	27198.935913
HLA B*7301	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.270351	0.225172	-4.045179	18635.931520
HLA A*0301	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.343357	0.298081	-4.045276	22047.363038
HLA A*0201	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.387616	0.342132	-4.045485	24412.724598
HLA B*1801	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.377208	0.331684	-4.045524	23834.609079
HLA B*3501	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.453054	0.407463	-4.045591	28382.726227
HLA A*0201	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.389764	0.344156	-4.045607	24533.735632
HLA B*3901	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.476354	0.430602	-4.045752	29947.043325

HLA B*0803	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.486234	0.440475	-4.045758	30636.104013
HLA A*0202	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.554322	0.508560	-4.045762	35836.171861
HLA A*0101	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.389064	0.343210	-4.045854	24494.215509
HLA B*0702	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.430349	0.384476	-4.045872	26936.966432
HLA B*0802	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.457969	0.411911	-4.046058	28705.771978
HLA B*1517	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.453559	0.407463	-4.046096	28415.758125
HLA B*4002	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.641485	0.595350	-4.046135	43801.113866
HLA A*2902	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.393617	0.347374	-4.046243	24752.372752
HLA B*5301	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.563062	0.516757	-4.046305	36564.673088
HLA B*1502	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.594622	0.548275	-4.046348	39320.798349
HLA A*0216	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.274308	0.227657	-4.046650	18806.485291
HLA B*7301	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.532979	0.486297	-4.046682	34117.632663
HLA B*1502	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.561502	0.514746	-4.046756	36433.562325
HLA A*0212	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.390936	0.344156	-4.046780	24600.054777
HLA A*3301	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.624071	0.577199	-4.046872	42079.519493
HLA A*0212	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.390165	0.343210	-4.046956	24556.442072
HLA B*0801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.337640	0.290570	-4.047071	21759.071355
HLA B*4501	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.654760	0.607629	-4.047131	45160.604342
HLA B*3801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.558901	0.511716	-4.047185	36216.022972
HLA A*6802	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-3.889206	-0.158117	-4.047323	7748.290615
HLA A*0203	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.345492	0.298081	-4.047412	22156.049933
HLA B*1801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.493973	0.446544	-4.047428	31186.938146
HLA A*0211	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.431568	0.384129	-4.047439	27012.704503
HLA B*1509	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.511425	0.463883	-4.047542	32465.695686
HLA A*2602	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.480950	0.433361	-4.047588	30265.617810
HLA A*0211	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.459675	0.411911	-4.047764	28818.737877
HLA A*3201	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.379468	0.331684	-4.047784	23958.975193
HLA B*5301	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.505473	0.457680	-4.047793	32023.844481
HLA A*0250	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.511765	0.463883	-4.047883	32491.172871
HLA A*3002	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.602925	0.554890	-4.048036	40079.787192
HLA A*0202	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.478640	0.430602	-4.048038	30105.094847
HLA A*1101	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.478654	0.430602	-4.048052	30106.072054
HLA B*1501	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.351817	0.303325	-4.048492	22481.078850
HLA A*3001	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.303030	0.254455	-4.048575	20092.320300
HLA B*4403	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.622029	0.573435	-4.048594	41882.159799
HLA A*0201	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.387915	0.339229	-4.048686	24429.503269
HLA A*0301	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.339327	0.290570	-4.048757	21843.754485
HLA A*3201	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.557397	0.508560	-4.048837	36090.848007
HLA A*3301	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.396281	0.347374	-4.048907	24904.690705
HLA B*5101	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.501822	0.452913	-4.048909	31755.749565
HLA B*3501	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.276573	0.227657	-4.048915	18904.819807
HLA A*0203	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.399420	0.350403	-4.049017	25085.344204
HLA B*1502	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.603910	0.554890	-4.049020	40170.740837
HLA B*4601	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.391209	0.342132	-4.049077	24615.497316
HLA B*5801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.351775	0.302627	-4.049148	22478.889794
HLA A*2402	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.581395	0.532233	-4.049161	38141.232816
HLA B*0801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.385835	0.336669	-4.049166	24312.820415
HLA A*2902	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.456764	0.407463	-4.049301	28626.216067
HLA A*2501	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.453284	0.403979	-4.049305	28397.777863
HLA B*5801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.348789	0.299099	-4.049690	22324.855816
HLA A*2602	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.539210	0.489404	-4.049806	34610.647417
HLA A*0202	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.598250	0.548275	-4.049975	39650.615361
HLA B*4601	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.397425	0.347374	-4.050052	24970.391512
HLA A*2601	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.392292	0.342132	-4.050160	24676.963971
HLA A*2501	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.424950	0.374749	-4.050200	26604.161070
HLA B*1503	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.336475	0.286262	-4.050213	21700.763393
HLA B*4801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.434740	0.384476	-4.050263	27210.709919
HLA A*0201	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.394782	0.344171	-4.050611	24818.880107
HLA B*1502	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.171445	0.120764	-4.050681	14840.373652
HLA B*5401	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.556121	0.505350	-4.050771	35984.984189
HLA B*7301	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.556222	0.505350	-4.050872	35993.356178
HLA B*1509	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.545828	0.494882	-4.050946	35142.141444
HLA A*0212	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.395189	0.344171	-4.051017	24842.119239
HLA A*2402	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.556572	0.505350	-4.051222	36022.381165
HLA B*1501	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.204394	0.153079	-4.051315	16010.098853

HLA A*2301	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.537722	0.486297	-4.051426	34492.327352
HLA A*0216	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.420044	0.368545	-4.051499	26305.335419
HLA A*2601	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.388319	0.336669	-4.051649	24452.245524
HLA B*4402	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.420218	0.368545	-4.051673	26315.868389
HLA A*2403	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.424872	0.373125	-4.051747	26599.411951
HLA A*6901	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.388605	0.336669	-4.051936	24468.389491
HLA B*4801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.428845	0.376904	-4.051941	26843.863060
HLA B*0801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.394153	0.342132	-4.052021	24782.922520
HLA A*2301	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.518668	0.466612	-4.052056	33011.721744
HLA A*3101	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.396389	0.344156	-4.052233	24910.889131
HLA B*1503	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.277592	0.225172	-4.052420	18949.258428
HLA A*3101	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.355776	0.303325	-4.052451	22686.945675
HLA B*4601	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.386533	0.334057	-4.052476	24351.916125
HLA A*0201	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.386545	0.334057	-4.052487	24352.574840
HLA A*2301	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.542104	0.489404	-4.052701	34842.097256
HLA B*4402	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.437204	0.384476	-4.052728	27365.568977
HLA A*2402	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.287519	0.234640	-4.052878	19387.365273
HLA B*1503	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.534673	0.481648	-4.053025	34250.969388
HLA B*4601	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.403461	0.350403	-4.053058	25319.852927
HLA A*0206	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.355713	0.302627	-4.053086	22683.632102
HLA A*0219	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.460641	0.407463	-4.053177	28882.886605
HLA A*0202	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.287838	0.234640	-4.053198	19401.634677
HLA A*6901	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.339478	0.286262	-4.053215	21851.318821
HLA B*3901	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.397432	0.344156	-4.053276	24970.796777
HLA A*0202	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.506796	0.453330	-4.053466	32121.530357
HLA A*2601	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.399129	0.345470	-4.053659	25068.521940
HLA A*2602	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.630884	0.577199	-4.053685	42744.897348
HLA A*6801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.494269	0.440475	-4.053794	31208.203846
HLA A*2601	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.397980	0.344171	-4.053809	25002.292416
HLA A*0212	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.422445	0.368545	-4.053900	26451.177968
HLA A*8001	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.390607	0.336669	-4.053938	24581.430132
HLA B*4402	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-3.844575	-0.209501	-4.054076	6991.576023
HLA A*6801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.438245	0.384129	-4.054117	27431.231428
HLA A*2601	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.357486	0.303325	-4.054162	22776.472105
HLA B*4001	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.398438	0.344171	-4.054267	25028.681961
HLA B*4402	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.443722	0.389429	-4.054293	27779.341947
HLA A*3002	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.388354	0.334057	-4.054297	24454.229863
HLA B*0802	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.473589	0.419078	-4.054511	29756.963142
HLA B*1801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.458658	0.403979	-4.054678	28751.309508
HLA B*4601	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.398851	0.344171	-4.054680	25052.524131
HLA B*0702	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.400174	0.345470	-4.054705	25128.944618
HLA A*0219	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.438866	0.384129	-4.054737	27470.436998
HLA B*0803	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.474054	0.419078	-4.054976	29788.854630
HLA B*4801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.439155	0.384129	-4.055026	27488.722359
HLA B*4403	1:362-370	9	GLPDDLKFT	1.003255	-0.395626	-4.662727	0.607629	-4.055098	45996.718433
HLA A*1101	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.495765	0.440475	-4.055290	31315.935939
HLA B*4801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.397637	0.342132	-4.055505	24982.552307
HLA B*4403	1:153-161	9	DVVASSAGA	0.915700	-0.320350	-4.650921	0.595350	-4.055571	44763.154757
HLA B*4001	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.403186	0.347374	-4.055813	25303.831619
HLA B*4403	1:385-393	9	AVGRELGLP	0.452847	0.153588	-4.662285	0.606435	-4.055851	45949.960830
HLA B*3901	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.389949	0.334057	-4.055892	24544.223131
HLA A*2501	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.432820	0.376904	-4.055917	27090.707256
HLA B*5101	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.430678	0.374749	-4.055928	26957.375800
HLA B*3501	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.429111	0.373125	-4.055986	26860.278200
HLA B*5801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.359357	0.303325	-4.056032	22874.765270
HLA A*2602	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.623418	0.567351	-4.056067	42016.281599
HLA B*4402	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.395304	0.339229	-4.056075	24848.705374
HLA B*4402	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.400294	0.344171	-4.056123	25135.878759
HLA B*0802	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.440329	0.384129	-4.056201	27563.178484
HLA B*1501	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.334285	0.278063	-4.056222	21591.623157
HLA A*0216	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.475438	0.419078	-4.056360	29883.925961
HLA B*1509	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.545772	0.489404	-4.056368	35137.578978
HLA B*1801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.460967	0.404390	-4.056578	28904.613970
HLA A*0250	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.460984	0.404390	-4.056594	28905.708586
HLA A*1101	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.446257	0.389429	-4.056828	27941.971672

HLA A*3301	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.571607	0.514746	-4.056861	37291.235465
HLA B*5701	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.402345	0.345470	-4.056875	25254.872094
HLA A*2301	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.490239	0.433361	-4.056878	30919.994448
HLA B*4002	1:486-494	9	TRVPYEVLE	1.162065	-0.588630	-4.630320	0.573435	-4.056885	42689.434524
HLA B*5401	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.249913	0.192958	-4.056955	17779.229495
HLA B*3901	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.503526	0.446544	-4.056981	31880.545577
HLA B*5801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.358955	0.301939	-4.057016	22853.613815
HLA A*0212	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.396323	0.339229	-4.057095	24907.115992
HLA B*3501	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.360435	0.303325	-4.057110	22931.637076
HLA B*0803	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.516016	0.458831	-4.057184	32810.708407
HLA B*4001	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.343505	0.286262	-4.057242	22054.878568
HLA A*0219	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.441746	0.384476	-4.057270	27653.240888
HLA B*3801	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.510278	0.452913	-4.057365	32380.098448
HLA B*0802	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.461773	0.404390	-4.057384	28958.298933
HLA A*6901	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.400630	0.343210	-4.057420	25155.331754
HLA B*0801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.356678	0.299099	-4.057579	22734.124465
HLA B*5801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.348370	0.290570	-4.057801	22303.368215
HLA B*4001	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.408224	0.350403	-4.057820	25599.034450
HLA A*0301	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.361210	0.303325	-4.057885	22972.612654
HLA B*0702	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.469909	0.411911	-4.057998	29505.930393
HLA B*1517	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.203586	0.145582	-4.058004	15980.331736
HLA A*2602	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.566581	0.508560	-4.058021	36862.197651
HLA B*1509	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.400292	0.342132	-4.058160	25135.742777
HLA B*1801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.516091	0.457680	-4.058411	32816.388972
HLA B*1517	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.431580	0.373125	-4.058455	27013.435192
HLA B*4801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.431617	0.373125	-4.058493	27015.773528
HLA A*6802	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.431690	0.373125	-4.058565	27020.304630
HLA B*7301	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.462574	0.403979	-4.058595	29011.769704
HLA A*3001	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.286133	0.227420	-4.058713	19325.582662
HLA B*1517	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.477792	0.419078	-4.058714	30046.357875
HLA A*2902	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.448174	0.389429	-4.058745	28065.593316
HLA B*4001	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.402221	0.343210	-4.059011	25247.631951
HLA B*1503	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.313532	0.254355	-4.059177	20584.119324
HLA B*5101	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.443315	0.384129	-4.059187	27753.355122
HLA A*3301	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.591500	0.532233	-4.059266	39039.105789
HLA A*6801	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.672870	0.613596	-4.059274	47083.590672
HLA B*1517	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.140497	0.081144	-4.059353	13819.661939
HLA A*2301	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.523496	0.463883	-4.059614	33380.771311
HLA A*2601	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.398931	0.339229	-4.059703	25057.132622
HLA A*0216	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.391392	0.331684	-4.059708	24625.886543
HLA A*3201	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.614713	0.554890	-4.059823	41182.506267
HLA B*4601	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.403050	0.343210	-4.059840	25295.893191
HLA B*5101	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.463923	0.403979	-4.059943	29101.999288
HLA A*2603	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.512874	0.452913	-4.059961	32574.244045
HLA B*3501	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.479230	0.419078	-4.060152	30146.001786
HLA A*3201	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.493625	0.433361	-4.060264	31161.977894
HLA B*1509	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.362893	0.302627	-4.060266	23061.769185
HLA B*7301	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.493632	0.433361	-4.060271	31162.483646
HLA B*4801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.428883	0.368545	-4.060338	26846.186718
HLA A*0219	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.404657	0.344156	-4.060501	25389.670606
HLA A*3001	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.217936	0.157255	-4.060682	16517.200665
HLA A*0201	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.112139	0.051389	-4.060750	12946.105307
HLA B*3801	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.557789	0.496961	-4.060828	36123.469071
HLA A*0201	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.397693	0.336669	-4.061024	24985.796186
HLA A*3301	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.628488	0.567351	-4.061137	42509.676869
HLA B*1503	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.491771	0.430602	-4.061169	31029.249499
HLA B*5701	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.411689	0.350403	-4.061286	25804.121325
HLA B*5801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.351390	0.289937	-4.061453	22458.954878
HLA A*2501	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.480696	0.419078	-4.061618	30247.939742
HLA B*4403	1:80-88	9	PALLDLGVP	0.807731	-0.194135	-4.675233	0.613596	-4.061637	47340.534535
HLA B*5401	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.556537	0.494882	-4.061655	36019.458127
HLA A*3201	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.548093	0.486297	-4.061796	35325.891113
HLA A*1101	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.407321	0.345470	-4.061852	25545.910281
HLA A*2301	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.543505	0.481648	-4.061856	34954.619724
HLA A*0219	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.438931	0.376904	-4.062028	27474.598449

HLA A*0206	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.515560	0.453330	-4.062230	32776.291026
HLA B*5101	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.199159	0.136752	-4.062407	15818.283719
HLA B*5801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.360494	0.298081	-4.062413	22934.738726
HLA A*0219	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.396817	0.334057	-4.062759	24935.428466
HLA B*4001	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.399657	0.336669	-4.062988	25099.054551
HLA B*0702	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.410512	0.347374	-4.063138	25734.277703
HLA B*5101	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.493773	0.430602	-4.063171	31172.600423
HLA A*8001	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.394864	0.331684	-4.063180	24823.579911
HLA A*3001	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.291527	0.228245	-4.063282	19567.124767
HLA B*7301	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.545022	0.481648	-4.063374	35076.992432
HLA A*2402	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.571945	0.508560	-4.063385	37320.297553
HLA A*0211	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.395092	0.331684	-4.063408	24836.609733
HLA A*8001	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.413980	0.350403	-4.063577	25940.588416
HLA A*3001	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.155318	0.091584	-4.063734	14299.405129
HLA A*0301	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.350097	0.286262	-4.063835	22392.228945
HLA B*0802	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.467931	0.403979	-4.063952	29371.832790
HLA B*4601	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.409556	0.345470	-4.064086	25677.677665
HLA B*1509	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.523076	0.458831	-4.064245	33348.462015
HLA B*5301	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.083800	0.019419	-4.064381	12128.292078
HLA B*1501	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.414840	0.350403	-4.064436	25992.002168
HLA A*2301	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.517381	0.452913	-4.064468	32913.999485
HLA B*5701	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.401215	0.336669	-4.064546	25189.240389
HLA B*0702	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.408745	0.344171	-4.064574	25629.797241
HLA B*0803	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.468622	0.403979	-4.064642	29418.586079
HLA B*5701	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.407925	0.343210	-4.064716	25581.452522
HLA A*0301	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.366694	0.301939	-4.064755	23264.519541
HLA B*4001	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.437895	0.373125	-4.064770	27409.128749
HLA A*3101	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.351112	0.286262	-4.064850	22444.622399
HLA A*2402	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.580977	0.516095	-4.064882	38104.522002
HLA A*3101	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.415326	0.350403	-4.064923	26021.125539
HLA A*0203	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.438269	0.373125	-4.065144	27432.715468
HLA A*2301	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.524013	0.458831	-4.065182	33420.523943
HLA A*2402	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.554766	0.489404	-4.065362	35872.831977
HLA A*6801	1:196-204	9	LHDFAGLGA	0.949062	-0.348292	-4.666275	0.600770	-4.065504	46374.001427
HLA B*1501	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.320040	0.254355	-4.065685	20894.903233
HLA A*3002	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.218820	0.153079	-4.065741	16550.832800
HLA A*0301	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.368663	0.302627	-4.066036	23370.228374
HLA B*4002	1:494-502	9	ERISTRITN	1.065751	-0.517476	-4.614370	0.548275	-4.066095	41149.991361
HLA B*1501	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.122190	0.055954	-4.066236	13249.217580
HLA B*1501	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.368891	0.302627	-4.066264	23382.495335
HLA A*0212	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.425708	0.359286	-4.066423	26650.689667
HLA B*5401	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.533078	0.466612	-4.066465	34125.385593
HLA B*5401	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.519873	0.453330	-4.066543	33103.465537
HLA B*2705	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.456054	0.389429	-4.066625	28579.485125
HLA B*4001	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.400691	0.334057	-4.066634	25158.870280
HLA A*1101	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.425929	0.359286	-4.066643	26664.245778
HLA A*0219	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.441647	0.374749	-4.066898	27646.958361
HLA A*2403	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.412518	0.345470	-4.067049	25853.446303
HLA A*0219	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.435630	0.368545	-4.067085	27266.558578
HLA B*5801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.352827	0.285427	-4.067401	22533.436387
HLA B*5301	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.278358	0.210953	-4.067405	18982.707279
HLA B*3801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.546550	0.479051	-4.067498	35200.555271
HLA B*4801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.442249	0.374749	-4.067499	27685.274034
HLA A*2301	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.546620	0.479051	-4.067569	35206.268667
HLA B*3901	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.472003	0.404390	-4.067613	29648.498538
HLA A*2403	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.370338	0.302627	-4.067711	23460.547289
HLA B*4601	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.303110	0.235291	-4.067819	20096.016345
HLA B*4801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.411043	0.343210	-4.067833	25765.760572
HLA B*5301	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.579555	0.511716	-4.067839	37980.010426
HLA B*4601	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.399559	0.331684	-4.067874	25093.352309
HLA A*3201	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.213472	0.145582	-4.067890	16348.293406
HLA B*5701	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.412117	0.344171	-4.067946	25829.540570
HLA A*0203	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.410106	0.342132	-4.067974	25710.203981
HLA A*2402	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.565035	0.496961	-4.068074	36731.212299
HLA B*4601	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.407331	0.339229	-4.068102	25546.463089

HLA B*3501	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.418545	0.350403	-4.068142	26214.698816
HLA B*1509	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.452669	0.384476	-4.068192	28357.555621
HLA B*4002	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.623509	0.555251	-4.068259	42025.147368
HLA A*2603	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.645655	0.577199	-4.068456	44223.742302
HLA B*4002	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.550231	0.481648	-4.068583	35500.229225
HLA A*1101	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.452730	0.384129	-4.068601	28361.544594
HLA A*8001	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.411879	0.343210	-4.068670	25815.431195
HLA B*4402	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.441798	0.373125	-4.068673	27656.532305
HLA A*0203	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.268864	0.200115	-4.068749	18572.222667
HLA A*0211	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.550471	0.481648	-4.068823	35519.823966
HLA A*2603	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.601067	0.532233	-4.068833	39908.643315
HLA B*5101	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.297196	0.228245	-4.068952	19824.229717
HLA A*3002	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.521892	0.452913	-4.068979	33257.658475
HLA A*0101	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.340114	0.270903	-4.069212	21883.378097
HLA B*1501	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.413392	0.344171	-4.069221	25905.528204
HLA A*2403	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.412659	0.343210	-4.069450	25861.839522
HLA B*0803	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.459109	0.389429	-4.069680	28781.188971
HLA B*7301	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.304990	0.235291	-4.069699	20183.178601
HLA B*5401	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.516387	0.446544	-4.069842	32838.765759
HLA B*1801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.331139	0.261282	-4.069857	21435.781986
HLA A*8001	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.459560	0.389429	-4.070131	28811.099486
HLA B*4601	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.414309	0.344156	-4.070152	25960.242857
HLA A*6802	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.342696	0.272539	-4.070158	22013.872566
HLA B*3501	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.454645	0.384476	-4.070168	28486.868413
HLA B*4002	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.627823	0.557541	-4.070282	42444.644407
HLA A*0211	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.523797	0.453330	-4.070467	33403.894359
HLA A*0250	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.556810	0.486297	-4.070513	36042.069129
HLA B*4001	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.373905	0.303325	-4.070580	23654.003535
HLA B*0801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.356056	0.285427	-4.070629	22701.555706
HLA B*5401	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.552280	0.481648	-4.070632	35668.094469
HLA B*2705	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.454765	0.384129	-4.070636	28494.729148
HLA B*3501	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.447608	0.376904	-4.070704	28029.025708
HLA B*5801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.210592	0.139834	-4.070758	16240.221747
HLA A*0212	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.407592	0.336669	-4.070922	25561.808288
HLA A*0101	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.373681	0.302627	-4.071054	23641.849932
HLA A*2902	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.407728	0.336669	-4.071059	25569.830166
HLA A*2403	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.430461	0.359286	-4.071176	26943.962188
HLA A*6801	1:439-447	9	LDNQIWQCP	0.718676	-0.141477	-4.648447	0.577199	-4.071248	44508.881312
HLA A*0216	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.414527	0.343210	-4.071318	25973.307253
HLA A*2602	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.626437	0.554890	-4.071547	42309.384102
HLA A*0212	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.403313	0.331684	-4.071629	25311.224809
HLA B*4403	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.586481	0.514746	-4.071735	38590.584933
HLA B*5801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.353295	0.281539	-4.071756	22557.708225
HLA A*2601	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.344414	0.272539	-4.071875	22101.101629
HLA B*4403	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.629437	0.557541	-4.071896	42602.687420
HLA B*3901	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.456092	0.384129	-4.071963	28581.959022
HLA A*2501	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.416205	0.344156	-4.072048	26073.827342
HLA B*5701	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.414309	0.342132	-4.072177	25960.242857
HLA A*3301	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.446992	0.374749	-4.072243	27989.325762
HLA B*1517	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.307699	0.235291	-4.072408	20309.466698
HLA B*0802	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.447176	0.374749	-4.072426	28001.138948
HLA B*1501	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.218073	0.145582	-4.072491	16522.384139
HLA B*4801	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.404192	0.331684	-4.072508	25362.488816
HLA B*0702	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.416701	0.344156	-4.072544	26103.607261
HLA B*4501	1:500-508	9	ITNEVAEVN	1.109580	-0.552039	-4.630111	0.557541	-4.072570	42668.885357
HLA B*4801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.406830	0.334057	-4.072773	25517.042690
HLA B*0702	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.462231	0.389429	-4.072802	28988.863984
HLA A*0212	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.300558	0.227657	-4.072901	19978.295595
HLA B*5801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.186618	0.113627	-4.072991	15368.016209
HLA A*0216	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.457570	0.384476	-4.073093	28679.383957
HLA A*0212	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.446219	0.373125	-4.073095	27939.553169
HLA A*0250	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.531278	0.457680	-4.073598	33984.263451
HLA A*0216	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.448487	0.374749	-4.073737	28085.794205
HLA A*6901	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.259593	0.185815	-4.073778	18179.955426
HLA B*1501	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.363717	0.289937	-4.073781	23105.602116

HLA A*2603	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.641253	0.567351	-4.073901	43777.661189
HLA B*1502	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.532852	0.458831	-4.074021	34107.667198
HLA B*0803	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.527688	0.453330	-4.074358	33704.496885
HLA B*2705	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.449147	0.374749	-4.074397	28128.522104
HLA B*0801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.418564	0.344156	-4.074407	26215.833390
HLA A*2601	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.372526	0.298081	-4.074445	23579.006908
HLA A*2603	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.418686	0.344156	-4.074530	26223.209314
HLA A*0202	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.571668	0.496961	-4.074706	37296.481112
HLA A*2402	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.591505	0.516757	-4.074748	39039.528186
HLA B*3801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.564180	0.489404	-4.074776	36658.952380
HLA A*2602	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.591657	0.516757	-4.074900	39053.258568
HLA B*0803	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.505643	0.430602	-4.075040	32036.320583
HLA B*5401	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.479657	0.404390	-4.075268	30175.698151
HLA A*2902	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.418521	0.343210	-4.075312	26213.280668
HLA A*2601	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.374548	0.299099	-4.075450	23689.092092
HLA B*1517	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.303058	0.227420	-4.075638	20093.624709
HLA B*4002	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.608209	0.532233	-4.075976	40570.410191
HLA B*5401	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.506611	0.430602	-4.076008	32107.805151
HLA A*3301	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.410282	0.334057	-4.076224	25720.637799
HLA A*2602	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.591025	0.514746	-4.076279	38996.467249
HLA B*2705	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.483762	0.407463	-4.076299	30462.242923
HLA A*2902	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.420490	0.344171	-4.076319	26332.388020
HLA B*5701	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.420525	0.344156	-4.076369	26334.524936
HLA A*0301	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.361962	0.285427	-4.076535	23012.416469
HLA A*0101	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.378503	0.301939	-4.076564	23905.762444
HLA A*0216	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.422187	0.345470	-4.076717	26435.441877
HLA B*1517	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.268070	0.191274	-4.076796	18538.293598
HLA A*0301	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.358349	0.281539	-4.076810	22821.738102
HLA A*2603	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.593760	0.516757	-4.077003	39242.807132
HLA B*7301	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.347992	0.270903	-4.077089	22283.950613
HLA B*5801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.331447	0.254355	-4.077092	21450.978812
HLA B*0702	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.379849	0.302627	-4.077222	23979.982092
HLA A*3002	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.461740	0.384476	-4.077264	28956.105760
HLA A*0216	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.484753	0.407463	-4.077290	30531.866852
HLA B*4801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.436605	0.359286	-4.077319	27327.843608
HLA A*0250	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.593457	0.516095	-4.077362	39215.430084
HLA B*0803	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.409248	0.331684	-4.077564	25659.486457
HLA A*0301	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.348678	0.270903	-4.077775	22319.180113
HLA A*0301	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.367740	0.289937	-4.077803	23320.594030
HLA A*6802	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.421035	0.343210	-4.077826	26365.458399
HLA B*0803	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.422017	0.344171	-4.077846	26425.146960
HLA B*1517	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.462457	0.384476	-4.077980	29003.923242
HLA A*0203	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.422140	0.344156	-4.077983	26432.581775
HLA B*5701	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.417365	0.339229	-4.078137	26143.602456
HLA B*5301	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.332671	0.254455	-4.078216	21511.524802
HLA B*1501	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.264736	0.186500	-4.078236	18396.526770
HLA B*1509	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.531741	0.453330	-4.078411	34020.501424
HLA A*6801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.274552	0.195916	-4.078636	18817.069332
HLA A*0216	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.176454	0.097746	-4.078708	15012.531712
HLA B*1509	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.482714	0.403979	-4.078735	30388.831901
HLA A*0101	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.377903	0.299099	-4.078805	23872.806662
HLA A*0219	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.420986	0.342132	-4.078854	26362.463250
HLA B*3501	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.468298	0.389429	-4.078868	29396.631397
HLA B*7301	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.611163	0.532233	-4.078929	40847.238519
HLA A*2501	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.438299	0.359286	-4.079013	27434.644839
HLA A*1101	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.490972	0.411911	-4.079061	30972.227925
HLA B*3501	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.381033	0.301939	-4.079094	24045.454748
HLA A*6901	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.354500	0.275316	-4.079184	22620.398979
HLA B*4501	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.646539	0.567351	-4.079188	44313.790179
HLA A*2603	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.634091	0.554890	-4.079202	43061.715317
HLA A*8001	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.413273	0.334057	-4.079215	25898.381742
HLA A*2602	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.543129	0.463883	-4.079246	34924.376716
HLA B*3801	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.512693	0.433361	-4.079332	32560.677696
HLA B*4801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.365656	0.286262	-4.079393	23208.956553
HLA A*2501	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.413493	0.334057	-4.079436	25911.555184

HLA A*8001	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.423681	0.344156	-4.079525	26526.554679
HLA B*2705	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.382375	0.302627	-4.079748	24119.847122
HLA A*0219	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.411440	0.331684	-4.079756	25789.328239
HLA A*3001	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.232837	0.153079	-4.079758	17093.731535
HLA A*3101	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.361323	0.281539	-4.079784	22978.578834
HLA B*5301	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.610345	0.530534	-4.079811	40770.410159
HLA A*6801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.381766	0.301939	-4.079827	24086.074992
HLA B*5401	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.558898	0.479051	-4.079847	36215.827048
HLA B*5401	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.538681	0.458831	-4.079850	34568.544099
HLA B*5801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.350788	0.270903	-4.079885	22427.872289
HLA A*6802	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.382527	0.302627	-4.079900	24128.330184
HLA A*2601	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.381912	0.301939	-4.079973	24094.155133
HLA A*0301	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.352560	0.272539	-4.080021	22519.543685
HLA B*1501	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.419332	0.339229	-4.080103	26262.251129
HLA B*0803	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.484533	0.404390	-4.080143	30516.344442
HLA B*5801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.352889	0.272539	-4.080350	22536.606099
HLA B*3501	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.412060	0.331684	-4.080376	25826.187149
HLA A*2402	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.575382	0.494882	-4.080501	37616.847309
HLA B*0801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.378606	0.298081	-4.080525	23911.453532
HLA A*0206	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.358607	0.278063	-4.080544	22835.323082
HLA A*6802	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.419778	0.339229	-4.080550	26289.259422
HLA B*5801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.350356	0.269777	-4.080579	22405.558253
HLA B*1801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.353180	0.272539	-4.080641	22551.729318
HLA A*2601	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.383425	0.302627	-4.080798	24178.244811
HLA A*2402	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.514171	0.433361	-4.080810	32671.664557
HLA A*0101	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.379097	0.298081	-4.081016	23938.504710
HLA B*5101	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.485580	0.404390	-4.081191	30590.063499
HLA B*1801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.488813	0.407463	-4.081350	30818.625814
HLA A*2902	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.423516	0.342132	-4.081385	26516.511181
HLA B*0702	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.420645	0.339229	-4.081417	26341.791749
HLA A*0219	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.440722	0.359286	-4.081436	27588.091731
HLA B*3501	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.354040	0.272539	-4.081501	22596.426416
HLA A*2301	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.534908	0.453330	-4.081578	34269.503796
HLA A*0219	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.471009	0.389429	-4.081580	29580.728985
HLA A*2602	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.415740	0.334057	-4.081682	26045.913105
HLA A*0203	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.425922	0.344171	-4.081751	26663.813029
HLA A*8001	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.425922	0.344171	-4.081751	26663.813029
HLA B*3501	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.336292	0.254455	-4.081837	21691.608225
HLA A*3101	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.359977	0.278063	-4.081914	22907.458596
HLA A*2902	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.466434	0.384476	-4.081958	29270.788739
HLA B*1801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.429399	0.347374	-4.082026	26878.157416
HLA A*0206	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.563795	0.481648	-4.082147	36626.442181
HLA A*0212	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.360271	0.278063	-4.082208	22922.954687
HLA A*6802	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.368644	0.286262	-4.082382	23369.216953
HLA B*0802	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.414316	0.331684	-4.082632	25960.664187
HLA B*1501	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.134022	0.051389	-4.082633	13615.143989
HLA B*1501	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.310929	0.228245	-4.082684	20461.103932
HLA A*3001	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.282836	0.200115	-4.082721	19179.455311
HLA A*1101	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.424886	0.342132	-4.082754	26600.275364
HLA B*7301	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.572251	0.489404	-4.082847	37346.553612
HLA B*5701	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.417107	0.334057	-4.083050	26128.049345
HLA A*3002	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.572579	0.489404	-4.083176	37374.850026
HLA A*0206	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.502264	0.419078	-4.083186	31788.063471
HLA A*3002	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.562589	0.479051	-4.083538	36524.934721
HLA B*3501	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.420429	0.336669	-4.083760	26328.684443
HLA A*6901	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.369203	0.285427	-4.083777	23399.325452
HLA B*0802	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.491271	0.407463	-4.083808	30993.514889
HLA B*3901	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.495777	0.411911	-4.083866	31316.783029
HLA A*0301	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.338247	0.254355	-4.083891	21789.462813
HLA B*4501	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.639143	0.555251	-4.083892	43565.501551
HLA B*0801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.356495	0.272539	-4.083956	22724.533339
HLA A*3002	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.542847	0.458831	-4.084015	34901.711633
HLA B*3501	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.428295	0.344156	-4.084139	26809.902537
HLA B*5801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.362247	0.278063	-4.084184	23027.485250
HLA A*6802	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.428486	0.344171	-4.084314	26821.653238

HLA B*4601	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.382464	0.298081	-4.084383	24124.806089
HLA B*4501	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.542177	0.457680	-4.084497	34847.940994
HLA A*2501	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.427828	0.343210	-4.084618	26781.055386
HLA A*0219	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.421402	0.336669	-4.084733	26387.718727
HLA A*0201	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.387365	0.302627	-4.084738	24398.597183
HLA B*1517	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.496759	0.411911	-4.084848	31387.680856
HLA A*0250	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.416564	0.331684	-4.084880	26095.417923
HLA A*2402	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.571268	0.486297	-4.084972	37262.196009
HLA B*4601	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.387661	0.302627	-4.085034	24415.234060
HLA A*2603	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.366624	0.281539	-4.085085	23260.744093
HLA B*0802	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.462076	0.376904	-4.085173	28978.515280
HLA B*5101	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.458376	0.373125	-4.085251	28732.650597
HLA A*3101	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.387912	0.302627	-4.085285	24429.371108
HLA A*0206	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.427459	0.342132	-4.085327	26758.318484
HLA B*5701	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.432790	0.347374	-4.085416	27088.802073
HLA B*4002	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.653075	0.567535	-4.085540	44985.770602
HLA B*0801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.360867	0.275316	-4.085551	22954.475042
HLA A*3101	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.225441	0.139834	-4.085606	16805.084482
HLA B*1509	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.564868	0.479051	-4.085817	36717.106472
HLA A*0203	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.371278	0.285427	-4.085851	23511.369842
HLA A*6901	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.363959	0.278063	-4.085896	23118.480574
HLA A*2301	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.543643	0.457680	-4.085963	34965.778441
HLA B*4801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.433347	0.347374	-4.085973	27123.556085
HLA B*4801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.430335	0.344171	-4.086163	26936.092090
HLA A*0206	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.429491	0.343210	-4.086281	26883.828921
HLA B*1501	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.347600	0.261282	-4.086318	22263.827237
HLA A*0250	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.583300	0.496961	-4.086339	38308.942064
HLA B*4402	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.445637	0.359286	-4.086351	27902.093132
HLA B*4402	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.420448	0.334057	-4.086391	26329.823949
HLA B*4402	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.431892	0.345470	-4.086423	27032.878764
HLA B*0702	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.428556	0.342132	-4.086424	26826.006656
HLA A*2603	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.565489	0.479051	-4.086438	36769.583703
HLA B*1503	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.459637	0.373125	-4.086512	28816.243486
HLA A*0219	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.432198	0.345470	-4.086728	27051.897285
HLA A*8001	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.459919	0.373125	-4.086794	28834.956681
HLA B*1509	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.385948	0.299099	-4.086849	24319.134659
HLA A*3002	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.544534	0.457680	-4.086854	35037.544002
HLA A*2902	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.384961	0.298081	-4.086881	24263.940582
HLA A*0101	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.376912	0.289937	-4.086975	23818.367849
HLA B*5801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.362298	0.275316	-4.086982	23030.226088
HLA A*2603	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.584003	0.496961	-4.087041	38370.959100
HLA A*0211	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.539983	0.452913	-4.087070	34672.304153
HLA A*0216	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.385239	0.298081	-4.087158	24279.434824
HLA B*0803	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.430666	0.343210	-4.087456	26956.646628
HLA A*2902	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.460772	0.373125	-4.087647	28891.638111
HLA A*0206	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.472146	0.384476	-4.087670	29658.284253
HLA B*1801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.357571	0.269777	-4.087794	22780.908392
HLA A*0101	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.360383	0.272539	-4.087845	22928.907971
HLA B*1801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.464773	0.376904	-4.087870	29159.047901
HLA B*4801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.427113	0.339229	-4.087885	26737.047292
HLA A*2602	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.604030	0.516095	-4.087935	40181.825648
HLA A*3101	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.378557	0.290570	-4.087987	23908.737162
HLA A*0211	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.342454	0.254455	-4.087999	22001.609444
HLA B*3501	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.378615	0.290570	-4.088046	23911.970971
HLA B*1801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.472254	0.384129	-4.088125	29665.665781
HLA B*5401	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.541052	0.452913	-4.088139	34757.755141
HLA A*3001	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.274049	0.185815	-4.088234	18795.297110
HLA A*3001	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.299633	0.211398	-4.088234	19935.757283
HLA B*4501	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.574569	0.486297	-4.088273	37546.501138
HLA A*0301	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.366363	0.278063	-4.088300	23246.780263
HLA A*3001	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.274902	0.186500	-4.088402	18832.243388
HLA B*7301	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.528926	0.440475	-4.088451	33800.725906
HLA A*0101	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.366518	0.278063	-4.088455	23255.082070
HLA A*3101	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.316114	0.227657	-4.088457	20706.866082
HLA A*0203	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.390513	0.301939	-4.088574	24576.111395

HLA A*1101	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.496061	0.407463	-4.088598	31337.289599
HLA B*5301	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.604782	0.516095	-4.088687	40251.447245
HLA A*0201	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.392252	0.303325	-4.088927	24674.694581
HLA A*3201	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.466040	0.376904	-4.089136	29244.197735
HLA B*0803	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.466044	0.376904	-4.089141	29244.514153
HLA B*4403	1:466-474	9	YGHPIVLRP	0.630864	-0.063513	-4.656559	0.567351	-4.089208	45348.137058
HLA B*5101	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.501219	0.411911	-4.089307	31711.628907
HLA A*0101	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.364728	0.275316	-4.089411	23159.414142
HLA B*2705	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.473948	0.384476	-4.089472	29781.603564
HLA B*5101	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.508974	0.419078	-4.089896	32283.023382
HLA A*2403	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.437454	0.347374	-4.090080	27381.266215
HLA A*2501	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.497645	0.407463	-4.090182	31451.762242
HLA B*5301	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.523581	0.433361	-4.090220	33387.273050
HLA B*5301	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.595694	0.505350	-4.090343	39417.918942
HLA A*0206	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.435922	0.345470	-4.090452	27284.855838
HLA B*3801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.509569	0.419078	-4.090491	32327.239471
HLA B*4402	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.380476	0.289937	-4.090540	24014.644775
HLA B*1502	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.585448	0.494882	-4.090566	38498.835029
HLA A*3002	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.437985	0.347374	-4.090611	27414.763982
HLA A*2403	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.324598	0.233980	-4.090618	21115.353919
HLA A*3201	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.580025	0.489404	-4.090621	38021.126194
HLA B*4001	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.392588	0.301939	-4.090649	24693.790660
HLA A*3301	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.554639	0.463883	-4.090756	35862.353833
HLA A*0216	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.441389	0.350403	-4.090986	27630.510888
HLA A*2501	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.475355	0.384129	-4.091227	29878.268091
HLA B*5801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.236836	0.145582	-4.091254	17251.851149
HLA A*0206	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.435485	0.344156	-4.091328	27257.414550
HLA B*1502	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.607486	0.516095	-4.091391	40502.866201
HLA B*4402	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.434768	0.343210	-4.091558	27212.476459
HLA A*2403	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.377943	0.286262	-4.091681	23875.002300
HLA B*1502	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.522383	0.430602	-4.091780	33295.283073
HLA A*2501	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.476392	0.384476	-4.091915	29949.635600
HLA B*4001	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.394634	0.302627	-4.092007	24810.422703
HLA A*8001	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.434319	0.342132	-4.092188	27184.372634
HLA A*0202	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.451494	0.359286	-4.092208	28280.953654
HLA A*3301	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.496245	0.403979	-4.092265	31350.515828
HLA B*5101	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.499917	0.407463	-4.092454	31616.728946
HLA B*1801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.436735	0.344156	-4.092578	27335.976051
HLA A*0301	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.368007	0.275316	-4.092691	23334.980915
HLA A*1101	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.477235	0.384476	-4.092759	30007.858812
HLA B*0802	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.461334	0.368545	-4.092789	28929.018105
HLA A*2902	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.424658	0.331684	-4.092974	26586.320285
HLA B*5701	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.392160	0.299099	-4.093061	24669.489123
HLA A*2301	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.469987	0.376904	-4.093083	29511.198449
HLA A*0201	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.395057	0.301939	-4.093118	24834.594365
HLA A*2902	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.371200	0.278063	-4.093137	23507.172818
HLA B*5801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.354481	0.261282	-4.093199	22619.420009
HLA A*8001	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.440578	0.347374	-4.093205	27578.989073
HLA B*0801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.375023	0.281539	-4.093484	23714.993625
HLA A*2603	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.092789	-0.000735	-4.093524	12381.942329
HLA B*1503	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.229162	0.135619	-4.093543	16949.710479
HLA A*0203	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.379811	0.286262	-4.093549	23977.906517
HLA B*4403	1:434-442	9	LTAAGLDNQ	0.675174	-0.119923	-4.648811	0.555251	-4.093560	44546.219122
HLA A*3301	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.648494	0.554890	-4.093604	44513.697335
HLA B*7301	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.572732	0.479051	-4.093681	37387.994934
HLA B*4801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.444121	0.350403	-4.093718	27804.901836
HLA B*0702	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.371821	0.278063	-4.093758	23540.770001
HLA B*4001	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.392858	0.299099	-4.093759	24709.158367
HLA B*3801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.551561	0.457680	-4.093881	35609.097421
HLA B*4601	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.369227	0.275316	-4.093911	23400.591363
HLA A*6901	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.348279	0.254355	-4.093924	22298.663020
HLA B*0702	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.131048	0.037065	-4.093983	13522.213562
HLA B*0801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.294100	0.200115	-4.093985	19683.381062
HLA B*4402	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.372128	0.278063	-4.094066	23557.459151
HLA A*6802	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.207434	0.113362	-4.094073	16122.569103

HLA A*2603	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.206659	0.112320	-4.094339	16093.811747
HLA A*3001	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.305347	0.210953	-4.094393	20199.782118
HLA B*5101	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.471446	0.376904	-4.094542	29610.509260
HLA A*2902	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.440043	0.345470	-4.094573	27544.992610
HLA A*2501	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.426317	0.331684	-4.094633	26688.057755
HLA A*0206	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.431368	0.336669	-4.094699	27000.285821
HLA B*4801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.440287	0.345470	-4.094817	27560.494567
HLA A*2403	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.428939	0.334057	-4.094882	26849.672582
HLA B*4501	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.606642	0.511716	-4.094926	40424.279889
HLA A*0203	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.398274	0.303325	-4.094949	25019.205588
HLA B*5101	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.454360	0.359286	-4.095075	28468.227108
HLA A*3002	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.438405	0.343210	-4.095195	27441.324479
HLA B*4501	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.662877	0.567535	-4.095342	46012.646767
HLA A*2403	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.439526	0.344156	-4.095369	27512.228732
HLA A*6802	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.365209	0.269777	-4.095432	23185.112812
HLA A*2602	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.590327	0.494882	-4.095446	38933.860489
HLA A*0202	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.306874	0.211398	-4.095475	20270.938230
HLA B*4001	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.393558	0.298081	-4.095477	24749.025288
HLA A*0219	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.439667	0.344171	-4.095496	27521.160468
HLA A*0212	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.370813	0.275316	-4.095497	23486.198932
HLA B*4501	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.626315	0.530534	-4.095780	42297.483544
HLA B*5401	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.480372	0.384476	-4.095895	30225.366125
HLA A*1101	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.440106	0.344171	-4.095935	27549.016318
HLA A*0219	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.469155	0.373125	-4.096030	29454.735613
HLA A*3101	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.368618	0.272539	-4.096080	23367.826321
HLA B*1509	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.443456	0.347374	-4.096083	27762.365139
HLA A*2403	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.386752	0.290570	-4.096182	24364.171136
HLA B*4801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.374283	0.278063	-4.096220	23674.614961
HLA B*0803	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.480675	0.384129	-4.096546	30246.467036
HLA B*4402	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.443936	0.347374	-4.096562	27793.021081
HLA A*6901	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.386568	0.289937	-4.096632	24353.892323
HLA B*0802	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.481121	0.384476	-4.096645	30277.572726
HLA B*1801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.438894	0.342132	-4.096762	27472.220400
HLA A*3101	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.332081	0.235291	-4.096791	21482.334509
HLA B*4001	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.372204	0.275316	-4.096888	23561.537688
HLA B*1801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.196462	0.099536	-4.096926	15720.347867
HLA B*3901	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.504397	0.407463	-4.096934	31944.596284
HLA A*0101	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.383307	0.286262	-4.097045	24171.705614
HLA A*0202	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.290129	0.192958	-4.097171	19504.241722
HLA B*5301	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.594263	0.496961	-4.097301	39288.265477
HLA B*4801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.434002	0.336669	-4.097333	27164.526182
HLA B*1801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.470490	0.373125	-4.097365	29545.383828
HLA B*7301	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.605926	0.508560	-4.097366	40357.634172
HLA A*6801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.550701	0.453330	-4.097371	35538.660473
HLA A*0216	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.400111	0.302627	-4.097484	25125.274376
HLA A*0211	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.516659	0.419078	-4.097581	32859.380100
HLA B*4402	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.448231	0.350403	-4.097827	28069.237514
HLA B*4801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.400630	0.302627	-4.098003	25155.331754
HLA B*4402	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.401431	0.303325	-4.098106	25201.780441
HLA B*1503	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.506066	0.407463	-4.098602	32067.532106
HLA A*2603	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.430297	0.331684	-4.098613	26933.760650
HLA A*3301	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.593502	0.494882	-4.098620	39219.461163
HLA A*2402	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.562538	0.463883	-4.098655	36520.587871
HLA B*4501	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.613416	0.514746	-4.098670	41059.708090
HLA A*3201	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.510656	0.411911	-4.098745	32408.313545
HLA A*2601	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.385018	0.286262	-4.098755	24267.091152
HLA A*0203	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.401401	0.302627	-4.098774	25200.008099
HLA B*1503	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.396916	0.298081	-4.098835	24941.094822
HLA A*0301	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.333538	0.234640	-4.098898	21554.510054
HLA A*0301	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.368738	0.269777	-4.098961	23374.274495
HLA A*0212	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.449518	0.350403	-4.099115	28152.575588
HLA A*0219	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.220272	0.120764	-4.099508	16606.259993
HLA B*1501	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.374950	0.275316	-4.099634	23711.016798
HLA B*1801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.484131	0.384476	-4.099654	30488.127099
HLA B*4402	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.441936	0.342132	-4.099805	27665.361222

HLA B*0702	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.484063	0.384129	-4.099934	30483.344290
HLA A*0219	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.381496	0.281539	-4.099957	24071.094808
HLA A*0101	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.327380	0.227420	-4.099960	21251.038366
HLA B*3501	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.327568	0.227420	-4.100148	21260.237618
HLA A*2902	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.450683	0.350403	-4.100280	28228.218977
HLA B*4001	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.439533	0.339229	-4.100304	27512.675250
HLA B*3901	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.468939	0.368545	-4.100394	29440.079350
HLA A*2603	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.293463	0.192958	-4.100505	19654.544794
HLA A*0201	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.386883	0.286262	-4.100621	24371.553473
HLA A*2601	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.390584	0.289937	-4.100647	24580.100339
HLA A*2301	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.541233	0.440475	-4.100757	34772.236898
HLA B*4002	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.615587	0.514746	-4.100841	41265.468638
HLA A*2602	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.579912	0.479051	-4.100861	38011.254352
HLA B*3901	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.391662	0.290570	-4.101092	24641.211991
HLA A*6802	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.399260	0.298081	-4.101180	25076.117694
HLA B*0802	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.474420	0.373125	-4.101295	29814.005328
HLA B*0801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.213637	0.112320	-4.101317	16354.485551
HLA A*2402	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.505786	0.404390	-4.101396	32046.894417
HLA A*0250	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.560498	0.458831	-4.101667	36349.497104
HLA A*2603	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.632301	0.530534	-4.101767	42884.565864
HLA A*0101	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.371785	0.269777	-4.102008	23538.859784
HLA A*0250	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.222776	0.120764	-4.102013	16702.304002
HLA A*0250	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.568625	0.466612	-4.102013	37036.102331
HLA A*0216	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.491475	0.389429	-4.102046	31008.105741
HLA A*0216	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.446205	0.344156	-4.102049	27938.646284
HLA A*3001	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.249885	0.147675	-4.102210	17778.075329
HLA B*0801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.329915	0.227657	-4.102258	21375.449180
HLA B*1517	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.242096	0.139834	-4.102262	17462.089076
HLA B*1503	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.363659	0.261282	-4.102377	23102.477358
HLA B*0801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.313779	0.211398	-4.102381	20595.815214
HLA B*1503	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.470971	0.368545	-4.102426	29578.168641
HLA B*1509	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.514413	0.411911	-4.102502	32689.874889
HLA A*2403	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.441748	0.339229	-4.102520	27653.390490
HLA B*5801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.330204	0.227657	-4.102547	21389.677487
HLA A*0212	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.388042	0.285427	-4.102615	24436.641000
HLA B*1517	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.446788	0.344171	-4.102617	27976.155396
HLA A*0211	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.330416	0.227657	-4.102759	21400.094443
HLA A*2501	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.492345	0.389429	-4.102915	31070.235555
HLA A*0219	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.405557	0.302627	-4.102930	25442.332225
HLA B*1501	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.384470	0.281539	-4.102931	24236.521653
HLA A*0301	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.364225	0.261282	-4.102943	23132.617626
HLA B*1509	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.549496	0.446544	-4.102951	35440.167719
HLA A*1101	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.453724	0.350403	-4.103320	28426.520990
HLA A*6801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.534140	0.430602	-4.103537	34208.933478
HLA A*3101	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.325825	0.222188	-4.103637	21175.067153
HLA A*3101	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.401755	0.298081	-4.103675	25220.602226
HLA B*0702	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.478440	0.374749	-4.103691	30091.254485
HLA B*0802	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.493672	0.389429	-4.104243	31165.349733
HLA B*1801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.523550	0.419078	-4.104472	33384.925054
HLA A*6801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.516462	0.411911	-4.104551	32844.451182
HLA B*1509	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.448726	0.344156	-4.104570	28101.296467
HLA A*0201	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.382642	0.278063	-4.104579	24134.727080
HLA A*2403	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.448773	0.344171	-4.104602	28104.337129
HLA B*5701	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.407246	0.302627	-4.104619	25541.488246
HLA B*4601	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.386169	0.281539	-4.104630	24331.504803
HLA A*0219	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.447928	0.343210	-4.104718	28049.655509
HLA A*3002	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.551263	0.446544	-4.104718	35584.640383
HLA B*4601	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.406661	0.301939	-4.104722	25507.105431
HLA B*3501	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.407427	0.302627	-4.104800	25552.130062
HLA B*7301	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.599866	0.494882	-4.104985	39798.470087
HLA A*6901	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.403066	0.298081	-4.104986	25296.851145
HLA B*5801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.338968	0.233980	-4.104988	21825.681605
HLA A*0203	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.444281	0.339229	-4.105052	27815.132375
HLA B*0803	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.479805	0.374749	-4.105056	30185.984476
HLA B*1501	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.305274	0.200115	-4.105159	20196.394766

HLA A*2902	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.376099	0.270903	-4.105196	23773.825813
HLA B*0702	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.455629	0.350403	-4.105226	28551.514078
HLA A*0201	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.395308	0.289937	-4.105372	24848.974233
HLA A*0201	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.403574	0.298081	-4.105493	25326.428705
HLA B*4001	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.396072	0.290570	-4.105502	24892.702478
HLA B*5801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.301550	0.195916	-4.105634	20023.957612
HLA A*2301	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.517547	0.411911	-4.105636	32926.644250
HLA B*0802	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.465170	0.359286	-4.105884	29185.719371
HLA A*2402	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.546401	0.440475	-4.105926	35188.560156
HLA A*2402	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.584992	0.479051	-4.105941	38458.450985
HLA B*2705	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.474589	0.368545	-4.106044	29825.620503
HLA B*1503	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.341738	0.235291	-4.106447	21965.336366
HLA A*0201	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.392123	0.285427	-4.106696	24667.353868
HLA A*0101	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.392148	0.285427	-4.106722	24668.821836
HLA A*8001	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.397306	0.290570	-4.106736	24963.503023
HLA A*3201	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.623507	0.516757	-4.106750	42024.920017
HLA A*6801	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.438586	0.331684	-4.106902	27452.757859
HLA B*5401	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.397653	0.290570	-4.107083	24983.498395
HLA B*7301	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.491614	0.384476	-4.107137	31018.004596
HLA A*3201	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.560137	0.452913	-4.107224	36319.226116
HLA B*0803	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.491900	0.384476	-4.107424	31038.483437
HLA A*3002	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.560872	0.453330	-4.107542	36380.777388
HLA A*2902	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.335213	0.227657	-4.107556	21637.811763
HLA A*2501	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.480945	0.373125	-4.107820	30265.290344
HLA B*0801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.409976	0.301939	-4.108037	25702.555205
HLA A*6802	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.386115	0.278063	-4.108052	24328.477485
HLA A*6901	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.335561	0.227420	-4.108141	21655.143309
HLA A*6901	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.377962	0.269777	-4.108185	23876.035611
HLA B*2705	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.450439	0.342132	-4.108307	28212.341444
HLA B*2705	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.467762	0.359286	-4.108476	29360.394336
HLA B*3901	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.407700	0.299099	-4.108601	25568.170261
HLA B*0802	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.407758	0.299099	-4.108660	25571.628519
HLA A*3101	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.308805	0.200115	-4.108690	20361.282379
HLA A*0101	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.390288	0.281539	-4.108749	24563.351121
HLA A*2902	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.448038	0.339229	-4.108809	28056.788456
HLA A*2403	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.412143	0.303325	-4.108818	25831.077700
HLA A*8001	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.412192	0.303325	-4.108867	25834.012476
HLA A*3101	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.334107	0.225172	-4.108934	21582.747552
HLA A*3101	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.370237	0.261282	-4.108955	23455.090408
HLA A*3201	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.562329	0.453330	-4.108999	36503.008166
HLA A*0250	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.443179	0.334057	-4.109122	27744.648219
HLA B*4402	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.445945	0.336669	-4.109275	27921.874228
HLA B*3901	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.486252	0.376904	-4.109349	30637.429945
HLA B*4001	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.381893	0.272539	-4.109354	24093.112382
HLA A*2402	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.591152	0.481648	-4.109504	39007.861108
HLA B*4403	1:8-16	9	DVPETPARP	0.603076	-0.035541	-4.677164	0.567535	-4.109629	47551.523303
HLA A*0250	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.599500	0.489404	-4.110096	39764.896627
HLA B*2705	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.483292	0.373125	-4.110167	30429.301276
HLA B*3501	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.454431	0.344171	-4.110260	28472.847781
HLA A*2902	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.258073	0.147675	-4.110398	18116.433213
HLA A*6802	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.395936	0.285427	-4.110509	24884.893031
HLA A*3301	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.577142	0.466612	-4.110530	37769.580265
HLA A*2501	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.479190	0.368545	-4.110645	30143.229442
HLA A*6901	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.247434	0.136752	-4.110682	17678.044761
HLA A*1101	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.483825	0.373125	-4.110700	30466.692776
HLA B*1509	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.470017	0.359286	-4.110731	29513.274002
HLA B*0801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.224106	0.113362	-4.110745	16753.524790
HLA A*6901	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.338432	0.227657	-4.110775	21798.777211
HLA B*0803	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.456282	0.345470	-4.110813	28594.486410
HLA A*2601	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.396321	0.285427	-4.110894	24906.981248
HLA B*4001	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.392449	0.281539	-4.110910	24685.910068
HLA A*6801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.263639	0.152623	-4.111015	18350.108110
HLA A*3101	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.413031	0.301939	-4.111092	25883.954702
HLA A*0202	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.530249	0.419078	-4.111171	33903.832000
HLA B*4601	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.397484	0.286262	-4.111222	24973.768917

HLA A*0201	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.366109	0.254455	-4.111654	23233.201879
HLA A*0216	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.453881	0.342132	-4.111749	28436.826408
HLA B*4402	1:289-297	9	AETFLEALS	0.785461	-0.921388	-3.975883	-0.135927	-4.111810	9459.824995
HLA B*2705	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.398088	0.286262	-4.111826	25008.515133
HLA A*8001	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.410987	0.299099	-4.111888	25762.415432
HLA B*4501	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.628142	0.516095	-4.112048	42475.884330
HLA B*0802	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.456388	0.344171	-4.112217	28601.448442
HLA B*3901	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.487249	0.374749	-4.112499	30707.786528
HLA B*3901	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.502001	0.389429	-4.112572	31768.808676
HLA B*5301	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.607476	0.494882	-4.112595	40501.989747
HLA B*4001	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.390746	0.278063	-4.112683	24589.277370
HLA A*3301	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.559394	0.446544	-4.112850	36257.190533
HLA B*4001	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.383763	0.270903	-4.112860	24197.087583
HLA A*2403	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.410942	0.298081	-4.112861	25759.767503
HLA B*3501	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.388229	0.275316	-4.112913	24447.219251
HLA B*4402	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.382706	0.269777	-4.112929	24138.252625
HLA B*4402	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.383986	0.270903	-4.113083	24209.526618
HLA A*0212	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.347769	0.234640	-4.113129	22272.500954
HLA B*1517	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.502605	0.389429	-4.113176	31813.008889
HLA B*0803	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.449852	0.336669	-4.113182	28174.210826
HLA B*4601	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.367561	0.254355	-4.113206	23311.007702
HLA B*0801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.416802	0.303325	-4.113477	26109.680325
HLA B*0802	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.458947	0.345470	-4.113477	28770.447466
HLA B*4601	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.398960	0.285427	-4.113533	25058.759351
HLA A*0301	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.368205	0.254455	-4.113750	23345.587456
HLA A*0212	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.417196	0.303325	-4.113871	26133.421192
HLA B*0803	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.482542	0.368545	-4.113997	30376.833055
HLA A*2902	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.299870	0.185815	-4.114055	19946.653133
HLA B*3901	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.498611	0.384476	-4.114134	31521.771920
HLA B*2705	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.461540	0.347374	-4.114167	28942.793628
HLA B*0702	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.399608	0.285427	-4.114181	25096.203268
HLA B*3501	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.453475	0.339229	-4.114246	28410.224525
HLA A*0101	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.375566	0.261282	-4.114284	23744.648408
HLA A*0211	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.491205	0.376904	-4.114301	30988.820443
HLA B*0802	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.457593	0.343210	-4.114384	28680.935522
HLA A*2402	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.567772	0.453330	-4.114442	36963.442580
HLA A*0216	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.487594	0.373125	-4.114469	30732.216722
HLA B*4402	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.446311	0.331684	-4.114627	27945.448636
HLA A*0212	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.384588	0.269777	-4.114811	24243.078385
HLA B*4002	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.645388	0.530534	-4.114854	44196.476718
HLA A*0216	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.349858	0.234640	-4.115217	22379.876127
HLA B*4001	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.400722	0.285427	-4.115295	25160.639729
HLA A*0201	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.385328	0.269777	-4.115551	24284.426601
HLA A*3301	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.631678	0.516095	-4.115584	42823.129714
HLA A*2403	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.405555	0.289937	-4.115618	25442.194585
HLA B*1502	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.579550	0.463883	-4.115668	37979.599493
HLA B*5801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.370310	0.254455	-4.115855	23459.024311
HLA A*6802	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.344123	0.228245	-4.115878	22086.280602
HLA B*1503	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.349862	0.233980	-4.115882	22380.118274
HLA A*2301	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.519895	0.403979	-4.115915	33105.077351
HLA B*1517	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.460211	0.344156	-4.116054	28854.306417
HLA A*3101	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.307452	0.191274	-4.116178	20297.933417
HLA B*5701	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.387146	0.270903	-4.116244	24386.324856
HLA B*4002	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.575223	0.458831	-4.116391	37603.011652
HLA A*6901	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.228735	0.112320	-4.116415	16933.030010
HLA B*5301	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.218848	0.101982	-4.116866	16551.907292
HLA A*8001	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.262471	0.145582	-4.116889	18300.836170
HLA A*0202	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.598741	0.481648	-4.117093	39695.472351
HLA B*1501	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.419130	0.301939	-4.117191	26250.035446
HLA A*0203	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.325905	0.208642	-4.117262	21178.962373
HLA A*6801	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.629202	0.511716	-4.117486	42579.646072
HLA A*0219	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.467964	0.350403	-4.117561	29374.057451
HLA A*0201	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.392924	0.275316	-4.117608	24712.901517
HLA B*0802	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.461966	0.344156	-4.117809	28971.148000
HLA B*5101	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.507292	0.389429	-4.117863	32158.217589

HLA B*1503	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.451926	0.334057	-4.117869	28309.119085
HLA B*3801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.576712	0.458831	-4.117881	37732.206517
HLA B*0802	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.460034	0.342132	-4.117903	28842.601396
HLA B*5701	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.419983	0.301939	-4.118044	26301.635646
HLA A*2902	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.462243	0.344156	-4.118087	28989.648127
HLA B*0702	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.404441	0.286262	-4.118179	25377.037062
HLA A*0101	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.345838	0.227657	-4.118181	22173.676622
HLA B*5301	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.584907	0.466612	-4.118295	38450.961700
HLA A*0201	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.389242	0.270903	-4.118339	24504.288415
HLA A*0203	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.216297	0.097746	-4.118550	16454.947631
HLA B*5701	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.352635	0.233980	-4.118655	22523.442526
HLA B*4501	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.597733	0.479051	-4.118682	39603.452238
HLA A*2601	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.388504	0.269777	-4.118727	24462.698188
HLA B*3901	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.478029	0.359286	-4.118743	30062.779655
HLA B*4501	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.559274	0.440475	-4.118799	36247.188396
HLA B*5801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.353495	0.234640	-4.118854	22568.083560
HLA B*4501	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.615890	0.496961	-4.118928	41294.276857
HLA A*2301	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.538115	0.419078	-4.119037	34523.503577
HLA A*0301	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.354425	0.235291	-4.119134	22616.483354
HLA B*4501	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.627701	0.508560	-4.119141	42432.705804
HLA A*2301	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.549745	0.430602	-4.119143	35460.496649
HLA B*0702	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.347421	0.228245	-4.119176	22254.675311
HLA A*2601	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.397294	0.278063	-4.119231	24962.827783
HLA A*3101	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.394568	0.275316	-4.119252	24806.664782
HLA A*0250	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.601039	0.481648	-4.119391	39906.052583
HLA A*0212	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.240369	0.120764	-4.119606	17392.792982
HLA A*0216	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.310906	0.191274	-4.119632	20459.997039
HLA A*2402	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.577316	0.457680	-4.119636	37784.703656
HLA A*6802	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.401213	0.281539	-4.119674	25189.104119
HLA A*8001	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.417755	0.298081	-4.119675	26167.091044
HLA B*4403	1:235-243	9	GVDSAVAAA	0.870938	-0.338705	-4.652055	0.532233	-4.119822	44880.272773
HLA A*3001	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.272557	0.152623	-4.119934	18730.840786
HLA A*3002	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.462109	0.342132	-4.119977	28980.710151
HLA A*0206	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.470642	0.350403	-4.120239	29555.775076
HLA B*1517	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.462440	0.342132	-4.120309	29002.824907
HLA A*2501	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.457020	0.336669	-4.120351	28643.101292
HLA B*5301	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.602023	0.481648	-4.120375	39996.611969
HLA A*8001	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.459694	0.339229	-4.120465	28819.985153
HLA A*6901	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.381813	0.261282	-4.120531	24088.681193
HLA B*4002	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.632249	0.511716	-4.120533	42879.462151
HLA B*0702	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.311820	0.191274	-4.120546	20503.099353
HLA A*2603	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.629129	0.508560	-4.120569	42572.505784
HLA A*0201	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.402134	0.281539	-4.120595	25242.578742
HLA B*4801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.411167	0.290570	-4.120598	25773.149297
HLA B*3501	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.418695	0.298081	-4.120615	26223.776779
HLA B*4601	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.398694	0.278063	-4.120631	25043.445174
HLA A*2501	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.419741	0.299099	-4.120642	26286.983969
HLA A*0211	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.489196	0.368545	-4.120651	30845.814032
HLA B*3501	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.466157	0.345470	-4.120688	29252.109199
HLA B*4801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.419807	0.299099	-4.120708	26290.966141
HLA A*2402	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.573677	0.452913	-4.120764	37469.393907
HLA A*0219	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.375375	0.254455	-4.120920	23734.245758
HLA A*3301	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.637679	0.516757	-4.120922	43418.917246
HLA B*5701	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.393481	0.272539	-4.120942	24744.607330
HLA B*1801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.495751	0.374749	-4.121002	31314.919461
HLA B*1503	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.260869	0.139834	-4.121034	18233.438832
HLA B*4001	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.411092	0.289937	-4.121156	25768.687927
HLA A*0216	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.465495	0.344171	-4.121323	29207.516534
HLA A*1101	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.424661	0.303325	-4.121336	26586.464115
HLA A*0216	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.403005	0.281539	-4.121466	25293.293213
HLA B*0702	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.403015	0.281539	-4.121476	25293.840554
HLA B*4001	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.356147	0.234640	-4.121507	22706.345915
HLA B*5801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.349172	0.227420	-4.121752	22344.550823
HLA B*5301	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.187910	0.066046	-4.121864	15413.810900
HLA B*4002	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.638821	0.516757	-4.122064	43533.224732

HLA A*0206	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.173700	0.051389	-4.122311	14917.647524
HLA B*4601	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.395036	0.272539	-4.122497	24833.385223
HLA B*4402	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.408014	0.285427	-4.122588	25586.711990
HLA B*1501	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.392437	0.269777	-4.122660	24685.242337
HLA B*1502	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.482120	0.359286	-4.122834	30347.267098
HLA B*0702	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.392639	0.269777	-4.122862	24696.729829
HLA A*2301	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.527267	0.404390	-4.122878	33671.874254
HLA B*5401	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.542111	0.419078	-4.123033	34842.662736
HLA B*7301	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.569605	0.446544	-4.123061	37119.747268
HLA A*2601	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.398414	0.275316	-4.123098	25027.327974
HLA B*1509	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.392900	0.269777	-4.123123	24711.564612
HLA B*4403	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.309778	0.186500	-4.123278	20406.936530
HLA A*2501	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.425224	0.301939	-4.123286	26621.005692
HLA A*3002	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.535241	0.411911	-4.123330	34295.839889
HLA B*1801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.492027	0.368545	-4.123482	31047.552158
HLA B*2705	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.409037	0.285427	-4.123610	25646.996150
HLA B*5701	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.421724	0.298081	-4.123643	26407.283361
HLA B*0802	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.474049	0.350403	-4.123646	29788.532323
HLA A*3101	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.316622	0.192958	-4.123664	20731.076944
HLA A*0202	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.469496	0.345470	-4.124026	29477.849972
HLA A*0301	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.319968	0.195916	-4.124051	20891.399315
HLA B*5101	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.492847	0.368545	-4.124302	31106.226903
HLA A*6802	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.333087	0.208642	-4.124445	21532.133036
HLA A*3002	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.565005	0.440475	-4.124530	36728.629137
HLA B*5701	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.415122	0.290570	-4.124552	26008.881309
HLA A*3101	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.267840	0.143276	-4.124563	18528.467772
HLA B*0702	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.415258	0.290570	-4.124688	26017.043489
HLA B*3501	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.467997	0.343210	-4.124787	29376.282281
HLA B*7301	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.582478	0.457680	-4.124798	38236.474197
HLA B*1503	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.266063	0.141148	-4.124915	18452.843385
HLA A*0203	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.268265	0.143276	-4.124988	18546.619547
HLA A*0202	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.578026	0.452913	-4.125113	37846.486251
HLA A*2601	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.386402	0.261282	-4.125120	24344.539737
HLA B*3901	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.468448	0.343210	-4.125238	29406.811240
HLA A*6901	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.321222	0.195916	-4.125306	20951.839337
HLA B*1801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.462034	0.336669	-4.125365	28975.693547
HLA B*3901	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.457128	0.331684	-4.125444	28650.230155
HLA A*6901	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.263176	0.137730	-4.125446	18330.561934
HLA B*5401	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.500361	0.374749	-4.125612	31649.072605
HLA B*0802	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.459694	0.334057	-4.125636	28819.985153
HLA B*1503	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.500415	0.374749	-4.125666	31653.010863
HLA A*3301	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.634268	0.508560	-4.125708	43079.190795
HLA B*4002	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.622837	0.496961	-4.125876	41960.175147
HLA A*2601	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.353600	0.227657	-4.125943	22573.578316
HLA A*0301	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.360038	0.233980	-4.126058	22910.680920
HLA B*5301	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.584973	0.458831	-4.126142	38456.786574
HLA B*5701	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.411870	0.285427	-4.126443	25814.872567
HLA B*4402	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.429106	0.302627	-4.126479	26859.987579
HLA A*0211	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.468666	0.342132	-4.126535	29421.610109
HLA A*0202	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.429277	0.302627	-4.126650	26870.597272
HLA B*5301	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.510802	0.384129	-4.126673	32419.185542
HLA A*3301	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.560061	0.433361	-4.126700	36312.939205
HLA B*1801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.430165	0.303325	-4.126840	26925.602201
HLA B*5701	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.430180	0.303325	-4.126855	26926.476203
HLA A*2603	1:315-323	9	RAFEGAVRD	1.121906	-0.607160	-4.641668	0.514746	-4.126922	43819.600581
HLA B*0702	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.362432	0.235291	-4.127141	23037.328869
HLA A*3002	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.546317	0.419078	-4.127239	35181.707639
HLA B*0802	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.474702	0.347374	-4.127329	29833.366467
HLA A*2501	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.472867	0.345470	-4.127398	29707.582725
HLA B*2705	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.477853	0.350403	-4.127450	30050.584406
HLA A*3002	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.558598	0.430602	-4.127995	36190.757507
HLA A*2603	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.644154	0.516095	-4.128060	44071.128339
HLA B*4601	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.399002	0.270903	-4.128099	25061.199641
HLA A*0211	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.502898	0.374749	-4.128149	31834.529271
HLA B*3801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.574863	0.446544	-4.128319	37571.900026

HLA B*1517	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.478739	0.350403	-4.128335	30111.935964
HLA B*0802	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.465046	0.336669	-4.128377	29177.352320
HLA B*4501	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.645338	0.516757	-4.128581	44191.455945
HLA A*2403	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.407108	0.278063	-4.129045	25533.337126
HLA A*3001	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.272325	0.143276	-4.129048	18720.811626
HLA B*4002	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.615413	0.486297	-4.129116	41248.952065
HLA B*3801	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.569661	0.440475	-4.129186	37124.567110
HLA A*2601	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.383559	0.254355	-4.129204	24185.701653
HLA A*2501	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.471493	0.342132	-4.129361	29613.713225
HLA B*1502	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.618824	0.489404	-4.129421	41574.245085
HLA B*4801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.432748	0.303325	-4.129423	27086.164348
HLA B*5301	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.608503	0.479051	-4.129452	40597.854647
HLA A*6802	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.404782	0.275316	-4.129466	25396.951481
HLA B*3801	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.560160	0.430602	-4.129558	36321.190999
HLA B*1517	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.468871	0.339229	-4.129642	29435.460953
HLA B*1509	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.498221	0.368545	-4.129676	31493.476765
HLA A*0301	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.357418	0.227657	-4.129761	22772.899058
HLA A*0212	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.419736	0.289937	-4.129800	26286.699551
HLA B*5801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.355088	0.225172	-4.129915	22651.013139
HLA B*1509	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.271145	0.141148	-4.129997	18670.039287
HLA B*0801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.416280	0.286262	-4.130018	26078.341542
HLA B*3801	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.583396	0.453330	-4.130066	38317.440138
HLA A*0250	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.514286	0.384129	-4.130158	32680.326459
HLA B*4403	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.609281	0.479051	-4.130230	40670.617269
HLA B*4001	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.384614	0.254355	-4.130259	24244.521103
HLA A*6802	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-3.955137	-0.175217	-4.130354	9018.558974
HLA A*0201	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.391763	0.261282	-4.130481	24646.944826
HLA B*5801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.365773	0.235291	-4.130482	23215.235296
HLA B*1509	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.432466	0.301939	-4.130527	27068.586076
HLA B*7301	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.583892	0.453330	-4.130562	38361.203956
HLA B*0702	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.434012	0.303325	-4.130687	27165.114017
HLA A*0212	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.412542	0.281539	-4.131003	25854.844983
HLA A*2402	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.589843	0.458831	-4.131012	38890.495317
HLA B*5401	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.538477	0.407463	-4.131013	34552.277884
HLA B*1503	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.401920	0.270903	-4.131017	25230.154881
HLA B*5801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.359361	0.228245	-4.131117	22875.012772
HLA B*4801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.412669	0.281539	-4.131130	25862.399166
HLA A*2601	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.385591	0.254455	-4.131136	24299.145178
HLA A*2902	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.434533	0.303325	-4.131208	27197.758793
HLA A*6801	1:72-80	9	ADGAPKLDP	0.674928	-0.120038	-4.686104	0.554890	-4.131215	48540.497644
HLA B*4501	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.620643	0.489404	-4.131239	41748.691989
HLA A*0203	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.402256	0.270903	-4.131353	25249.680838
HLA B*1801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.490686	0.359286	-4.131400	30951.792798
HLA B*4501	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.550506	0.419078	-4.131428	35522.706457
HLA B*4501	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.590273	0.458831	-4.131442	38929.016350
HLA B*4002	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.640104	0.508560	-4.131544	43662.003247
HLA A*6801	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.647650	0.516095	-4.131556	44427.328946
HLA B*4002	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.647655	0.516095	-4.131560	44427.809643
HLA A*0301	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.340293	0.208642	-4.131651	21892.377332
HLA A*0301	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.356880	0.225172	-4.131708	22744.703988
HLA B*3901	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.505055	0.373125	-4.131930	31993.021634
HLA B*4001	1:289-297	9	AETFLEALS	0.785461	-0.921388	-3.996051	-0.135927	-4.131978	9909.484926
HLA B*4402	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.431239	0.299099	-4.132140	26992.253246
HLA A*0101	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.367533	0.235291	-4.132242	23309.494432
HLA A*0211	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.491602	0.359286	-4.132316	31017.165587
HLA B*1503	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.422896	0.290570	-4.132326	26478.667046
HLA B*3501	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.366443	0.233980	-4.132463	23251.056581
HLA B*4403	1:272-280	9	QRDFVAATG	1.082447	-0.566352	-4.648604	0.516095	-4.132509	44525.017040
HLA B*4801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.417969	0.285427	-4.132542	26179.976272
HLA B*7301	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.591408	0.458831	-4.132577	39030.869966
HLA B*0801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.325606	0.192958	-4.132648	21164.416239
HLA A*0211	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.478363	0.345470	-4.132893	30085.882883
HLA B*2705	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.469592	0.336669	-4.132923	29484.389045
HLA B*0702	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.431075	0.298081	-4.132994	26982.033424
HLA B*1517	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.431103	0.298081	-4.133022	26983.785119

HLA B*0803	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.540509	0.407463	-4.133046	34714.346046
HLA B*5801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.318950	0.185815	-4.133135	20842.518861
HLA A*2902	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.329232	0.195916	-4.133315	21341.824760
HLA B*5301	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.586815	0.453330	-4.133485	38620.241775
HLA B*2705	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.432604	0.299099	-4.133505	27077.227300
HLA A*0211	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.541099	0.407463	-4.133635	34761.516056
HLA B*4402	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.419929	0.286262	-4.133666	26298.363204
HLA B*5801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.355872	0.222188	-4.133684	22691.978321
HLA A*2603	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.628652	0.494882	-4.133771	42525.778002
HLA B*1503	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.523254	0.389429	-4.133825	33362.176106
HLA A*3301	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.623352	0.489404	-4.133948	42009.917585
HLA B*4601	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.423949	0.289937	-4.134012	26542.919377
HLA A*2402	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.511091	0.376904	-4.134188	32440.764978
HLA A*6801	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.623716	0.489404	-4.134312	42045.159053
HLA B*7301	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.538745	0.404390	-4.134355	34573.593792
HLA B*5301	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.587273	0.452913	-4.134360	38661.004861
HLA A*2403	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.409680	0.275316	-4.134364	25685.041130
HLA B*1503	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.518593	0.384129	-4.134464	33006.007367
HLA A*1101	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.473910	0.339229	-4.134682	29779.025833
HLA B*0803	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.425276	0.290570	-4.134706	26624.174247
HLA B*5701	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.424731	0.289937	-4.134795	26590.779360
HLA A*3001	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.271998	0.137191	-4.134807	18706.739343
HLA B*5701	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.404643	0.269777	-4.134866	25388.846487
HLA A*2602	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.575368	0.440475	-4.134893	37615.626311
HLA A*6801	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.651689	0.516757	-4.134932	44842.412373
HLA A*2403	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.327998	0.192958	-4.135040	21281.295882
HLA B*0702	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.406100	0.270903	-4.135197	25474.146986
HLA B*5401	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.494572	0.359286	-4.135286	31229.990894
HLA A*0250	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.588652	0.453330	-4.135322	38783.972083
HLA B*3901	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.482738	0.347374	-4.135364	30390.475947
HLA B*4001	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.405172	0.269777	-4.135394	25419.769244
HLA A*2403	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.420850	0.285427	-4.135423	26354.192704
HLA A*0203	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.389916	0.254455	-4.135461	24542.364260
HLA A*3002	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.479676	0.344171	-4.135505	30177.004157
HLA A*0301	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.363121	0.227420	-4.135701	23073.874238
HLA A*3201	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.617351	0.481648	-4.135703	41433.464125
HLA B*1502	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.588831	0.452913	-4.135918	38799.921453
HLA A*0203	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.413996	0.278063	-4.135933	25941.570785
HLA A*0203	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.411308	0.275316	-4.135992	25781.516447
HLA A*0211	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.520562	0.384476	-4.136085	33155.979367
HLA A*3201	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.599986	0.463883	-4.136104	39809.452173
HLA B*5801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.347654	0.211398	-4.136255	22266.597640
HLA A*0250	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.589186	0.452913	-4.136273	38831.629797
HLA B*5401	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.439011	0.302627	-4.136384	27479.652488
HLA A*3001	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.290961	0.154429	-4.136532	19541.630100
HLA A*0101	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.391039	0.254455	-4.136584	24605.911151
HLA A*3101	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.406438	0.269777	-4.136661	25493.999691
HLA B*1509	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.511436	0.374749	-4.136687	32466.573877
HLA B*4002	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.626159	0.489404	-4.136756	42282.383810
HLA A*3201	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.567413	0.430602	-4.136811	36932.860115
HLA A*2403	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.438800	0.301939	-4.136861	27466.276176
HLA A*2301	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.544334	0.407463	-4.136871	35021.436021
HLA B*4501	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.642244	0.505350	-4.136894	43877.718588
HLA B*0801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.406746	0.269777	-4.136969	25512.073576
HLA A*0101	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.365259	0.228245	-4.137014	23187.746968
HLA A*0101	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.371680	0.234640	-4.137039	23533.130063
HLA B*1801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.526490	0.389429	-4.137060	33611.632880
HLA B*4801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.435294	0.298081	-4.137214	27245.472940
HLA B*4001	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.364892	0.227657	-4.137235	23168.186093
HLA A*2403	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.398591	0.261282	-4.137309	25037.484664
HLA A*0301	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.365606	0.228245	-4.137362	23206.319987
HLA A*0203	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.407204	0.269777	-4.137427	25539.001188
HLA A*0212	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.435529	0.298081	-4.137449	27260.216426
HLA A*0216	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.476749	0.339229	-4.137520	29974.273408
HLA B*5401	1:66-74	9	GPASVYADG	0.573341	-0.821310	-3.889563	-0.247969	-4.137532	7754.664679

HLA A*3101	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.427595	0.289937	-4.137659	26766.715855
HLA B*0803	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.497036	0.359286	-4.137751	31407.724110
HLA A*0212	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.424134	0.286262	-4.137872	26554.265748
HLA A*0206	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.423354	0.285427	-4.137927	26506.614882
HLA B*4801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.407747	0.269777	-4.137969	25570.936830
HLA A*0219	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.413381	0.275316	-4.138065	25904.827483
HLA B*1517	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.258832	0.120764	-4.138068	18148.117437
HLA B*4801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.413519	0.275316	-4.138203	25913.097195
HLA B*0802	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.477456	0.339229	-4.138227	30023.122576
HLA A*0250	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.481448	0.343210	-4.138238	30300.349254
HLA B*5101	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.488649	0.350403	-4.138246	30806.957250
HLA B*4403	1:457-465	9	VGVQGDGRT	0.855552	-0.338795	-4.655157	0.516757	-4.138400	45201.912266
HLA B*2705	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.399733	0.261282	-4.138451	25103.399987
HLA B*4403	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.440564	0.301939	-4.138625	27578.093892
HLA B*1501	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.334649	0.195916	-4.138733	21609.736035
HLA A*0219	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.424440	0.285427	-4.139013	26572.947549
HLA B*1502	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.592379	0.453330	-4.139049	39118.173516
HLA B*1801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.410068	0.270903	-4.139165	25707.978648
HLA A*0203	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.393699	0.254355	-4.139344	24757.059961
HLA A*6801	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.597190	0.457680	-4.139510	39553.991333
HLA B*4002	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.644866	0.505350	-4.139516	44143.428815
HLA A*2501	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.374894	0.235291	-4.139603	23707.938423
HLA A*0206	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.410620	0.270903	-4.139717	25740.682601
HLA B*1502	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.621423	0.481648	-4.139775	41823.743492
HLA A*3101	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.425297	0.285427	-4.139870	26625.470583
HLA B*4601	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.401163	0.261282	-4.139881	25186.242606
HLA B*3501	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.425323	0.285427	-4.139896	26627.055080
HLA B*5701	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.417988	0.278063	-4.139925	26181.109342
HLA A*3301	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.619149	0.479051	-4.140098	41605.294538
HLA A*0219	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.367761	0.227657	-4.140104	23321.729515
HLA B*0801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.430041	0.289937	-4.140104	26917.883088
HLA B*4601	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.410101	0.269777	-4.140324	25709.925804
HLA A*2301	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.524908	0.384476	-4.140432	33489.480290
HLA A*0206	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.487953	0.347374	-4.140580	30757.664709
HLA B*1503	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.368832	0.228245	-4.140587	23379.333132
HLA B*4002	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.635635	0.494882	-4.140753	43215.041772
HLA A*8001	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.336701	0.195916	-4.140784	21712.036598
HLA A*1101	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.431394	0.290570	-4.140824	27001.892623
HLA A*3002	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.622504	0.481648	-4.140856	41927.953540
HLA B*4801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.442925	0.301939	-4.140987	27728.442643
HLA B*4403	1:353-361	9	NIKSHHNVG	0.997802	-0.467268	-4.671535	0.530534	-4.141001	46939.133472
HLA B*1509	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.545483	0.404390	-4.141093	35114.205635
HLA B*5801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.352087	0.210953	-4.141134	22495.069519
HLA A*2602	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.571745	0.430602	-4.141143	37303.140111
HLA B*5301	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.587994	0.446544	-4.141450	38725.267799
HLA A*0212	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.443391	0.301939	-4.141452	27758.160101
HLA A*0203	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.262231	0.120764	-4.141468	18290.740395
HLA B*0801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.239331	0.097746	-4.141584	17351.253524
HLA A*1101	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.444239	0.302627	-4.141612	27812.423925
HLA B*1502	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.369558	0.227657	-4.141901	23418.448012
HLA A*2403	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.414656	0.272539	-4.142118	25981.036602
HLA A*0212	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.413026	0.270903	-4.142123	25883.674645
HLA A*1101	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.396601	0.254355	-4.142246	24923.020947
HLA B*3901	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.445573	0.303325	-4.142248	27898.017855
HLA A*0301	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.364471	0.222188	-4.142283	23145.761573
HLA A*6801	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.608907	0.466612	-4.142295	40635.648570
HLA A*3201	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.546275	0.403979	-4.142295	35178.281882
HLA A*2602	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.519657	0.376904	-4.142754	33086.993717
HLA A*0202	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.474641	0.331684	-4.142957	29829.170487
HLA A*6901	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.376950	0.233980	-4.142970	23820.429614
HLA B*1501	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.334276	0.191274	-4.143002	21591.155929
HLA B*5401	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.554982	0.411911	-4.143070	35890.690681
HLA B*5101	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.490505	0.347374	-4.143131	30938.902159
HLA A*3101	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.339088	0.195916	-4.143171	21831.704237
HLA A*0211	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.286485	0.143276	-4.143209	19341.271416

HLA A*3002	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.520200	0.376904	-4.143296	33128.367863
HLA B*3501	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.194771	0.051389	-4.143382	15659.234322
HLA A*2602	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.590055	0.446544	-4.143511	38909.435321
HLA B*4402	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.418848	0.275316	-4.143532	26232.999803
HLA A*3301	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.584115	0.440475	-4.143640	38380.924360
HLA B*4403	1:336-344	9	GTLYPDVVE	1.275887	-0.778926	-4.640653	0.496961	-4.143692	43717.310591
HLA A*0201	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.416285	0.272539	-4.143746	26078.623705
HLA A*3101	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.414687	0.270903	-4.143784	25982.863875
HLA B*5401	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.527923	0.384129	-4.143794	33722.735577
HLA A*0201	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.398175	0.254355	-4.143820	25013.521486
HLA A*8001	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.430170	0.286262	-4.143908	26925.893532
HLA A*1101	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.480602	0.336669	-4.143933	30241.394930
HLA A*3002	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.551505	0.407463	-4.144041	35604.474331
HLA B*3901	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.355193	0.210953	-4.144240	22656.528086
HLA B*0702	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.446187	0.301939	-4.144248	27937.437151
HLA A*0211	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.487516	0.343210	-4.144307	30726.730701
HLA A*8001	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.434402	0.289937	-4.144465	27189.520377
HLA A*0101	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.378491	0.233980	-4.144511	23905.115815
HLA A*6801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.487740	0.343210	-4.144530	30742.526440
HLA A*3001	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.290794	0.146138	-4.144656	19534.125560
HLA B*5801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.337737	0.192958	-4.144779	21763.898171
HLA A*0203	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.434768	0.289937	-4.144832	27212.476459
HLA B*3901	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.490432	0.345470	-4.144962	30933.713937
HLA A*0216	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.415885	0.270903	-4.144982	26054.650712
HLA A*8001	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.446997	0.301939	-4.145058	27989.628602
HLA A*0219	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.416252	0.270903	-4.145349	26076.648625
HLA B*3801	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.557315	0.411911	-4.145404	36084.014992
HLA B*4402	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.380746	0.235291	-4.145456	24029.589828
HLA B*5401	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.522606	0.376904	-4.145702	33312.399231
HLA B*5701	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.421106	0.275316	-4.145790	26369.737772
HLA A*0219	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.447730	0.301939	-4.145791	28036.911781
HLA A*3001	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.282550	0.136752	-4.145797	19166.800922
HLA A*0301	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.227020	0.081144	-4.145875	16866.289638
HLA B*7301	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.609777	0.463883	-4.145894	40717.068741
HLA A*2402	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.550132	0.403979	-4.146153	35492.163945
HLA A*6802	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.400569	0.254355	-4.146214	25151.793727
HLA B*5101	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.490392	0.344171	-4.146221	30930.869153
HLA A*2601	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.245848	0.099536	-4.146312	17613.608006
HLA A*2902	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.448943	0.302627	-4.146316	28115.286239
HLA B*0801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.368517	0.222188	-4.146329	23362.391007
HLA B*1501	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.353539	0.207166	-4.146373	22570.403405
HLA A*0219	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.449708	0.303325	-4.146383	28164.914779
HLA A*2501	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.490597	0.344171	-4.146425	30945.430513
HLA B*1503	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.241990	0.095477	-4.146513	17457.838535
HLA B*0702	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.421942	0.275316	-4.146626	26420.572728
HLA B*0802	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.449438	0.302627	-4.146811	28147.397786
HLA B*5101	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.483529	0.336669	-4.146860	30445.932353
HLA B*5801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.338395	0.191274	-4.147121	21796.890430
HLA B*0803	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.520261	0.373125	-4.147136	33133.027932
HLA A*3001	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.284890	0.137730	-4.147160	19270.355167
HLA B*4002	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.600616	0.453330	-4.147286	39867.211780
HLA A*2902	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.274324	0.126963	-4.147361	18807.197492
HLA A*2501	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.497889	0.350403	-4.147486	31469.462878
HLA A*0206	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.536959	0.389429	-4.147530	34431.735742
HLA B*2705	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.481598	0.334057	-4.147541	30310.842048
HLA A*6802	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.304975	0.157255	-4.147721	20182.523479
HLA A*1101	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.495138	0.347374	-4.147764	31270.734589
HLA A*0301	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.339163	0.191274	-4.147889	21835.483991
HLA B*5801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.356674	0.208642	-4.148031	22733.878488
HLA B*3501	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.434298	0.286262	-4.148036	27183.049086
HLA B*4403	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.637550	0.489404	-4.148146	43406.000133
HLA A*0202	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.537582	0.389429	-4.148152	34481.133189
HLA B*5101	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.450174	0.301939	-4.148235	28195.100018
HLA B*1801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.491565	0.343210	-4.148355	31014.480912
HLA B*1517	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.495770	0.347374	-4.148396	31316.274772

HLA B*3801	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.552809	0.404390	-4.148419	35711.537002
HLA B*7301	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.434028	0.285427	-4.148601	27166.142758
HLA B*4801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.438574	0.289937	-4.148638	27452.015287
HLA A*6802	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.438598	0.289937	-4.148661	27453.500451
HLA A*0202	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.305965	0.157255	-4.148710	20228.542840
HLA A*8001	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.430417	0.281539	-4.148878	26941.192817
HLA B*3801	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.480705	0.331684	-4.149021	30248.594301
HLA A*2501	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.488268	0.339229	-4.149040	30779.969797
HLA B*4402	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.094039	-0.055017	-4.149055	12417.629645
HLA B*0801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.251071	0.101982	-4.149089	17826.711331
HLA B*4403	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.657955	0.508560	-4.149395	45494.096518
HLA B*0801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.410707	0.261282	-4.149425	25745.835524
HLA A*6801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.497008	0.347374	-4.149635	31405.685229
HLA B*4402	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.431230	0.281539	-4.149691	26991.669152
HLA A*3001	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.285338	0.135619	-4.149719	19290.277301
HLA A*0201	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.341071	0.191274	-4.149797	21931.614548
HLA B*3901	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.447949	0.298081	-4.149868	28051.021252
HLA A*2603	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.613839	0.463883	-4.149956	41099.710688
HLA A*0202	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.420930	0.270903	-4.150027	26359.040640
HLA B*4002	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.451987	0.301939	-4.150049	28313.101244
HLA B*0803	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.452753	0.302627	-4.150126	28363.078963
HLA B*1502	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.607838	0.457680	-4.150158	40535.746943
HLA B*4403	1:294-302	9	EALSGVSAP	0.479426	0.006871	-4.636680	0.486297	-4.150384	43319.203021
HLA B*1517	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.440978	0.290570	-4.150408	27604.364617
HLA B*1509	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.534654	0.384129	-4.150525	34249.487068
HLA A*2301	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.523696	0.373125	-4.150571	33396.124674
HLA A*3001	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.292030	0.141148	-4.150881	19589.791064
HLA B*1801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.450136	0.299099	-4.151037	28192.659605
HLA B*0702	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.450155	0.299099	-4.151056	28193.879785
HLA A*1101	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.429122	0.278063	-4.151059	26861.004765
HLA A*3301	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.487775	0.336669	-4.151106	30745.021246
HLA B*1509	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.495286	0.344171	-4.151115	31281.394191
HLA A*0201	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.351251	0.200115	-4.151136	22451.787495
HLA A*2402	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.563247	0.411911	-4.151336	36580.303483
HLA B*4501	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.646248	0.494882	-4.151366	44284.073294
HLA A*3002	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.297408	0.145582	-4.151826	19833.884287
HLA B*1503	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.499297	0.347374	-4.151923	31571.605824
HLA A*0212	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.380293	0.228245	-4.152048	24004.513420
HLA A*6901	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.386702	0.234640	-4.152062	24361.403337
HLA A*0202	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.528966	0.376904	-4.152062	33803.834638
HLA A*2501	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.454819	0.302627	-4.152192	28498.274895
HLA B*5701	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.433770	0.281539	-4.152231	27149.981327
HLA B*3901	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.387525	0.235291	-4.152234	24407.574407
HLA B*5801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.352494	0.200115	-4.152379	22516.132753
HLA A*2301	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.527159	0.374749	-4.152410	33663.495886
HLA A*0203	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.413712	0.261282	-4.152430	25924.595078
HLA B*3901	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.489166	0.336669	-4.152496	30843.644767
HLA A*6901	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.374718	0.222188	-4.152530	23698.321075
HLA A*0203	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.292432	0.139834	-4.152597	19607.921789
HLA A*6901	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.025659	-0.127048	-4.152708	10608.629724
HLA B*1801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.496888	0.344171	-4.152717	31397.021459
HLA A*3201	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.611574	0.458831	-4.152743	40885.928161
HLA B*4002	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.537328	0.384476	-4.152851	34460.992849
HLA A*6802	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.204286	0.051389	-4.152897	16006.115157
HLA A*2603	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.583502	0.430602	-4.152900	38326.769463
HLA B*1801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.455627	0.302627	-4.153000	28551.359618
HLA A*2601	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.387715	0.234640	-4.153075	24418.272174
HLA B*4501	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.605991	0.452913	-4.153079	40363.747884
HLA A*6901	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.378258	0.225172	-4.153086	23892.316164
HLA B*5101	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.497271	0.344156	-4.153115	31424.719938
HLA A*0203	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.434740	0.281539	-4.153201	27210.709919
HLA B*5301	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.527951	0.374749	-4.153202	33724.924883
HLA B*1517	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.438802	0.285427	-4.153375	27466.424766
HLA B*3901	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.503883	0.350403	-4.153480	31906.771832
HLA A*2902	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.426059	0.272539	-4.153520	26672.180742

HLA A*0216	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.296874	0.143276	-4.153598	19809.542338
HLA B*4601	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.408099	0.254455	-4.153644	25591.695641
HLA B*0802	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.456992	0.303325	-4.153667	28641.241880
HLA A*3002	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.504146	0.350403	-4.153743	31926.110245
HLA B*5301	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.572838	0.419078	-4.153760	37397.097963
HLA A*1101	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.487843	0.334057	-4.153785	30749.845112
HLA A*0301	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.364782	0.210953	-4.153828	23162.295988
HLA B*5401	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.543432	0.389429	-4.154003	34948.758096
HLA A*2402	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.513290	0.359286	-4.154004	32605.450463
HLA A*2602	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.620664	0.466612	-4.154052	41750.724741
HLA A*0201	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.379290	0.225172	-4.154117	23949.126447
HLA B*1509	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.543573	0.389429	-4.154143	34960.104072
HLA A*6901	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.299764	0.145582	-4.154182	19941.797811
HLA B*3801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.498383	0.344171	-4.154212	31505.234918
HLA A*2902	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.440482	0.286262	-4.154220	27572.872581
HLA A*3101	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.382548	0.228245	-4.154304	24129.504997
HLA A*2301	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.543777	0.389429	-4.154348	34976.562280
HLA A*2602	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.607822	0.453330	-4.154492	40534.211915
HLA A*0206	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.294396	0.139834	-4.154561	19696.802734
HLA B*7301	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.585191	0.430602	-4.154589	38476.139809
HLA A*0206	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.562094	0.407463	-4.154630	36483.265784
HLA A*2403	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.382344	0.227657	-4.154687	24118.150868
HLA A*0101	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.409130	0.254355	-4.154775	25652.546647
HLA B*4402	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.453002	0.298081	-4.154922	28379.348386
HLA A*3201	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.612648	0.457680	-4.154968	40987.136290
HLA A*2402	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.574118	0.419078	-4.155040	37507.521883
HLA A*0101	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.351032	0.195916	-4.155116	22440.494399
HLA B*1801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.233549	0.078424	-4.155125	17121.774496
HLA B*1501	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.380307	0.225172	-4.155135	24005.292604
HLA A*2602	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.612843	0.457680	-4.155163	41005.544499
HLA A*2402	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.562775	0.407463	-4.155312	36540.548129
HLA B*1501	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.409833	0.254455	-4.155378	25694.074678
HLA B*5801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.268791	0.113362	-4.155429	18569.108245
HLA A*0202	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.433617	0.278063	-4.155554	27140.435910
HLA A*6802	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.416841	0.261282	-4.155560	26112.081693
HLA B*4501	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.539743	0.384129	-4.155614	34653.176952
HLA B*1502	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.567528	0.411911	-4.155617	36942.651744
HLA B*1801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.501249	0.345470	-4.155779	31713.859219
HLA A*2601	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.380953	0.225172	-4.155781	24041.032324
HLA B*5701	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.383227	0.227420	-4.155807	24167.259970
HLA A*1101	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.426789	0.270903	-4.155886	26717.093805
HLA A*0101	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.378103	0.222188	-4.155915	23883.786872
HLA B*5801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.363184	0.207166	-4.156018	23077.244816
HLA A*2603	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.532923	0.376904	-4.156019	34113.203208
HLA B*4403	1:136-144	9	PVWMSHGDA	0.838199	-0.326483	-4.667783	0.511716	-4.156067	46535.345259
HLA B*1517	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.490237	0.334057	-4.156180	30919.827174
HLA B*1801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.082282	-0.073933	-4.156214	12085.980242
HLA B*3901	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.222415	0.066046	-4.156368	16688.394724
HLA B*1801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.384630	0.228245	-4.156385	24245.439242
HLA A*0202	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.531264	0.374749	-4.156514	33983.160362
HLA A*0301	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.367986	0.211398	-4.156588	23333.844786
HLA A*0101	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.368010	0.211398	-4.156611	23335.107155
HLA A*2301	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.540753	0.384129	-4.156625	34733.882821
HLA B*1501	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.293949	0.137191	-4.156759	19676.567207
HLA A*6802	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.391448	0.234640	-4.156808	24629.084110
HLA A*2403	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.426611	0.269777	-4.156833	26706.111288
HLA A*0201	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.277719	0.120764	-4.156955	18954.794959
HLA A*0219	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.435071	0.278063	-4.157008	27231.474014
HLA B*5701	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.418411	0.261282	-4.157129	26206.616401
HLA A*2602	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.569041	0.411911	-4.157130	37071.583249
HLA B*0803	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.501298	0.344156	-4.157142	31717.462361
HLA A*2902	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.392562	0.235291	-4.157271	24692.321206
HLA B*0801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.368428	0.210953	-4.157475	23357.588759
HLA B*4001	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.411990	0.254455	-4.157535	25821.995985
HLA A*2603	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.616414	0.458831	-4.157583	41344.124553

HLA A*0250	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.576682	0.419078	-4.157604	37729.552958
HLA B*7301	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.530801	0.373125	-4.157676	33946.962164
HLA B*4402	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.448414	0.290570	-4.157844	28081.084428
HLA A*2403	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.278661	0.120764	-4.157898	18995.959473
HLA B*4001	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.391986	0.233980	-4.158006	24659.615119
HLA B*1801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.436251	0.278063	-4.158188	27305.528792
HLA A*3101	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.260302	0.101982	-4.158320	18209.681869
HLA A*0216	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.461836	0.303325	-4.158512	28962.529094
HLA A*3301	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.611463	0.452913	-4.158551	40875.533631
HLA B*1502	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.605101	0.446544	-4.158557	40281.072940
HLA B*5701	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.393201	0.234640	-4.158561	24728.682452
HLA B*1501	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.306406	0.147675	-4.158732	20249.126931
HLA A*8001	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.429681	0.270903	-4.158779	26895.612024
HLA B*3901	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.444488	0.285427	-4.159061	27828.377484
HLA A*0206	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.462407	0.303325	-4.159082	29000.628361
HLA A*0219	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.457177	0.298081	-4.159097	28653.485226
HLA A*0212	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.431723	0.272539	-4.159184	27022.351184
HLA A*0101	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.384372	0.225172	-4.159199	24231.015369
HLA A*0201	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.386620	0.227420	-4.159200	24356.791036
HLA A*2902	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.258787	0.099536	-4.159251	18146.252126
HLA A*2501	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.449838	0.290570	-4.159268	28173.296324
HLA A*6901	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.312101	0.152623	-4.159478	20516.414014
HLA B*5401	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.501672	0.342132	-4.159540	31744.756583
HLA A*0212	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.420845	0.261282	-4.159563	26353.907559
HLA A*8001	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.462266	0.302627	-4.159639	28991.216477
HLA A*0203	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.432202	0.272539	-4.159664	27052.189983
HLA A*0201	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.387931	0.228245	-4.159686	24430.428413
HLA B*1517	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.461641	0.301939	-4.159703	28949.527236
HLA A*2602	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.641361	0.481648	-4.159713	43788.556830
HLA A*2601	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.387959	0.228245	-4.159715	24432.014455
HLA A*6801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.432369	0.272539	-4.159831	27062.582782
HLA A*0202	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.445454	0.285427	-4.160027	27890.321732
HLA B*1501	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.371447	0.211398	-4.160049	23520.529587
HLA A*0211	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.533348	0.373125	-4.160223	34146.622872
HLA A*1101	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.504447	0.344156	-4.160290	31948.225641
HLA A*2301	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.510725	0.350403	-4.160321	32413.398380
HLA A*0301	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.367505	0.207166	-4.160338	23307.981260
HLA B*4801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.432896	0.272539	-4.160357	27095.397509
HLA A*0219	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.446703	0.286262	-4.160441	27970.707402
HLA A*3201	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.519808	0.359286	-4.160522	33098.451506
HLA B*3801	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.564549	0.403979	-4.160569	36690.101982
HLA A*0216	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.462600	0.301939	-4.160661	29013.496210
HLA B*1503	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.502819	0.342132	-4.160687	31828.674286
HLA A*0211	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.511192	0.350403	-4.160789	32448.312396
HLA B*1501	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.241981	0.081144	-4.160837	17457.460759
HLA B*1501	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.369502	0.208642	-4.160859	23415.407621
HLA A*2602	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.619964	0.458831	-4.161133	41683.470663
HLA A*2902	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.446635	0.285427	-4.161209	27966.319512
HLA B*4002	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.386486	0.225172	-4.161314	24349.281444
HLA A*0206	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.536134	0.374749	-4.161385	34366.416351
HLA A*6801	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.640510	0.479051	-4.161459	43702.886117
HLA A*2902	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.386813	0.225172	-4.161640	24367.598371
HLA B*5101	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.504895	0.343210	-4.161686	31981.254447
HLA B*0802	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.447223	0.285427	-4.161796	28004.168773
HLA A*0219	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.431585	0.269777	-4.161807	27013.727473
HLA A*0201	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.373287	0.211398	-4.161888	23620.372529
HLA A*2501	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.460058	0.298081	-4.161977	28844.161791
HLA A*2603	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.509355	0.347374	-4.161981	32311.328691
HLA B*5101	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.504132	0.342132	-4.162000	31925.073962
HLA A*2403	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.433006	0.270903	-4.162103	27102.287791
HLA A*0201	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.396098	0.233980	-4.162118	24894.183856
HLA B*4801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.433036	0.270903	-4.162134	27104.193923
HLA B*1503	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.384360	0.222188	-4.162172	24230.359942
HLA B*5101	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.501484	0.339229	-4.162255	31731.020707
HLA A*2601	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.384489	0.222188	-4.162301	24237.570611

HLA B*0801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.387522	0.225172	-4.162350	24407.442365
HLA A*2902	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.432130	0.269777	-4.162352	27047.653533
HLA B*1501	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.384550	0.222188	-4.162362	24240.980037
HLA B*4403	1:28-36	9	QLIARRVRE	1.072167	-0.566817	-4.667811	0.505350	-4.162461	46538.366370
HLA B*1509	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.496527	0.334057	-4.162469	31370.874774
HLA A*2403	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.444145	0.281539	-4.162606	27806.406091
HLA A*6801	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.609189	0.446544	-4.162645	40662.037257
HLA B*0801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.397486	0.234640	-4.162846	24973.904023
HLA B*3801	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.506066	0.343210	-4.162856	32067.532106
HLA A*2902	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.438177	0.275316	-4.162861	27426.928168
HLA A*0101	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.371511	0.208642	-4.162868	23523.965411
HLA A*0219	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.435557	0.272539	-4.163019	27261.986181
HLA A*3301	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.644807	0.481648	-4.163159	44137.458942
HLA A*6801	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.622116	0.458831	-4.163285	41890.544018
HLA A*2902	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.465293	0.301939	-4.163354	29193.930884
HLA A*0201	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.398645	0.235291	-4.163354	25040.600209
HLA A*2601	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.391021	0.227420	-4.163601	24604.846253
HLA B*4402	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.418012	0.254355	-4.163657	26182.525750
HLA A*6801	1:9-17	9	VPETPARPV	0.601332	-0.092772	-4.672263	0.508560	-4.163704	47017.919526
HLA A*2403	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.418270	0.254455	-4.163815	26198.111288
HLA A*2902	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.355231	0.191274	-4.163957	22658.489280
HLA A*2902	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.453930	0.289937	-4.163994	28440.057233
HLA A*0211	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.553459	0.389429	-4.164030	35765.092260
HLA A*2603	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.568433	0.404390	-4.164043	37019.676356
HLA A*8001	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.442110	0.278063	-4.164047	27676.438763
HLA B*7301	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.576172	0.411911	-4.164260	37685.286491
HLA A*0301	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.357219	0.192958	-4.164261	22762.429562
HLA B*5301	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.201429	0.037065	-4.164364	15901.165705
HLA A*3201	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.548511	0.384129	-4.164383	35359.924927
HLA B*1509	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.571882	0.407463	-4.164418	37314.846687
HLA A*0203	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.355741	0.191274	-4.164467	22685.104741
HLA B*4002	1:243-251	9	ALVQRAIGD	1.095737	-0.616686	-4.643759	0.479051	-4.164708	44031.091989
HLA A*0101	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.350666	0.185815	-4.164851	22421.563897
HLA A*3002	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.549078	0.384129	-4.164949	35406.056672
HLA A*2301	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.464061	0.299099	-4.164963	29111.289647
HLA A*2603	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.605496	0.440475	-4.165021	40317.699493
HLA A*2902	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.392510	0.227420	-4.165090	24689.382561
HLA A*2601	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.376581	0.211398	-4.165182	23800.206259
HLA A*0216	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.450968	0.285427	-4.165541	28246.703122
HLA B*4601	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.399655	0.233980	-4.165675	25098.918769
HLA B*0803	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.507835	0.342132	-4.165703	32198.430333
HLA B*0702	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.438283	0.272539	-4.165744	27433.605930
HLA A*3001	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.265337	0.099536	-4.165801	18422.022352
HLA A*3101	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.420319	0.254455	-4.165864	26321.990836
HLA B*4001	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.373064	0.207166	-4.165897	23608.236207
HLA A*0203	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.394157	0.228245	-4.165912	24783.190667
HLA A*0250	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.525287	0.359286	-4.166001	33518.662071
HLA A*3001	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.278363	0.112320	-4.166043	18982.912669
HLA A*2902	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.420565	0.254355	-4.166210	26336.946984
HLA A*8001	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.436117	0.269777	-4.166340	27297.110057
HLA A*2301	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.525693	0.359286	-4.166407	33550.047235
HLA B*4403	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.391697	0.225172	-4.166525	24643.211666
HLA B*4601	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.394817	0.228245	-4.166573	24820.894200
HLA B*0801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.421096	0.254355	-4.166741	26369.167149
HLA A*8001	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.442131	0.275316	-4.166815	27677.786334
HLA B*2705	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.312449	0.145582	-4.166867	20532.847338
HLA B*5801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.353370	0.186500	-4.166870	22561.613674
HLA A*6802	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.377826	0.210953	-4.166873	23868.545118
HLA B*4002	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.619821	0.452913	-4.166908	41669.717252
HLA A*2601	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.400992	0.233980	-4.167012	25176.297970
HLA B*4601	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.394705	0.227420	-4.167285	24814.449679
HLA A*0211	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.511490	0.344156	-4.167334	32470.613862
HLA A*2402	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.598078	0.430602	-4.167476	39634.959556
HLA B*5101	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.499174	0.331684	-4.167490	31562.725531
HLA A*0216	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.392693	0.225172	-4.167521	24699.802971

HLA B*4402	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.422095	0.254455	-4.167640	26429.864965
HLA B*5701	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.422104	0.254455	-4.167649	26430.436902
HLA B*4002	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.175918	0.007934	-4.167985	14994.025849
HLA A*6901	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.359286	0.191274	-4.168013	22871.053073
HLA B*5101	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.466207	0.298081	-4.168126	29255.432652
HLA B*3801	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.527507	0.359286	-4.168221	33690.459814
HLA A*3101	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.289006	0.120764	-4.168242	19453.870333
HLA B*2705	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.314427	0.146138	-4.168289	20626.590402
HLA A*2902	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.422781	0.254455	-4.168326	26471.648890
HLA B*4001	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.395771	0.227420	-4.168351	24875.471099
HLA A*0216	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.446417	0.278063	-4.168354	27952.252645
HLA B*3901	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.470523	0.301939	-4.168584	29547.621634
HLA B*1509	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.507823	0.339229	-4.168594	32197.559395
HLA A*0301	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.354470	0.185815	-4.168655	22618.808174
HLA A*3301	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.627499	0.458831	-4.168667	42412.968559
HLA A*0201	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.314371	0.145582	-4.168789	20623.912474
HLA A*6801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.094866	-0.073933	-4.168798	12441.298830
HLA A*0206	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.282228	0.113362	-4.168866	19152.600619
HLA B*1509	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.542085	0.373125	-4.168961	34840.589354
HLA B*1503	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.312318	0.143276	-4.169041	20526.627776
HLA A*6801	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.664003	0.494882	-4.169121	46132.035658
HLA B*0702	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.377767	0.208642	-4.169125	23865.317181
HLA B*0801	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.306096	0.136752	-4.169344	20234.672083
HLA A*2902	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.378124	0.208642	-4.169482	23884.949778
HLA B*0702	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.403710	0.233980	-4.169730	25334.376716
HLA A*2602	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.588868	0.419078	-4.169790	38803.280051
HLA A*0212	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.380758	0.210953	-4.169805	24030.239824
HLA A*3001	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.296999	0.126963	-4.170036	19815.223026
HLA A*0101	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.361363	0.191274	-4.170090	22980.692228
HLA A*2301	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.538693	0.368545	-4.170148	34569.479172
HLA A*0206	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.514406	0.344171	-4.170235	32689.344347
HLA B*4402	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.218872	0.048624	-4.170248	16552.802757
HLA B*5101	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.515811	0.345470	-4.170342	32795.269341
HLA A*0202	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.577824	0.407463	-4.170360	37828.882251
HLA A*0101	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.381463	0.210953	-4.170510	24069.271769
HLA A*0201	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.392708	0.222188	-4.170520	24700.604724
HLA A*3201	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.611118	0.440475	-4.170643	40843.040134
HLA B*0803	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.521051	0.350403	-4.170647	33193.309361
HLA A*0206	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.456997	0.286262	-4.170734	28641.551774
HLA B*0803	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.518132	0.347374	-4.170759	32971.028382
HLA B*4801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.425147	0.254355	-4.170792	26616.253565
HLA A*2601	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.366718	0.195916	-4.170801	23265.778159
HLA A*3301	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.575270	0.404390	-4.170880	37607.080434
HLA B*5701	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.310774	0.139834	-4.170940	20453.799544
HLA B*4402	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.398673	0.227657	-4.171016	25042.225864
HLA A*2603	1:15-23	9	RPVLVVDFG	1.020076	-0.530672	-4.660786	0.489404	-4.171383	45791.637499
HLA B*4601	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.364396	0.192958	-4.171438	23141.755008
HLA B*1503	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.516977	0.345470	-4.171507	32883.387222
HLA B*5101	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.382476	0.210953	-4.171522	24125.458660
HLA B*4403	1:419-427	9	RLDTLRHAD	1.201394	-0.706512	-4.666416	0.494882	-4.171534	46389.056563
HLA A*6901	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.328893	0.157255	-4.171639	21325.205440
HLA A*3101	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.399232	0.227420	-4.171812	25074.489839
HLA A*3002	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.426315	0.254355	-4.171960	26687.913376
HLA A*2602	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.367937	0.195916	-4.172021	23331.194032
HLA B*5101	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.471159	0.299099	-4.172060	29590.972580
HLA B*0702	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.462031	0.289937	-4.172095	28975.536792
HLA B*5701	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.368031	0.195916	-4.172115	23336.243346
HLA A*3301	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.629940	0.457680	-4.172260	42652.037806
HLA A*0219	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.270093	0.097746	-4.172346	18624.844803
HLA B*0803	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.506693	0.334057	-4.172635	32113.885215
HLA B*5101	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.506721	0.334057	-4.172664	32115.970073
HLA A*0212	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.427153	0.254455	-4.172698	26739.506360
HLA A*2403	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.427088	0.254355	-4.172733	26735.456250
HLA B*4601	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.384207	0.211398	-4.172809	24221.841009
HLA B*5701	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.408146	0.235291	-4.172855	25594.464756

HLA B*4601	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.400642	0.227657	-4.172985	25156.012201
HLA A*2403	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.401410	0.228245	-4.173165	25200.553422
HLA B*3801	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.557489	0.384129	-4.173360	36098.463462
HLA B*4601	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.408033	0.234640	-4.173393	25587.819384
HLA A*2403	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.408766	0.235291	-4.173476	25631.045161
HLA A*6802	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.427964	0.254455	-4.173509	26789.459892
HLA A*2601	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.384463	0.210953	-4.173510	24236.128306
HLA A*1101	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.471606	0.298081	-4.173525	29621.404155
HLA B*3801	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.542215	0.368545	-4.173670	34850.957501
HLA B*4001	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.409260	0.235291	-4.173969	25660.180542
HLA A*2902	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.396227	0.222188	-4.174039	24901.592071
HLA A*0101	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.367150	0.192958	-4.174192	23288.948902
HLA B*0801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.428688	0.254455	-4.174233	26834.134928
HLA B*4402	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.402521	0.228245	-4.174277	25265.121128
HLA A*1101	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.460739	0.286262	-4.174477	28889.449986
HLA B*5701	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.402279	0.227657	-4.174622	25251.046854
HLA A*0211	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.518833	0.344171	-4.174661	33024.225394
HLA A*0212	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.226052	0.051389	-4.174663	16828.738661
HLA A*0216	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.447209	0.272539	-4.174670	28003.259791
HLA B*0801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.402174	0.227420	-4.174754	25244.900361
HLA A*0206	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.476699	0.301939	-4.174760	29970.868294
HLA B*4001	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.367989	0.192958	-4.175031	23333.971019
HLA A*3002	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.474491	0.299099	-4.175392	29818.844434
HLA A*2403	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.402909	0.227420	-4.175489	25287.683644
HLA B*4402	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.410141	0.234640	-4.175500	25712.290406
HLA A*3301	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.628897	0.453330	-4.175567	42549.710948
HLA A*6802	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.241697	0.066046	-4.175650	17446.036904
HLA A*6901	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.384348	0.208642	-4.175706	24229.704533
HLA B*0702	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.430335	0.254355	-4.175980	26936.092090
HLA B*1502	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.560599	0.384476	-4.176123	36357.953898
HLA B*4402	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.448696	0.272539	-4.176157	28099.320213
HLA B*5301	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.606800	0.430602	-4.176197	40438.934834
HLA A*6901	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.383415	0.207166	-4.176249	24177.721610
HLA A*0201	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.387207	0.210953	-4.176254	24389.755208
HLA B*3501	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.430734	0.254355	-4.176379	26960.876101
HLA B*0702	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.437773	0.261282	-4.176491	27401.419256
HLA B*1503	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.330991	0.154429	-4.176562	21428.477423
HLA A*6802	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.410634	0.233980	-4.176654	25741.518140
HLA B*0801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.313887	0.137191	-4.176696	20600.941222
HLA B*4001	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.363240	0.186500	-4.176741	23080.241298
HLA A*3201	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.411440	0.234640	-4.176800	25789.328239
HLA B*4402	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.173776	-0.003120	-4.176895	14920.230238
HLA A*0101	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.384179	0.207166	-4.177013	24220.268610
HLA A*0250	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.553939	0.376904	-4.177035	35804.585026
HLA B*5101	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.479688	0.302627	-4.177061	30177.820439
HLA B*0702	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.108159	-0.069030	-4.177189	12828.004622
HLA B*2705	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.480578	0.303325	-4.177253	30239.758948
HLA A*0206	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.550518	0.373125	-4.177393	35523.667340
HLA A*0206	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.459264	0.281539	-4.177725	28791.467207
HLA B*4501	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.582121	0.404390	-4.177731	38205.045148
HLA A*0201	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.370775	0.192958	-4.177817	23484.166097
HLA B*1503	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.450397	0.272539	-4.177858	28209.594317
HLA A*8001	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.304983	0.126963	-4.178020	20182.851037
HLA A*0212	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.321307	0.143276	-4.178030	20955.920231
HLA B*0802	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.456151	0.278063	-4.178088	28585.824914
HLA A*2501	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.464484	0.286262	-4.178222	29139.651447
HLA B*5101	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.468883	0.290570	-4.178313	29436.257177
HLA A*3001	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.280343	0.101982	-4.178361	19069.682644
HLA B*4001	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.400553	0.222188	-4.178364	25150.841266
HLA B*4002	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.642362	0.463883	-4.178479	43889.588873
HLA A*0203	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.324234	0.145582	-4.178652	21097.655423
HLA B*1509	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.529194	0.350403	-4.178791	33821.578168
HLA B*1801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.365430	0.186500	-4.178930	23196.906126
HLA B*4801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.414335	0.235291	-4.179044	25961.787766
HLA A*0202	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.481018	0.301939	-4.179079	30270.366458

HLA A*0211	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.406567	0.227420	-4.179147	25501.586403
HLA B*5301	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.583549	0.404390	-4.179160	38330.916559
HLA B*1503	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.044159	-0.135106	-4.179265	11070.293527
HLA A*0203	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.401563	0.222188	-4.179375	25209.416573
HLA B*2705	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.451957	0.272539	-4.179418	28311.110095
HLA B*4501	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.632823	0.453330	-4.179493	42936.100970
HLA B*0802	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.481471	0.301939	-4.179532	30301.988513
HLA B*4601	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.404742	0.225172	-4.179569	25394.615878
HLA B*5701	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.407829	0.228245	-4.179584	25575.779046
HLA A*2601	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.388486	0.208642	-4.179843	24461.639487
HLA A*0219	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.371175	0.191274	-4.179901	23505.773976
HLA A*0216	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.455263	0.275316	-4.179947	28527.428401
HLA B*4002	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.637639	0.457680	-4.179959	43414.924273
HLA B*1801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.530470	0.350403	-4.180066	33921.077486
HLA B*1503	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.530606	0.350403	-4.180203	33931.722694
HLA B*1517	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.408456	0.228245	-4.180211	25612.748428
HLA A*1101	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.470196	0.289937	-4.180259	29525.410926
HLA A*1101	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.414950	0.234640	-4.180310	25998.611860
HLA A*2602	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.539680	0.359286	-4.180394	34648.115636
HLA A*0301	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.366894	0.186500	-4.180394	23275.219971
HLA A*3201	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.527779	0.347374	-4.180406	33711.608801
HLA B*2705	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.451315	0.270903	-4.180413	28269.328285
HLA A*0202	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.527794	0.347374	-4.180420	33712.703076
HLA A*3001	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.275997	0.095477	-4.180519	18879.779525
HLA A*1101	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.466009	0.285427	-4.180582	29242.141105
HLA A*0216	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.470602	0.289937	-4.180666	29553.057012
HLA B*0802	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.466982	0.286262	-4.180720	29307.707954
HLA A*6801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.557764	0.376904	-4.180860	36121.319471
HLA A*1101	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.326504	0.145582	-4.180922	21208.199374
HLA A*2902	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.409227	0.228245	-4.180982	25658.237153
HLA B*5801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.318325	0.137191	-4.181134	20812.547411
HLA B*1517	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.459207	0.278063	-4.181144	28787.729242
HLA A*3002	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.484471	0.303325	-4.181146	30512.052403
HLA B*7301	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.515266	0.334057	-4.181209	32754.134005
HLA B*1509	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.524441	0.343210	-4.181231	33453.445990
HLA B*3901	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.452182	0.270903	-4.181280	28325.817270
HLA B*0802	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.462873	0.281539	-4.181334	29031.709261
HLA A*0202	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.484706	0.303325	-4.181381	30528.563551
HLA B*4403	1:498-506	9	TRITNEVAE	0.997488	-0.544575	-4.634315	0.452913	-4.181402	43083.852120
HLA B*1503	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.367984	0.186500	-4.181484	23333.718552
HLA A*2301	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.518201	0.336669	-4.181531	32976.201506
HLA B*1502	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.463108	0.281539	-4.181569	29047.419343
HLA B*5701	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.372944	0.191274	-4.181670	23601.723490
HLA A*3001	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.253169	0.071401	-4.181768	17913.041089
HLA A*2603	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.452986	0.270903	-4.182083	28378.273702
HLA B*1503	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.375042	0.192958	-4.182084	23716.020011
HLA A*2601	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.382210	0.200115	-4.182095	24110.714853
HLA B*0803	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.521565	0.339229	-4.182336	33232.658962
HLA A*0101	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.322235	0.139834	-4.182400	21000.748947
HLA B*4801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.436892	0.254455	-4.182437	27345.886115
HLA A*2602	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.481624	0.299099	-4.182525	30312.645863
HLA A*0216	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.234014	0.051389	-4.182625	17140.124449
HLA A*2603	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.664334	0.481648	-4.182686	46167.238340
HLA A*0216	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.410120	0.227420	-4.182700	25711.038531
HLA B*4403	1:104-112	9	GGIVAHTGT	0.908578	-0.449747	-4.641567	0.458831	-4.182736	43809.408222
HLA A*3301	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.555870	0.373125	-4.182745	35964.160016
HLA A*0216	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.469082	0.286262	-4.182820	29449.796275
HLA A*8001	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.437228	0.254355	-4.182873	27367.049464
HLA B*5401	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.551563	0.368545	-4.183018	35609.290063
HLA A*0219	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.417849	0.234640	-4.183209	26172.754099
HLA A*0219	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.473227	0.289937	-4.183290	29732.182258
HLA A*3101	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.392181	0.208642	-4.183539	24670.690285
HLA A*2402	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.556683	0.373125	-4.183558	36031.541552
HLA B*4001	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.411816	0.228245	-4.183571	25811.660688
HLA B*0802	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.453392	0.269777	-4.183615	28404.845668

HLA A*2603	1:311-319	9	RQFIRAFEG	0.897662	-0.431050	-4.650315	0.466612	-4.183702	44700.720103
HLA A*0203	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.418994	0.235291	-4.183703	26241.800171
HLA A*6901	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.103432	-0.080273	-4.183705	12689.132839
HLA B*3801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.526010	0.342132	-4.183879	33574.558959
HLA A*0212	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.419172	0.235291	-4.183882	26252.591747
HLA A*2501	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.462039	0.278063	-4.183976	28976.007059
HLA A*0250	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.329716	0.145582	-4.184133	21365.622140
HLA A*8001	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.469707	0.285427	-4.184280	29492.205938
HLA A*0201	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.392933	0.208642	-4.184291	24713.436299
HLA B*4501	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.648176	0.463883	-4.184294	44481.199291
HLA B*4001	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.395332	0.210953	-4.184379	24850.318572
HLA A*2601	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.391566	0.207166	-4.184400	24635.747042
HLA B*2705	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.411929	0.227420	-4.184509	25818.364193
HLA B*3801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.568992	0.384476	-4.184515	37067.371872
HLA B*4403	1:392-400	9	LPEEIVARQ	0.716878	-0.252995	-4.648437	0.463883	-4.184555	44507.918170
HLA A*2602	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.588615	0.403979	-4.184635	38780.615157
HLA A*8001	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.445935	0.261282	-4.184653	27921.270017
HLA A*2402	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.569135	0.384476	-4.184659	37079.606244
HLA A*3201	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.603783	0.419078	-4.184705	40159.007311
HLA A*3101	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.337380	0.152623	-4.184756	21746.009005
HLA B*1502	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.603973	0.419078	-4.184895	40176.608885
HLA A*2301	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.529145	0.344171	-4.184973	33817.735995
HLA B*4601	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.370792	0.185815	-4.184977	23485.055441
HLA B*3801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.592473	0.407463	-4.185009	39126.639432
HLA A*6802	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.412563	0.227420	-4.185143	25856.103861
HLA A*0219	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.396807	0.211398	-4.185409	24934.888881
HLA B*1501	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.412854	0.227420	-4.185434	25873.454633
HLA A*3002	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.283238	0.097746	-4.185492	19197.206262
HLA B*2705	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.483604	0.298081	-4.185524	30451.203501
HLA A*2501	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.413228	0.227657	-4.185571	25895.719838
HLA A*1101	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.460913	0.275316	-4.185597	28901.017667
HLA B*1517	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.447084	0.261282	-4.185802	27995.231732
HLA B*3801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.575319	0.389429	-4.185890	37611.353130
HLA A*3002	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.531386	0.345470	-4.185916	33992.721654
HLA B*1503	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.244385	0.058419	-4.185966	17554.343717
HLA A*0301	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.343319	0.157255	-4.186064	22045.454740
HLA A*3301	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.529276	0.343210	-4.186066	33827.982759
HLA B*3901	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.467642	0.281539	-4.186103	29352.294793
HLA B*7301	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.563111	0.376904	-4.186207	36568.827351
HLA B*0802	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.461576	0.275316	-4.186260	28945.142383
HLA B*1502	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.593870	0.407463	-4.186407	39252.786464
HLA A*3101	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.343827	0.157255	-4.186572	22071.230706
HLA B*1517	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.441039	0.254455	-4.186584	27608.247640
HLA B*0801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.377892	0.191274	-4.186618	23872.160925
HLA B*1517	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.468182	0.281539	-4.186643	29388.839836
HLA B*4801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.411985	0.225172	-4.186813	25821.716598
HLA B*4002	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.627337	0.440475	-4.186861	42397.139501
HLA B*0802	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.459724	0.272539	-4.187186	28822.012092
HLA A*3201	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.521260	0.334057	-4.187202	33209.295129
HLA B*0702	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.398309	0.210953	-4.187355	25021.235937
HLA B*7301	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.594949	0.407463	-4.187486	39350.377710
HLA A*2601	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.373329	0.185815	-4.187514	23622.672746
HLA A*0212	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.441983	0.254355	-4.187628	27668.354715
HLA B*1517	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.398718	0.210953	-4.187764	25044.800034
HLA A*0216	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.399185	0.211398	-4.187787	25071.776981
HLA B*0702	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.415479	0.227657	-4.187822	26030.277290
HLA A*0212	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.412998	0.225172	-4.187825	25881.994366
HLA B*0803	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.486976	0.299099	-4.187877	30688.521990
HLA B*1517	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.463249	0.275316	-4.187932	29056.849472
HLA A*2301	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.519627	0.331684	-4.187943	33084.666838
HLA A*0202	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.561147	0.373125	-4.188022	36403.812146
HLA B*0803	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.489983	0.301939	-4.188044	30901.766984
HLA A*2402	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.556737	0.368545	-4.188192	36036.025144
HLA A*3002	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.478856	0.290570	-4.188286	30120.082177
HLA A*2902	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.449654	0.261282	-4.188372	28161.410508

HLA A*2402	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.563217	0.374749	-4.188467	36577.730934
HLA A*2501	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.461261	0.272539	-4.188722	28924.166925
HLA A*0212	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.400191	0.211398	-4.188792	25129.896249
HLA B*5401	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.528087	0.339229	-4.188859	33735.508534
HLA B*5301	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.592874	0.403979	-4.188895	39162.851883
HLA B*0803	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.443532	0.254355	-4.189177	27767.171677
HLA A*0206	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.487335	0.298081	-4.189255	30713.933795
HLA B*4403	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.608508	0.419078	-4.189430	40598.293909
HLA B*5401	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.533630	0.344156	-4.189473	34168.797603
HLA A*8001	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.411919	0.222188	-4.189731	25817.805501
HLA B*4001	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.401340	0.211398	-4.189941	25196.463788
HLA A*2402	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.579501	0.389429	-4.190072	37975.284964
HLA B*5701	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.412300	0.222188	-4.190112	25840.442196
HLA A*0250	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.597698	0.407463	-4.190235	39600.238614
HLA A*3002	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.425086	0.234640	-4.190446	26612.510063
HLA A*0201	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.397686	0.207166	-4.190520	24985.390678
HLA B*5801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.347800	0.157255	-4.190545	22274.067402
HLA A*8001	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.401629	0.210953	-4.190675	25213.235506
HLA A*0250	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.559312	0.368545	-4.190767	36250.326024
HLA B*0802	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.481426	0.290570	-4.190857	30298.873996
HLA A*0203	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.424896	0.233980	-4.190916	26600.850988
HLA B*4402	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.424924	0.233980	-4.190944	26602.577936
HLA A*0206	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.426272	0.235291	-4.190982	26685.314687
HLA B*4601	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.413251	0.222188	-4.191063	25897.120806
HLA B*4801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.425083	0.233980	-4.191104	26612.366092
HLA A*0211	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.272332	0.081144	-4.191188	18721.115461
HLA B*4601	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.400003	0.208642	-4.191360	25119.022606
HLA B*3901	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.242850	0.051389	-4.191462	17492.439638
HLA A*6802	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.377354	0.185815	-4.191539	23842.604861
HLA B*4801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.419001	0.227420	-4.191581	26242.226070
HLA B*1517	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.464127	0.272539	-4.191589	29115.699669
HLA A*0211	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.382906	0.191274	-4.191632	24149.354925
HLA A*2402	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.534863	0.343210	-4.191653	34265.981487
HLA A*2402	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.575857	0.384129	-4.191728	37657.977379
HLA B*4801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.413935	0.222188	-4.191747	25937.922175
HLA B*1502	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.535904	0.344156	-4.191748	34348.201167
HLA A*0101	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.391923	0.200115	-4.191808	24656.013426
HLA A*3001	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.289570	0.097746	-4.191824	19479.145125
HLA B*7301	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.528564	0.336669	-4.191895	33772.577473
HLA A*0219	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.377713	0.185815	-4.191898	23862.347866
HLA B*4402	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.414245	0.222188	-4.192057	25956.451199
HLA B*3801	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.569027	0.376904	-4.192123	37070.379950
HLA B*1801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.399455	0.207166	-4.192289	25087.379921
HLA A*3201	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.534447	0.342132	-4.192316	34233.185787
HLA B*1517	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.495004	0.302627	-4.192377	31261.093317
HLA A*0219	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.427825	0.235291	-4.192535	26780.910504
HLA A*0212	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.414734	0.222188	-4.192546	25985.675315
HLA B*1502	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.534715	0.342132	-4.192583	34254.304841
HLA A*3301	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.483210	0.290570	-4.192640	30423.540151
HLA A*0250	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.567624	0.374749	-4.192875	36950.846735
HLA A*0219	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.420347	0.227420	-4.192927	26323.699680
HLA B*1503	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.496306	0.303325	-4.192981	31354.925812
HLA B*3901	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.427642	0.234640	-4.193002	26769.612111
HLA A*0219	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.454285	0.261282	-4.193003	28463.299216
HLA B*5301	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.604925	0.411911	-4.193013	40264.732545
HLA A*1101	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.428490	0.235291	-4.193200	26821.943444
HLA B*4002	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.626733	0.433361	-4.193372	42338.233957
HLA B*1509	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.570319	0.376904	-4.193416	37180.844865
HLA B*4403	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-3.989581	-0.203931	-4.193512	9762.939537
HLA A*0211	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.475233	0.281539	-4.193694	29869.864091
HLA A*0219	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.421985	0.228245	-4.193740	26423.145636
HLA A*0211	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.428413	0.234640	-4.193772	26817.155448
HLA B*0702	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.419088	0.225172	-4.193915	26247.479395
HLA A*0212	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.427910	0.233980	-4.193930	26786.126755
HLA A*2603	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.528040	0.334057	-4.193983	33731.858624

HLA B*5101	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.231131	0.037065	-4.194066	17026.726215
HLA A*2603	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.651759	0.457680	-4.194079	44849.690738
HLA B*4801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.348678	0.154429	-4.194249	22319.180113
HLA A*2301	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.528329	0.334057	-4.194272	33754.311824
HLA A*2301	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.533602	0.339229	-4.194373	34166.579482
HLA A*2301	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.541900	0.347374	-4.194526	34825.702321
HLA A*3002	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.583989	0.389429	-4.194559	38369.713624
HLA A*2501	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.403226	0.208642	-4.194584	25306.158871
HLA B*3801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.538810	0.344156	-4.194654	34578.831289
HLA B*5401	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.430020	0.235291	-4.194729	26916.572515
HLA B*4801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.423263	0.228245	-4.195018	26501.022956
HLA B*4403	1:67-75	9	PASVYADGA	0.889795	-0.432115	-4.652746	0.457680	-4.195066	44951.711977
HLA B*5801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.342978	0.147675	-4.195304	22028.168319
HLA B*0802	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.493663	0.298081	-4.195582	31164.675336
HLA A*0216	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.456940	0.261282	-4.195658	28637.833272
HLA A*2601	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.352980	0.157255	-4.195725	22541.361501
HLA B*3801	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.570540	0.374749	-4.195791	37199.757232
HLA A*3301	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.494950	0.299099	-4.195851	31257.203821
HLA A*0211	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.381691	0.185815	-4.195876	24081.905657
HLA A*1101	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.497960	0.301939	-4.196021	31474.570682
HLA A*0201	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.381928	0.185815	-4.196113	24095.067577
HLA A*0201	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.392057	0.195916	-4.196141	24663.617617
HLA A*2301	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.539360	0.343210	-4.196150	34622.632837
HLA A*0301	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.317115	0.120764	-4.196352	20754.642422
HLA B*0803	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.471831	0.275316	-4.196515	29636.792008
HLA A*3001	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.283363	0.086816	-4.196546	19202.711354
HLA B*1801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.471991	0.275316	-4.196675	29647.696573
HLA A*0101	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.349801	0.153079	-4.196723	22376.970572
HLA A*6801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.389686	0.192958	-4.196728	24529.356105
HLA A*8001	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.469371	0.272539	-4.196833	29469.399173
HLA A*2602	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.580991	0.384129	-4.196862	38105.758870
HLA B*5101	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.482343	0.285427	-4.196916	30362.867765
HLA B*1502	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.601325	0.404390	-4.196936	39932.399530
HLA B*3901	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.483257	0.286262	-4.196994	30426.832089
HLA B*1502	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.495091	0.298081	-4.197010	31267.351348
HLA B*3801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.570152	0.373125	-4.197028	37166.566365
HLA A*6901	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.383756	0.186500	-4.197256	24196.694875
HLA A*2301	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.541439	0.344156	-4.197283	34788.794866
HLA A*0211	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.337269	0.139834	-4.197435	21740.480463
HLA B*0803	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.475642	0.278063	-4.197579	29897.994450
HLA B*5101	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.452084	0.254455	-4.197629	28319.381941
HLA A*0202	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.340920	0.143276	-4.197644	21924.022416
HLA B*0803	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.468568	0.270903	-4.197665	29414.925827
HLA B*4002	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.644286	0.446544	-4.197741	44084.481877
HLA B*1509	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.534450	0.336669	-4.197780	34233.370986
HLA B*5401	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.425203	0.227420	-4.197783	26619.709573
HLA B*4403	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.651254	0.453330	-4.197924	44797.555215
HLA B*5701	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.423108	0.225172	-4.197935	26491.562384
HLA B*4002	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.384609	0.186500	-4.198109	24244.258785
HLA B*5801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.352550	0.154429	-4.198121	22519.056377
HLA A*2501	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.452511	0.254355	-4.198156	28347.278931
HLA A*0202	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.077118	-0.121106	-4.198224	11943.117689
HLA A*2403	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.409624	0.211398	-4.198225	25681.706469
HLA A*0212	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.389592	0.191274	-4.198319	24524.048635
HLA A*2602	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.541599	0.343210	-4.198389	34801.595060
HLA A*2301	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.540535	0.342132	-4.198403	34716.411916
HLA B*5701	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.405597	0.207166	-4.198431	25444.672216
HLA B*3501	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.488419	0.289937	-4.198482	30790.628680
HLA A*0206	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.468262	0.269777	-4.198485	29394.246006
HLA A*1101	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.459788	0.261282	-4.198506	28826.222345
HLA A*2403	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.420791	0.222188	-4.198603	26350.628613
HLA A*0206	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.398783	0.200115	-4.198668	25048.594030
HLA B*4402	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.409687	0.210953	-4.198734	25685.457993
HLA B*4001	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.346418	0.147675	-4.198743	22203.325838
HLA B*7301	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.471385	0.272539	-4.198846	29606.344624

HLA B*4601	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.409871	0.210953	-4.198917	25696.298808
HLA B*5301	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.576033	0.376904	-4.199130	37673.259890
HLA A*0212	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.294755	0.095477	-4.199278	19713.112784
HLA A*0211	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.538528	0.339229	-4.199300	34556.390457
HLA A*2501	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.392292	0.192958	-4.199334	24676.963971
HLA B*1517	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.351975	0.152623	-4.199351	22489.228877
HLA A*6901	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.339186	0.139834	-4.199352	21836.665298
HLA B*1801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.501477	0.301939	-4.199538	31730.505727
HLA B*2705	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.433694	0.233980	-4.199714	27145.281625
HLA B*4001	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.352903	0.153079	-4.199824	22537.337634
HLA B*7301	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.531522	0.331684	-4.199838	34003.389345
HLA A*3201	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.478022	0.278063	-4.199959	30062.291750
HLA B*5701	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.408637	0.208642	-4.199995	25623.419934
HLA B*5401	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.550586	0.350403	-4.200183	35529.240971
HLA A*8001	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.434951	0.234640	-4.200311	27223.961768
HLA A*1101	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.434404	0.233980	-4.200424	27189.667469
HLA B*1517	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.435097	0.234640	-4.200457	27233.094574
HLA A*2603	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.647021	0.446544	-4.200476	44362.962643
HLA B*3901	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.461782	0.261282	-4.200500	28958.925585
HLA B*4801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.261484	0.060842	-4.200642	18259.301067
HLA A*2602	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.471636	0.270903	-4.200733	29623.487459
HLA B*5301	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.608235	0.407463	-4.200772	40572.824558
HLA B*4601	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.408014	0.207166	-4.200848	25586.711990
HLA A*0219	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.426113	0.225172	-4.200940	26675.499700
HLA A*3301	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.560233	0.359286	-4.200947	36327.282812
HLA A*3001	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.283713	0.082695	-4.201018	19218.196390
HLA A*2601	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.392332	0.191274	-4.201058	24679.233569
HLA A*0250	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.585556	0.384476	-4.201079	38508.416845
HLA B*1801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.436377	0.235291	-4.201087	27313.506831
HLA A*0211	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.499205	0.298081	-4.201124	31564.945370
HLA A*0250	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.574297	0.373125	-4.201172	37522.946330
HLA A*2402	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.499276	0.298081	-4.201195	31570.068672
HLA A*6901	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.354390	0.153079	-4.201311	22614.648139
HLA B*5401	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.548777	0.347374	-4.201403	35381.547675
HLA A*6901	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.401720	0.200115	-4.201605	25218.555699
HLA A*6802	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.423801	0.222188	-4.201613	26533.874481
HLA A*2301	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.547099	0.345470	-4.201630	35245.144366
HLA B*4601	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.392961	0.191274	-4.201688	24715.040714
HLA A*3002	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.429416	0.227657	-4.201759	26879.175291
HLA B*4403	1:199-207	9	FAGLGAQWT	0.896515	-0.456040	-4.642350	0.440475	-4.201875	43888.401700
HLA A*6801	1:393-401	9	PEEIVARQP	0.746903	-0.265255	-4.683536	0.481648	-4.201888	48254.324159
HLA B*5401	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.533580	0.331684	-4.201896	34164.915986
HLA A*0212	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.429329	0.227420	-4.201909	26873.795535
HLA B*5101	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.505278	0.303325	-4.201954	32009.468336
HLA A*6901	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.339386	0.137191	-4.202195	21846.708992
HLA A*8001	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.429886	0.227657	-4.202229	26908.273701
HLA B*1517	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.429888	0.227657	-4.202231	26908.419273
HLA B*2705	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.430523	0.228245	-4.202278	26947.752315
HLA A*0206	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.541536	0.339229	-4.202307	34796.512067
HLA B*3801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.547861	0.345470	-4.202391	35306.976372
HLA A*0211	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.477738	0.275316	-4.202422	30042.619516
HLA A*0101	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.389009	0.186500	-4.202510	24491.167946
HLA A*0203	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.430125	0.227420	-4.202705	26923.126018
HLA A*2402	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.546916	0.344171	-4.202745	35230.275062
HLA B*2705	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.492711	0.289937	-4.202775	31096.468122
HLA B*4601	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.398877	0.195916	-4.202961	25054.015021
HLA B*0802	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.438337	0.235291	-4.203046	27437.019636
HLA A*2603	1:279-287	9	TGANLVTVD	1.293049	-0.839719	-4.656628	0.453330	-4.203298	45355.252140
HLA B*4001	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.394766	0.191274	-4.203492	24817.940253
HLA B*7301	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.578244	0.374749	-4.203495	37865.532355
HLA A*6901	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.317125	0.113627	-4.203498	20755.091548
HLA B*2705	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.485214	0.281539	-4.203675	30564.258129
HLA B*7301	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.562991	0.359286	-4.203705	36558.739245
HLA A*0206	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.340497	0.136752	-4.203745	21902.683631
HLA B*4001	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.403863	0.200115	-4.203748	25343.286934

HLA A*2402	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.542978	0.339229	-4.203750	34912.286841
HLA A*0211	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.507301	0.303325	-4.203976	32158.913486
HLA A*0212	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.349822	0.145582	-4.204240	22378.060111
HLA B*1502	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.551883	0.347374	-4.204509	35635.499058
HLA B*0802	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.494494	0.289937	-4.204558	31224.416016
HLA B*4501	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.589035	0.384476	-4.204559	38818.187336
HLA B*4801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.411858	0.207166	-4.204692	25814.174298
HLA B*5401	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.548915	0.344171	-4.204744	35392.842682
HLA A*0202	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.285092	0.080331	-4.204761	19279.322795
HLA B*1801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.495606	0.290570	-4.205036	31304.417787
HLA A*0216	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.474820	0.269777	-4.205043	29841.437319
HLA B*5801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.348352	0.143276	-4.205075	22302.402965
HLA B*4002	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.624155	0.419078	-4.205077	42087.715530
HLA B*5301	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.578268	0.373125	-4.205143	37867.580893
HLA B*4801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.413872	0.208642	-4.205229	25934.133777
HLA B*1501	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.346383	0.141148	-4.205234	22201.524148
HLA A*0301	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.358062	0.152623	-4.205439	22806.680577
HLA B*5301	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.564725	0.359286	-4.205439	36704.991707
HLA B*5801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.358544	0.153079	-4.205465	22831.987838
HLA A*3101	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.416440	0.210953	-4.205486	26087.936810
HLA A*0219	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.351143	0.145582	-4.205561	22446.200952
HLA A*0203	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.430739	0.225172	-4.205566	26961.167813
HLA B*5701	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.398680	0.192958	-4.205722	25042.632294
HLA A*0202	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.549902	0.344171	-4.205731	35473.352082
HLA A*3001	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.286250	0.080331	-4.205919	19330.810832
HLA B*5801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.358652	0.152623	-4.206029	22837.670397
HLA A*2402	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.537805	0.331684	-4.206121	34498.858959
HLA A*0301	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.359350	0.153079	-4.206271	22874.394023
HLA A*0206	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.481589	0.275316	-4.206273	30310.186142
HLA A*2902	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.406447	0.200115	-4.206332	25494.551375
HLA B*0801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.359025	0.152623	-4.206402	22857.323181
HLA B*1501	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.343253	0.136752	-4.206501	22042.115616
HLA B*1503	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.354430	0.147675	-4.206755	22616.728061
HLA B*0803	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.504870	0.298081	-4.206789	31979.351338
HLA A*2501	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.492267	0.285427	-4.206840	31064.689195
HLA B*1501	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.417805	0.210953	-4.206851	26170.063995
HLA A*1101	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.488477	0.281539	-4.206938	30794.793309
HLA B*4601	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.393474	0.186500	-4.206974	24744.205736
HLA A*3001	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.289239	0.082233	-4.207006	19464.292209
HLA B*1502	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.583967	0.376904	-4.207064	38367.845487
HLA B*4601	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.407328	0.200115	-4.207213	25546.324886
HLA B*4402	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.434773	0.227420	-4.207353	27212.770894
HLA B*3801	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.554752	0.347374	-4.207378	35871.667587
HLA B*1509	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.265932	0.058419	-4.207513	18447.253873
HLA B*0803	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.435252	0.227657	-4.207595	27242.819959
HLA B*4001	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.416275	0.208642	-4.207633	26078.059381
HLA B*1502	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.576242	0.368545	-4.207697	37691.403184
HLA B*0803	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.511129	0.303325	-4.207804	32443.573114
HLA B*0801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.393647	0.185815	-4.207832	24754.113612
HLA B*5101	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.489455	0.281539	-4.207916	30864.175463
HLA A*3101	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.415119	0.207166	-4.207953	26008.740604
HLA B*3501	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.442627	0.234640	-4.207987	27709.398195
HLA B*4001	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.393828	0.185815	-4.208013	24764.427369
HLA A*0202	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.032821	-0.175217	-4.208037	10785.009244
HLA A*0201	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.394759	0.186500	-4.208259	24817.537470
HLA B*0802	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.479173	0.270903	-4.208270	30142.087963
HLA B*5101	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.479178	0.270903	-4.208275	30142.414096
HLA A*0301	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.356079	0.147675	-4.208404	22702.783869
HLA B*5701	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.408531	0.200115	-4.208416	25617.182800
HLA B*7301	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.494680	0.286262	-4.208418	31237.763598
HLA A*8001	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.462934	0.254455	-4.208479	29035.793064
HLA A*2601	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.320884	0.112320	-4.208564	20935.523707
HLA A*0212	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.417253	0.208642	-4.208610	26136.814506
HLA A*2403	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.400022	0.191274	-4.208748	25120.109759
HLA B*5801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.349923	0.141148	-4.208775	22383.266418

HLA B*1801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.329591	0.120764	-4.208827	21359.496979
HLA A*3201	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.289983	0.081144	-4.208839	19497.700840
HLA B*3501	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.405094	0.195916	-4.209178	25415.231550
HLA B*1502	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.593347	0.384129	-4.209218	39205.460249
HLA B*4501	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.434416	0.225172	-4.209243	27190.402945
HLA B*1517	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.499311	0.289937	-4.209374	31572.630634
HLA B*5801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.355579	0.146138	-4.209440	22676.638372
HLA A*0203	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.420507	0.210953	-4.209553	26333.385226
HLA A*2403	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.420535	0.210953	-4.209581	26335.094810
HLA B*5701	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.420587	0.210953	-4.209633	26338.229335
HLA A*0211	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.487733	0.278063	-4.209670	30742.027503
HLA A*2501	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.434944	0.225172	-4.209772	27223.519936
HLA A*0203	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.405700	0.195916	-4.209784	25450.729663
HLA A*0250	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.599241	0.389429	-4.209812	39741.240062
HLA B*5401	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.421230	0.211398	-4.209832	26377.299696
HLA B*1801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.421385	0.211398	-4.209987	26386.719463
HLA B*5301	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.594510	0.384476	-4.210033	39310.589059
HLA A*2602	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.594585	0.384476	-4.210108	39317.394957
HLA B*0802	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.464646	0.254355	-4.210291	29150.530795
HLA A*0101	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.261754	0.051389	-4.210365	18270.664393
HLA B*2705	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.401657	0.191274	-4.210383	25214.872369
HLA A*3002	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.583512	0.373125	-4.210387	38327.598847
HLA B*5101	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.482933	0.272539	-4.210394	30404.124967
HLA A*2602	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.331233	0.120764	-4.210470	21440.421096
HLA A*0250	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.508638	0.298081	-4.210558	32258.058436
HLA B*0801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.331558	0.120764	-4.210794	21456.433734
HLA B*1801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.509120	0.298081	-4.211039	32293.853348
HLA B*4402	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.358917	0.147675	-4.211243	22851.635732
HLA A*2403	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.436580	0.225172	-4.211407	27326.217410
HLA B*5401	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.548154	0.336669	-4.211485	35330.860301
HLA A*3301	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.630598	0.419078	-4.211520	42716.694747
HLA B*3801	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.545666	0.334057	-4.211609	35129.025951
HLA A*6802	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.437099	0.225172	-4.211926	27358.907777
HLA B*4002	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.267922	0.055954	-4.211968	18531.976398
HLA A*2403	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.398485	0.186500	-4.211985	25031.390156
HLA A*1101	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.481809	0.269777	-4.212032	30325.603688
HLA B*5701	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.423523	0.211398	-4.212125	26516.941538
HLA A*2402	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.562559	0.350403	-4.212156	36522.366065
HLA A*3201	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.091078	-0.121106	-4.212184	12333.273198
HLA A*2603	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.557672	0.345470	-4.212202	36113.699194
HLA A*1101	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.434505	0.222188	-4.212317	27195.993208
HLA A*2501	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.446969	0.234640	-4.212329	27987.811611
HLA A*3101	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.398165	0.185815	-4.212350	25012.980211
HLA B*1517	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.482190	0.269777	-4.212413	30352.192759
HLA B*0803	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.484955	0.272539	-4.212417	30546.075122
HLA A*0212	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.398414	0.185815	-4.212599	25027.327974
HLA B*4002	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.643214	0.430602	-4.212612	43975.863483
HLA A*0216	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.421296	0.208642	-4.212654	26381.295550
HLA A*2501	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.474063	0.261282	-4.212781	29789.499254
HLA B*0702	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.408780	0.195916	-4.212864	25631.877141
HLA B*3501	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.474155	0.261282	-4.212873	29795.785075
HLA B*4002	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.617300	0.404390	-4.212910	41428.533108
HLA B*4501	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.659529	0.446544	-4.212985	45659.294800
HLA A*3301	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.597251	0.384129	-4.213123	39559.555275
HLA B*5401	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.547226	0.334057	-4.213169	35255.442175
HLA A*0301	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.356455	0.143276	-4.213179	22722.443503
HLA B*0802	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.467788	0.254455	-4.213333	29362.141589
HLA A*3201	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.620810	0.407463	-4.213346	41764.730831
HLA B*0801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.361034	0.147675	-4.213359	22963.293598
HLA A*2601	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.399878	0.186500	-4.213378	25111.821409
HLA A*0206	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.294680	0.081144	-4.213536	19709.700415
HLA B*2705	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.515515	0.301939	-4.213576	32772.922193
HLA A*0101	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.370850	0.157255	-4.213596	23488.231944
HLA B*0803	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.499029	0.285427	-4.213602	31552.140754
HLA B*3901	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.503784	0.289937	-4.213848	31899.522947

HLA B*4001	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.439077	0.225172	-4.213905	27483.815336
HLA A*8001	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.441424	0.227420	-4.214004	27632.753149
HLA A*2601	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.351824	0.137730	-4.214094	22481.443714
HLA B*7301	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.582645	0.368545	-4.214100	38251.163729
HLA A*0301	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.368644	0.154429	-4.214215	23369.216953
HLA A*0101	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.366856	0.152623	-4.214233	23273.205396
HLA A*3201	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.517634	0.303325	-4.214309	32933.235701
HLA B*0802	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.448308	0.233980	-4.214328	28074.249060
HLA B*5301	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.564814	0.350403	-4.214411	36712.538140
HLA A*3001	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.093395	-0.121106	-4.214501	12399.236508
HLA A*2902	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.371764	0.157255	-4.214510	23537.713728
HLA A*3301	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.485421	0.270903	-4.214518	30578.812327
HLA A*8001	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.442775	0.228245	-4.214530	27718.843806
HLA A*3001	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.280668	0.066046	-4.214621	19083.924712
HLA B*4501	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.645381	0.430602	-4.214778	44195.759430
HLA B*5101	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.490162	0.275316	-4.214846	30914.474907
HLA A*2902	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.449509	0.234640	-4.214868	28151.966385
HLA B*3901	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.442460	0.227420	-4.215040	27698.757000
HLA B*0702	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.449718	0.234640	-4.215078	28165.524262
HLA A*0101	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.369636	0.154429	-4.215207	23422.629195
HLA B*1509	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.547137	0.331684	-4.215453	35248.195255
HLA A*0219	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.408426	0.192958	-4.215468	25610.947183
HLA A*2602	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.622955	0.407463	-4.215491	41971.526677
HLA B*1502	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.605023	0.389429	-4.215594	40273.882349
HLA B*4801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.426998	0.211398	-4.215600	26729.960652
HLA B*0801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.361210	0.145582	-4.215628	22972.612654
HLA A*0216	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.311138	0.095477	-4.215661	20470.957919
HLA A*3101	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.311141	0.095477	-4.215663	20471.068665
HLA B*1509	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.488207	0.272539	-4.215668	30775.640680
HLA A*8001	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.363635	0.147675	-4.215960	23101.227574
HLA A*3101	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.427395	0.211398	-4.215997	26754.410262
HLA B*1509	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.486917	0.270903	-4.216014	30684.371733
HLA A*2402	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.552787	0.336669	-4.216118	35709.798285
HLA A*8001	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.450199	0.233980	-4.216220	28196.777923
HLA A*3101	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.402740	0.186500	-4.216240	25277.835706
HLA B*7301	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.515539	0.299099	-4.216440	32774.695219
HLA B*5101	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.486226	0.269777	-4.216449	30635.606803
HLA A*0206	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.471218	0.254455	-4.216763	29594.974948
HLA B*5701	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.362446	0.145582	-4.216864	23038.076657
HLA A*0216	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.471234	0.254355	-4.216879	29596.095708
HLA B*3801	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.516023	0.299099	-4.216924	32811.240918
HLA B*0801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.424139	0.207166	-4.216973	26554.553060
HLA A*0250	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.561149	0.344171	-4.216978	36404.009088
HLA A*0203	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.402820	0.185815	-4.217005	25282.485643
HLA B*4501	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.650451	0.433361	-4.217090	44714.748209
HLA A*0219	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.471465	0.254355	-4.217110	29611.790805
HLA A*0219	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.451130	0.233980	-4.217150	28257.249086
HLA A*6901	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.371640	0.154429	-4.217211	23530.965865
HLA B*0702	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.471671	0.254455	-4.217216	29625.891453
HLA B*5801	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.354063	0.136752	-4.217311	22597.648890
HLA B*5301	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.606929	0.389429	-4.217500	40450.968982
HLA B*0801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.370582	0.153079	-4.217504	23473.750575
HLA B*0803	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.439709	0.222188	-4.217521	27523.840555
HLA A*0216	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.410526	0.192958	-4.217568	25735.113034
HLA B*5401	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.096477	-0.121106	-4.217583	12487.556561
HLA B*1502	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.592510	0.374749	-4.217761	39130.026311
HLA B*1517	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.442980	0.225172	-4.217807	27731.893037
HLA A*0206	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.479143	0.261282	-4.217861	30139.968188
HLA A*1101	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.443038	0.225172	-4.217866	27735.643952
HLA A*2403	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.425034	0.207166	-4.217868	26609.342895
HLA B*3901	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.490463	0.272539	-4.217924	30935.889537
HLA A*3002	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.557376	0.339229	-4.218147	36089.090822
HLA B*4402	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.411196	0.192958	-4.218238	25774.822510
HLA B*5401	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.563748	0.345470	-4.218278	36622.479496
HLA A*3001	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.309620	0.091322	-4.218299	20399.541119

HLA B*0803	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.499910	0.281539	-4.218371	31616.215821
HLA B*1503	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.427050	0.208642	-4.218408	26733.142176
HLA A*0212	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.405059	0.186500	-4.218559	25413.169230
HLA A*2602	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.491099	0.272539	-4.218561	30981.277288
HLA B*4403	1:332-340	9	FLVQGTLYP	0.460598	-0.027237	-4.651933	0.433361	-4.218572	44867.649090
HLA B*5101	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.508523	0.289937	-4.218587	32249.508456
HLA A*2902	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.452812	0.233980	-4.218832	28366.915250
HLA B*5101	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.454182	0.235291	-4.218891	28456.524757
HLA A*2501	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.488794	0.269777	-4.219017	30817.292040
HLA A*0211	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.489929	0.270903	-4.219026	30897.922196
HLA B*1502	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.372218	0.153079	-4.219139	23562.302492
HLA B*5801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.354766	0.135619	-4.219146	22634.231451
HLA B*4402	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.275158	0.055954	-4.219204	18843.351621
HLA B*0802	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.480567	0.261282	-4.219285	30238.940991
HLA B*1509	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.517435	0.298081	-4.219354	32918.095145
HLA B*0702	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.365331	0.145582	-4.219749	23191.636032
HLA A*2602	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.521739	0.301939	-4.219800	33245.965715
HLA A*2403	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.405620	0.185815	-4.219805	25446.048782
HLA A*2501	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.495211	0.275316	-4.219895	31275.979336
HLA A*0201	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.363261	0.143276	-4.219985	23081.365080
HLA A*0201	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.359836	0.139834	-4.220002	22900.024194
HLA A*3001	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.257069	0.037065	-4.220005	18074.632141
HLA B*4001	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.366499	0.146138	-4.220361	23254.075633
HLA B*3801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.557035	0.336669	-4.220366	36060.792416
HLA A*3201	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.557195	0.336669	-4.220526	36074.060629
HLA B*5801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.358372	0.137730	-4.220642	22822.972766
HLA B*0801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.301844	0.081144	-4.220700	20037.503115
HLA A*2902	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.431688	0.210953	-4.220734	27020.158454
HLA A*6801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.378171	0.157255	-4.220917	23887.534216
HLA B*1503	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.522864	0.301939	-4.220926	33332.228933
HLA A*3001	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.279378	0.058419	-4.220959	19027.328986
HLA B*4402	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.406856	0.185815	-4.221041	25518.561223
HLA B*1503	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.406953	0.185815	-4.221137	25524.222007
HLA A*1101	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.417072	0.195916	-4.221156	26125.929183
HLA B*4403	1:338-346	9	LYPDVVESG	0.937323	-0.490779	-4.667741	0.446544	-4.221196	46530.813961
HLA A*0250	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.571712	0.350403	-4.221309	37300.314936
HLA A*8001	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.456672	0.235291	-4.221382	28620.176982
HLA A*0202	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.358666	0.137191	-4.221475	22838.411705
HLA A*1101	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.449746	0.228245	-4.221501	28167.352789
HLA A*3201	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.596319	0.374749	-4.221569	39474.683363
HLA A*0219	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.430245	0.208642	-4.221603	26930.555251
HLA B*1509	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.567133	0.345470	-4.221664	36909.091248
HLA B*0802	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.449335	0.227657	-4.221678	28140.698514
HLA B*0702	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.443990	0.222188	-4.221802	27796.479511
HLA B*3501	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.374908	0.153079	-4.221829	23708.707979
HLA B*1509	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.503371	0.281539	-4.221832	31869.164575
HLA A*8001	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.413270	0.191274	-4.221997	25898.241635
HLA B*0802	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.444206	0.222188	-4.222018	27810.317535
HLA A*0301	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.362002	0.139834	-4.222168	23014.532975
HLA B*5401	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.500272	0.278063	-4.222209	31642.566990
HLA A*0101	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.359415	0.137191	-4.222225	22877.859228
HLA A*3101	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.376663	0.154429	-4.222234	23804.713163
HLA B*1509	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.507828	0.285427	-4.222401	32197.907767
HLA A*2402	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.567916	0.345470	-4.222446	36975.642649
HLA A*2403	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.368092	0.145582	-4.222510	23339.525985
HLA A*0301	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.368672	0.146138	-4.222534	23370.734101
HLA B*4601	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.375270	0.152623	-4.222646	23728.468478
HLA B*5401	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.565968	0.343210	-4.222758	36810.185655
HLA B*3801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.573355	0.350403	-4.222952	37441.633574
HLA B*1503	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.513006	0.289937	-4.223069	32584.114031
HLA A*2602	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.335460	0.112320	-4.223140	21650.106362
HLA A*6901	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.370881	0.147675	-4.223206	23489.883896
HLA B*4601	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.376350	0.153079	-4.223272	23787.591469
HLA B*4501	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.591824	0.368545	-4.223279	39068.261889
HLA B*3501	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.149360	-0.073933	-4.223292	14104.564356

HLA A*0101	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.371071	0.147675	-4.223396	23500.179442
HLA B*4801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.409262	0.185815	-4.223447	25660.319361
HLA B*0802	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.458197	0.234640	-4.223557	28720.839551
HLA A*2501	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.513530	0.289937	-4.223593	32623.447399
HLA B*5701	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.409448	0.185815	-4.223633	25671.288444
HLA B*1502	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.325630	0.101982	-4.223648	21165.561242
HLA B*3801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.563015	0.339229	-4.223786	36560.717085
HLA A*3301	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.631300	0.407463	-4.223837	42785.847343
HLA B*5701	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.376489	0.152623	-4.223866	23795.185286
HLA A*3001	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.302400	0.078424	-4.223977	20063.210551
HLA A*2403	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.424120	0.200115	-4.224005	26553.403828
HLA B*0801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.092131	-0.132020	-4.224151	12363.200745
HLA A*0301	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.337537	0.113362	-4.224175	21753.892548
HLA B*2705	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.478626	0.254355	-4.224271	30104.117671
HLA A*3201	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.568527	0.344171	-4.224355	37027.688116
HLA B*1509	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.377041	0.152623	-4.224418	23825.455913
HLA B*2705	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.478901	0.254455	-4.224446	30123.178316
HLA B*4402	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.433088	0.208642	-4.224446	27107.419990
HLA B*1509	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.499814	0.275316	-4.224497	31609.203949
HLA B*4801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.435511	0.210953	-4.224557	27259.036654
HLA B*5801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.345323	0.120764	-4.224560	22147.421566
HLA A*2602	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.570049	0.345470	-4.224579	37157.720470
HLA A*0219	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.367911	0.143276	-4.224635	23329.805663
HLA A*0202	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.575293	0.350403	-4.224890	37609.114991
HLA A*0301	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.366222	0.141148	-4.225073	23239.235737
HLA A*2601	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.377859	0.152623	-4.225236	23870.352953
HLA B*2705	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.425452	0.200115	-4.225337	26634.978976
HLA B*4001	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.421280	0.195916	-4.225363	26380.296530
HLA A*6901	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.368647	0.143276	-4.225370	23369.343378
HLA A*2501	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.436800	0.211398	-4.225402	27340.117133
HLA B*1517	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.432569	0.207166	-4.225403	27075.030118
HLA B*7301	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.572913	0.347374	-4.225539	37403.572576
HLA A*2902	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.418514	0.192958	-4.225556	26212.855239
HLA A*2403	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.421658	0.195916	-4.225742	26403.283570
HLA A*0216	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.411644	0.185815	-4.225829	25801.469110
HLA B*5701	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.412401	0.186500	-4.225901	25846.454034
HLA A*3101	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.307083	0.081144	-4.225939	20280.700634
HLA A*0219	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.426101	0.200115	-4.225986	26674.778152
HLA B*3901	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.374093	0.147675	-4.226418	23664.242993
HLA A*0211	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.512844	0.286262	-4.226582	32571.953226
HLA B*1501	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.383925	0.157255	-4.226670	24206.121615
HLA A*2603	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.568816	0.342132	-4.226684	37052.335145
HLA A*2601	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.374396	0.147675	-4.226721	23680.763457
HLA B*4402	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.426883	0.200115	-4.226768	26722.875891
HLA B*0801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.366633	0.139834	-4.226799	23261.247451
HLA A*3301	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.566043	0.339229	-4.226815	36816.558655
HLA B*5401	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.307146	0.080331	-4.226815	20283.663192
HLA A*3002	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.571351	0.344156	-4.227194	37269.252129
HLA A*0212	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.434392	0.207166	-4.227226	27188.932014
HLA B*7301	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.616658	0.389429	-4.227229	41367.392479
HLA A*6801	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.646370	0.419078	-4.227292	44296.532786
HLA B*5101	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.513683	0.286262	-4.227420	32634.921217
HLA A*0203	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.434606	0.207166	-4.227440	27202.320418
HLA B*0801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.278943	0.051389	-4.227554	19008.295401
HLA A*3001	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.288423	0.060842	-4.227582	19427.787500
HLA A*3201	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.612086	0.384476	-4.227610	40934.175664
HLA A*0203	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.340972	0.113362	-4.227610	21926.631914
HLA A*3201	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.463044	0.235291	-4.227753	29043.176783
HLA A*8001	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.428091	0.200115	-4.227976	26797.287148
HLA A*6802	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.365221	0.137191	-4.228030	23185.739965
HLA A*2902	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.369182	0.141148	-4.228034	23398.186190
HLA A*6802	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.428204	0.200115	-4.228088	26804.246628
HLA B*4002	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.572293	0.344156	-4.228136	37350.190522
HLA B*5801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.355189	0.126963	-4.228226	22656.282949
HLA A*0201	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.381064	0.152623	-4.228440	24047.145890

HLA B*5101	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.462457	0.233980	-4.228477	29003.923242
HLA A*0211	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.453721	0.225172	-4.228549	28426.367206
HLA B*5101	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.506620	0.278063	-4.228557	32108.499957
HLA B*1501	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.381202	0.152623	-4.228579	24054.822566
HLA B*0702	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.456170	0.227420	-4.228750	28587.062110
HLA A*0202	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.572911	0.344156	-4.228754	37403.370227
HLA B*5101	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.456430	0.227657	-4.228773	28604.233730
HLA A*0250	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.483325	0.254455	-4.228870	30431.606031
HLA A*2602	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.603814	0.374749	-4.229064	40161.831735
HLA A*0301	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.341656	0.112320	-4.229336	21961.177708
HLA B*3801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.499146	0.269777	-4.229369	31560.676588
HLA B*3901	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.463354	0.233980	-4.229374	29063.924078
HLA A*2501	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.456846	0.227420	-4.229426	28631.636843
HLA B*1509	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.365136	0.135619	-4.229517	23181.224842
HLA B*5301	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.598161	0.368545	-4.229616	39642.464993
HLA A*0301	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.366819	0.137191	-4.229628	23271.190996
HLA A*0301	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.367368	0.137730	-4.229638	23300.668978
HLA B*1509	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.331663	0.101982	-4.229681	21461.657831
HLA A*0219	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.451903	0.222188	-4.229715	28307.587635
HLA A*0101	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.373061	0.143276	-4.229785	23608.108489
HLA A*3101	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.366595	0.136752	-4.229843	23259.234085
HLA A*8001	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.441309	0.211398	-4.229911	27625.429103
HLA A*8001	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.415897	0.185815	-4.230082	26055.355485
HLA A*0203	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.383293	0.153079	-4.230214	24170.921029
HLA A*0301	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.367112	0.136752	-4.230360	23286.933139
HLA A*3001	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.281838	0.051389	-4.230449	19135.408507
HLA B*4002	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.614602	0.384129	-4.230474	41172.036337
HLA A*0250	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.512068	0.281539	-4.230529	32513.855585
HLA A*3301	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.615018	0.384476	-4.230542	41211.479517
HLA A*2602	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.533888	0.303325	-4.230563	34189.137089
HLA A*2403	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.343946	0.113362	-4.230585	22077.321095
HLA A*6901	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.311897	0.081144	-4.230753	20506.760023
HLA A*0202	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.517024	0.286262	-4.230761	32886.945324
HLA B*2705	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.466105	0.235291	-4.230815	29248.627891
HLA B*1502	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.562535	0.331684	-4.230851	36520.390299
HLA A*0211	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.532807	0.301939	-4.230869	34104.161522
HLA B*3801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.528964	0.298081	-4.230883	33803.651763
HLA A*0216	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.465044	0.233980	-4.231064	29177.194475
HLA A*3201	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.604328	0.373125	-4.231203	40209.442295
HLA B*1501	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.197205	-0.034103	-4.231308	15747.245178
HLA A*0301	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.366934	0.135619	-4.231314	23277.360647
HLA A*2403	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.326849	0.095477	-4.231372	21225.071981
HLA A*2402	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.575634	0.344156	-4.231477	37638.628431
HLA A*0216	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.466820	0.235291	-4.231529	29296.769945
HLA B*1501	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.230868	-0.000735	-4.231603	17016.412718
HLA A*0101	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.368414	0.136752	-4.231662	23356.830599
HLA A*2602	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.600240	0.368545	-4.231695	39832.718359
HLA A*0202	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.571031	0.339229	-4.231802	37241.841551
HLA B*3801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.517411	0.285427	-4.231984	32916.314360
HLA A*8001	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.440644	0.208642	-4.232002	27583.166969
HLA B*0803	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.518304	0.286262	-4.232042	32984.051935
HLA A*1101	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.313199	0.081144	-4.232055	20568.312588
HLA B*4001	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.384710	0.152623	-4.232087	24249.899267
HLA A*6801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.344513	0.112320	-4.232193	22106.123909
HLA B*4402	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.428239	0.195916	-4.232323	26806.421836
HLA A*0301	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.359293	0.126963	-4.232330	22871.424266
HLA A*2601	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.385452	0.153079	-4.232374	24291.390530
HLA A*1101	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.423716	0.191274	-4.232443	26528.707353
HLA B*4002	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.644401	0.411911	-4.232490	44096.169542
HLA B*3901	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.373651	0.141148	-4.232502	23640.187293
HLA B*3901	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-3.972406	-0.260222	-4.232628	9384.386030
HLA B*2705	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.441318	0.208642	-4.232676	27626.026912
HLA A*6801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.460354	0.227657	-4.232697	28863.830002
HLA B*5101	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.487072	0.254355	-4.232717	30695.329626
HLA A*6901	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.378879	0.146138	-4.232740	23926.463806

HLA B*1509	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.468060	0.235291	-4.232770	29380.573500
HLA A*8001	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.457943	0.225172	-4.232771	28704.063784
HLA B*4002	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.564523	0.331684	-4.232839	36687.918664
HLA A*2403	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.386014	0.153079	-4.232935	24322.818725
HLA B*0802	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.461228	0.228245	-4.232983	28921.976337
HLA B*3901	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.487394	0.254355	-4.233039	30718.088050
HLA B*0702	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.386251	0.153079	-4.233172	24336.112316
HLA B*4403	1:328-336	9	KTAEFLVQG	0.978642	-0.574252	-4.637808	0.404390	-4.233419	43431.838202
HLA B*7301	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.535702	0.301939	-4.233763	34332.224367
HLA B*4801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.433896	0.200115	-4.233781	27157.913919
HLA A*6801	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.578120	0.344156	-4.233963	37854.676949
HLA B*7301	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.618143	0.384129	-4.234014	41509.071726
HLA B*1509	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.461439	0.227420	-4.234019	28936.061587
HLA A*0101	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.347461	0.113362	-4.234100	22256.722125
HLA A*2601	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.388622	0.154429	-4.234193	24469.316107
HLA A*0211	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.519667	0.285427	-4.234240	33087.709712
HLA A*0101	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.379945	0.145582	-4.234363	23985.301572
HLA A*2403	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.377654	0.143276	-4.234378	23859.120767
HLA B*4801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.425699	0.191274	-4.234426	26650.112964
HLA B*4601	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.355238	0.120764	-4.234474	22658.857023
HLA A*6801	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.532892	0.298081	-4.234811	34110.804160
HLA B*0803	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.524777	0.289937	-4.234840	33479.336062
HLA A*3201	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.603386	0.368545	-4.234841	40122.307864
HLA A*3001	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.278034	0.043160	-4.234873	18968.540749
HLA B*0702	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.435055	0.200115	-4.234940	27230.442798
HLA B*3501	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.372182	0.137191	-4.234992	23560.390528
HLA B*1517	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.382750	0.147675	-4.235076	24140.733872
HLA B*4501	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.609863	0.374749	-4.235114	40725.219726
HLA A*3201	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.624576	0.389429	-4.235147	42128.491758
HLA A*6901	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.376301	0.141148	-4.235153	23784.889170
HLA A*0250	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.580629	0.345470	-4.235159	38074.025309
HLA B*0702	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.442378	0.207166	-4.235212	27693.512845
HLA A*3001	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.291198	0.055954	-4.235244	19552.310541
HLA A*0101	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.362303	0.126963	-4.235340	23030.475272
HLA A*0206	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.421204	0.185815	-4.235389	26375.730062
HLA A*3002	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.469470	0.233980	-4.235490	29476.095833
HLA B*7301	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.586225	0.350403	-4.235822	38567.835626
HLA B*1503	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.349531	0.113627	-4.235905	22363.053355
HLA A*2501	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.490427	0.254455	-4.235972	30933.379243
HLA A*0219	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.446936	0.210953	-4.235983	27985.691938
HLA A*2602	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.575237	0.339229	-4.236008	37604.232240
HLA B*5301	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.580234	0.344171	-4.236063	38039.437019
HLA B*1503	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.517651	0.281539	-4.236112	32934.482881
HLA B*1801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.490639	0.254355	-4.236284	30948.444064
HLA B*0702	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.447718	0.211398	-4.236320	28036.153408
HLA B*5401	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.539649	0.303325	-4.236324	34645.678970
HLA A*8001	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.393607	0.157255	-4.236353	24751.837127
HLA B*1801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.427703	0.191274	-4.236430	26773.377712
HLA B*0702	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.357284	0.120764	-4.236521	22765.877806
HLA A*2603	1:108-116	9	AHTGTREYG	0.954176	-0.535098	-4.655697	0.419078	-4.236619	45258.190858
HLA A*0301	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.334419	0.097746	-4.236673	21598.282256
HLA A*2402	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.584101	0.347374	-4.236728	38379.678561
HLA A*2501	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.465074	0.228245	-4.236829	29179.246537
HLA B*0802	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.464416	0.227420	-4.236996	29135.080179
HLA A*1101	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.491590	0.254455	-4.237135	31016.326601
HLA B*4801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.430168	0.192958	-4.237210	26925.747866
HLA B*3901	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.459438	0.222188	-4.237250	28802.995654
HLA A*2301	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.535436	0.298081	-4.237356	34311.242892
HLA B*0801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.433281	0.195916	-4.237365	27119.447804
HLA B*5101	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.498653	0.261282	-4.237371	31524.841597
HLA B*5401	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.522862	0.285427	-4.237435	33332.048610
HLA A*0206	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.465694	0.228245	-4.237450	29220.950424
HLA B*4402	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.364479	0.126963	-4.237516	23146.137224
HLA A*2603	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.645005	0.407463	-4.237541	44157.520916
HLA A*6901	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.364561	0.126963	-4.237598	23150.520270

HLA A*2902	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.289022	0.051389	-4.237634	19454.607050
HLA A*6802	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.444836	0.207166	-4.237669	27850.667575
HLA A*0211	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.510323	0.272539	-4.237784	32383.426901
HLA A*0201	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.395064	0.157255	-4.237809	24834.997425
HLA B*1502	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.588241	0.350403	-4.237838	38747.271486
HLA A*2301	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.540485	0.302627	-4.237859	34712.468089
HLA A*2902	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.449318	0.211398	-4.237920	28139.632867
HLA B*5701	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.375178	0.137191	-4.237987	23723.462639
HLA A*6901	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.339987	0.101982	-4.238005	21876.986151
HLA A*0202	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.513455	0.275316	-4.238139	32617.800232
HLA B*3901	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.424360	0.185815	-4.238545	26568.060270
HLA B*4501	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.650564	0.411911	-4.238652	44726.361004
HLA A*8001	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.446036	0.207166	-4.238870	27927.765965
HLA A*0211	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.334358	0.095477	-4.238881	21595.244518
HLA B*4801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.434883	0.195916	-4.238967	27219.691023
HLA B*3801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.541630	0.302627	-4.239003	34804.042692
HLA A*0101	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.380192	0.141148	-4.239043	23998.930014
HLA B*5401	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.525324	0.286262	-4.239062	33521.563513
HLA B*3901	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.295054	0.055954	-4.239100	19726.661448
HLA B*4002	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.643080	0.403979	-4.239101	43962.305014
HLA A*0101	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.374866	0.135619	-4.239246	23706.399385
HLA B*1801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.525524	0.286262	-4.239262	33536.981633
HLA A*6802	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.295227	0.055954	-4.239274	19734.560239
HLA B*5301	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.586686	0.347374	-4.239312	38608.752267
HLA A*6901	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.339111	0.099536	-4.239575	21832.885340
HLA A*2403	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.379750	0.139834	-4.239916	23974.534091
HLA A*1101	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.467832	0.227657	-4.240175	29365.159817
HLA B*5301	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.579473	0.339229	-4.240244	37972.819739
HLA B*4002	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.647822	0.407463	-4.240358	44444.877737
HLA A*2603	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.624520	0.384129	-4.240391	42123.022262
HLA A*1101	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.426209	0.185815	-4.240394	26681.417127
HLA A*1101	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.513123	0.272539	-4.240585	32592.929045
HLA A*0206	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.474613	0.233980	-4.240633	29827.234080
HLA A*2301	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.530658	0.289937	-4.240721	33935.761405
HLA B*0801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.384014	0.143276	-4.240738	24211.098319
HLA B*1801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.468507	0.227657	-4.240850	29410.788699
HLA B*5801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.322200	0.081144	-4.241055	20999.044841
HLA B*5301	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.584325	0.343210	-4.241115	38399.408462
HLA B*3901	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.434254	0.192958	-4.241296	27180.255141
HLA A*2601	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.387478	0.146138	-4.241339	24404.933704
HLA A*2301	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.544726	0.303325	-4.241401	35053.090486
HLA A*2601	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.387059	0.145582	-4.241477	24381.444034
HLA A*2603	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.653390	0.411911	-4.241479	45018.393742
HLA A*0201	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.395952	0.154429	-4.241523	24885.835420
HLA A*2602	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.614694	0.373125	-4.241569	41180.723963
HLA B*1509	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.495944	0.254355	-4.241589	31328.814183
HLA B*1517	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.441765	0.200115	-4.241650	27654.437722
HLA A*2501	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.452617	0.210953	-4.241664	28354.180775
HLA B*5401	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.543721	0.301939	-4.241782	34972.021311
HLA B*0702	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.427604	0.185815	-4.241789	26767.295081
HLA B*5801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.354331	0.112320	-4.242011	22611.589777
HLA A*3002	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.467276	0.225172	-4.242103	29327.533588
HLA A*0211	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.477414	0.235291	-4.242123	30020.199127
HLA B*4601	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.385485	0.143276	-4.242209	24293.230392
HLA A*0212	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.378991	0.136752	-4.242239	23932.677710
HLA B*4403	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.610869	0.368545	-4.242324	40819.625478
HLA A*0211	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.435301	0.192958	-4.242343	27245.915129
HLA A*3101	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.390086	0.147675	-4.242411	24551.925668
HLA B*0803	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.470873	0.228245	-4.242628	29571.448790
HLA B*5701	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.399883	0.157255	-4.242628	25112.093115
HLA A*3301	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.611207	0.368545	-4.242662	40851.437337
HLA B*1501	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.397139	0.154429	-4.242710	24953.916330
HLA B*3501	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.467955	0.225172	-4.242782	29373.421817
HLA B*7301	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.524441	0.281539	-4.242902	33453.445990
HLA A*0201	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.390659	0.147675	-4.242984	24584.355928

HLA A*0203	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.390668	0.147675	-4.242993	24584.887928
HLA B*4402	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.454429	0.211398	-4.243030	28472.693747
HLA B*4402	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.395727	0.152623	-4.243103	24872.914333
HLA A*2301	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.477829	0.234640	-4.243189	30048.958747
HLA B*4002	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.632766	0.389429	-4.243337	42930.526623
HLA B*4403	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.582633	0.339229	-4.243404	38250.129071
HLA B*3501	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.452058	0.208642	-4.243416	28317.696739
HLA A*0212	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.439453	0.195916	-4.243537	27507.615138
HLA B*2705	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.436666	0.192958	-4.243708	27331.687734
HLA B*4402	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.384865	0.141148	-4.243717	24258.559304
HLA B*1509	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.455124	0.211398	-4.243726	28518.324370
HLA B*4501	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.521903	0.278063	-4.243840	33258.558089
HLA A*6802	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.381630	0.137730	-4.243900	24078.518604
HLA A*0250	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.586033	0.342132	-4.243901	38550.730307
HLA B*5101	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.471359	0.227420	-4.243939	29604.582839
HLA B*1509	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.534661	0.290570	-4.244091	34250.042931
HLA A*3201	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.588269	0.344156	-4.244113	38749.786989
HLA B*1502	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.617457	0.373125	-4.244332	41443.552123
HLA B*4501	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.648355	0.403979	-4.244376	44499.491567
HLA A*2301	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.546376	0.301939	-4.244437	35186.466190
HLA A*0216	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.440489	0.195916	-4.244573	27573.320083
HLA B*3901	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.499203	0.254455	-4.244748	31564.774608
HLA A*2602	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.542936	0.298081	-4.244855	34908.887317
HLA A*3002	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.340497	0.095477	-4.245020	21902.683631
HLA A*2603	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.649001	0.403979	-4.245022	44565.743599
HLA B*5401	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.544207	0.299099	-4.245108	35011.206563
HLA A*8001	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.431643	0.186500	-4.245144	27017.381251
HLA A*3001	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.264600	0.019419	-4.245181	18390.755331
HLA A*0202	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.543486	0.298081	-4.245405	34953.106952
HLA A*2902	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.398534	0.153079	-4.245456	25034.234075
HLA A*0203	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.432047	0.186500	-4.245548	27042.532650
HLA A*0250	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.589902	0.344156	-4.245746	38895.755504
HLA A*3201	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.543935	0.298081	-4.245854	34989.242273
HLA B*4001	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.400322	0.154429	-4.245893	25137.510600
HLA A*0250	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.548871	0.302627	-4.246244	35389.204914
HLA A*2602	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.635743	0.389429	-4.246314	43225.797386
HLA A*0201	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.399683	0.153079	-4.246604	25100.548210
HLA B*1801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.532077	0.285427	-4.246650	34046.830348
HLA B*0803	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.482042	0.235291	-4.246751	30341.849795
HLA A*0301	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.360423	0.113627	-4.246797	22931.016796
HLA B*0702	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.359157	0.112320	-4.246837	22864.248943
HLA B*3801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.522228	0.275316	-4.246912	33283.397025
HLA B*4403	1:6-14	9	DIDVPETPA	0.752912	-0.322310	-4.677566	0.430602	-4.246964	47595.533145
HLA A*3201	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.528576	0.281539	-4.247037	33773.491015
HLA B*4001	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.392630	0.145582	-4.247048	24696.195409
HLA A*0219	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.443083	0.195916	-4.247167	27738.494987
HLA A*2603	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.482496	0.235291	-4.247205	30373.546526
HLA A*0201	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.393560	0.146138	-4.247422	24749.159178
HLA A*3002	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.529062	0.281539	-4.247523	33811.333344
HLA B*0801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.401979	0.154429	-4.247550	25233.567420
HLA A*2402	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.581663	0.334057	-4.247605	38164.762813
HLA A*0101	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.368508	0.120764	-4.247744	23361.885461
HLA B*5301	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.589919	0.342132	-4.247787	38897.228484
HLA B*1502	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.592036	0.344171	-4.247864	39087.288468
HLA B*0802	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.473060	0.225172	-4.247888	29720.764256
HLA A*2601	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.391216	0.143276	-4.247939	24615.896821
HLA A*6901	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.383568	0.135619	-4.247949	24186.225026
HLA A*2403	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.389113	0.141148	-4.247964	24496.998398
HLA A*1101	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.475499	0.227420	-4.248079	29888.129643
HLA A*0212	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.401232	0.153079	-4.248153	25190.194304
HLA B*5701	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.389461	0.141148	-4.248312	24516.620107
HLA A*0212	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.385605	0.137191	-4.248414	24299.933925
HLA B*4501	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.655918	0.407463	-4.248455	45281.211840
HLA A*6802	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.435132	0.186500	-4.248632	27235.304584
HLA A*2601	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.369419	0.120764	-4.248656	23410.974424

HLA B*5101	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.441741	0.192958	-4.248783	27652.941688
HLA A*6802	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.401476	0.152623	-4.248853	25204.371012
HLA A*2603	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.608167	0.359286	-4.248881	40566.459718
HLA B*3501	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.449130	0.200115	-4.249015	28127.456919
HLA B*1503	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.305001	0.055954	-4.249048	20183.724552
HLA B*5401	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.521652	0.272539	-4.249113	33239.311673
HLA A*3101	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.268601	0.019419	-4.249182	18560.973025
HLA B*5301	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.594665	0.345470	-4.249195	39324.627516
HLA A*2301	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.539790	0.290570	-4.249220	34656.926552
HLA A*2403	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.362864	0.113627	-4.249238	23060.272095
HLA B*5801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.340970	0.091584	-4.249386	21926.513294
HLA A*6901	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.340981	0.091584	-4.249398	21927.106402
HLA A*0301	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.351411	0.101982	-4.249428	22460.048408
HLA B*0803	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.510715	0.261282	-4.249433	32412.696976
HLA A*0212	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.390762	0.141148	-4.249614	24590.208564
HLA B*4402	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.440938	0.191274	-4.249664	27601.826012
HLA A*6901	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.341021	0.091322	-4.249700	21929.123090
HLA A*3301	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.349832	0.099536	-4.250296	22378.544368
HLA A*2602	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.594542	0.344171	-4.250371	39313.566494
HLA B*4002	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.540356	0.289937	-4.250420	34702.141142
HLA A*3201	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.512005	0.261282	-4.250723	32509.106730
HLA A*8001	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.443729	0.192958	-4.250771	27779.792800
HLA A*0101	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.363123	0.112320	-4.250803	23073.999065
HLA B*4001	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.388049	0.137191	-4.250858	24437.037602
HLA A*2602	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.350621	0.099536	-4.251085	22419.259350
HLA A*0201	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.387863	0.136752	-4.251111	24426.595902
HLA B*5401	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.526443	0.275316	-4.251127	33607.996373
HLA B*2705	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.476399	0.225172	-4.251226	29950.121677
HLA A*3201	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.590501	0.339229	-4.251273	38949.450072
HLA A*2602	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.601746	0.350403	-4.251343	39971.087603
HLA A*2601	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.364730	0.113362	-4.251368	23159.539432
HLA B*0802	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.437989	0.186500	-4.251489	27415.060605
HLA B*4801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.437999	0.186500	-4.251499	27415.653861
HLA B*1509	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.537979	0.286262	-4.251716	34512.672714
HLA B*4601	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.389021	0.137191	-4.251830	24491.830428
HLA B*7301	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.486619	0.234640	-4.251979	30663.297094
HLA A*0211	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.541940	0.289937	-4.252003	34828.905322
HLA A*2402	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.594150	0.342132	-4.252018	39278.064634
HLA B*0801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.393182	0.141148	-4.252034	24727.612240
HLA A*2603	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.553983	0.301939	-4.252044	35808.265493
HLA B*0803	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.521934	0.269777	-4.252157	33260.897198
HLA A*0216	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.480442	0.228245	-4.252197	30230.272000
HLA A*3002	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.445162	0.192958	-4.252204	27871.618446
HLA A*2402	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.551326	0.299099	-4.252227	35589.838504
HLA A*2601	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.389026	0.136752	-4.252274	24492.095425
HLA A*2403	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.460920	0.208642	-4.252278	28901.486724
HLA A*2403	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.406774	0.154429	-4.252345	25513.729840
HLA A*0201	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.389705	0.137191	-4.252514	24530.417737
HLA B*4601	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.406983	0.154429	-4.252554	25526.017152
HLA B*3501	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.120564	-0.132020	-4.252584	13199.709963
HLA A*2603	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.637164	0.384476	-4.252688	43367.506462
HLA A*0201	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.394028	0.141148	-4.252880	24775.817677
HLA B*1503	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.389684	0.136752	-4.252932	24529.223404
HLA B*5101	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.464348	0.211398	-4.252950	29130.509629
HLA B*4601	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.400773	0.147675	-4.253099	25163.634465
HLA A*2301	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.538535	0.285427	-4.253109	34556.951300
HLA A*3301	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.642549	0.389429	-4.253120	43908.588009
HLA B*5801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.352696	0.099536	-4.253160	22526.610831
HLA B*1801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.478398	0.225172	-4.253226	30088.324402
HLA B*2705	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.439079	0.185815	-4.253264	27483.964021
HLA B*4002	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.531426	0.278063	-4.253363	33995.848044
HLA B*5801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.355428	0.101982	-4.253446	22668.788333
HLA A*2301	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.539832	0.286262	-4.253570	34660.301539
HLA B*0801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.410895	0.157255	-4.253640	25756.980504
HLA A*0101	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.391439	0.137730	-4.253709	24628.551153

HLA B*4001	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.397200	0.143276	-4.253923	24957.426522
HLA B*3501	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.476171	0.222188	-4.253983	29934.409196
HLA A*2601	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.395144	0.141148	-4.253996	24839.565901
HLA A*0201	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.367413	0.113362	-4.254051	23303.064128
HLA B*3801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.532150	0.278063	-4.254087	34052.540704
HLA A*3101	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.407187	0.153079	-4.254109	25538.034064
HLA A*0211	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.515421	0.261282	-4.254139	32765.831045
HLA B*5401	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.508619	0.254455	-4.254164	32256.662366
HLA B*1501	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.297326	0.043160	-4.254165	19830.129174
HLA A*3201	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.462898	0.208642	-4.254256	29033.436954
HLA A*2403	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.391481	0.137191	-4.254290	24630.949549
HLA B*5301	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.598525	0.344156	-4.254368	39675.720441
HLA A*1101	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.454708	0.200115	-4.254593	28491.029708
HLA B*1801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.440433	0.185815	-4.254618	27569.740269
HLA B*7301	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.516105	0.261282	-4.254823	32817.454187
HLA B*1801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.482246	0.227420	-4.254826	30356.133862
HLA B*0803	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.441365	0.186500	-4.254866	27629.016148
HLA A*0203	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.412124	0.157255	-4.254869	25829.959779
HLA B*4501	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.644366	0.389429	-4.254936	44092.591356
HLA B*5401	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.489137	0.233980	-4.255158	30841.642503
HLA A*0206	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.545159	0.289937	-4.255222	35088.000392
HLA B*1801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.545170	0.289937	-4.255234	35088.949516
HLA B*0702	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.441922	0.186500	-4.255423	27664.463237
HLA B*7301	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.598692	0.343210	-4.255482	39690.962897
HLA A*3001	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.263514	0.007934	-4.255580	18344.847446
HLA B*4801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.401208	0.145582	-4.255626	25188.831580
HLA A*3101	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.396814	0.141148	-4.255666	24935.293569
HLA B*1501	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.393495	0.137730	-4.255765	24745.410536
HLA B*4402	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.391397	0.135619	-4.255777	24626.152991
HLA A*3001	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.304430	0.048624	-4.255806	20157.208399
HLA A*6801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.395642	0.139834	-4.255808	24868.070655
HLA B*3801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.559164	0.303325	-4.255839	36237.973184
HLA B*1501	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.347447	0.091584	-4.255863	22255.999699
HLA A*2501	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.441739	0.185815	-4.255924	27652.792089
HLA B*4001	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.357923	0.101982	-4.255941	22799.402223
HLA B*5401	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.554058	0.298081	-4.255978	35814.465030
HLA B*5301	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.590100	0.334057	-4.256042	38913.434946
HLA B*7301	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.598175	0.342132	-4.256043	39643.751782
HLA B*5401	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.546000	0.289937	-4.256063	35156.022586
HLA A*0216	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.392877	0.136752	-4.256125	24710.227780
HLA A*0250	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.595355	0.339229	-4.256127	39387.223394
HLA B*4601	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.395962	0.139834	-4.256127	24886.373944
HLA B*0702	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.399460	0.143276	-4.256184	25087.651362
HLA B*5801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.351718	0.095477	-4.256241	22475.971385
HLA B*2705	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.358255	0.101982	-4.256273	22816.800113
HLA A*0201	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.383491	0.126963	-4.256528	24181.907533
HLA B*7301	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.547102	0.290570	-4.256532	35245.335038
HLA B*4001	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.356100	0.099536	-4.256564	22703.889271
HLA A*0101	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.348159	0.091584	-4.256575	22292.511570
HLA B*1517	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.478812	0.222188	-4.256623	30116.986356
HLA A*0201	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.392393	0.135619	-4.256773	24682.705123
HLA B*4501	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.588504	0.331684	-4.256820	38770.755865
HLA B*5701	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.411301	0.154429	-4.256872	25781.098025
HLA A*0216	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.467856	0.210953	-4.256902	29366.748483
HLA B*5701	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.370324	0.113362	-4.256962	23459.785788
HLA B*4002	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.631739	0.374749	-4.256990	42829.153516
HLA A*6801	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.560315	0.303325	-4.256990	36334.161893
HLA A*3101	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.403137	0.146138	-4.256999	25300.957073
HLA B*2705	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.468467	0.211398	-4.257068	29408.083969
HLA B*4403	1:329-337	9	TAEFLVQGT	0.696455	-0.312326	-4.641241	0.384129	-4.257112	43776.477043
HLA A*6802	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.378005	0.120764	-4.257241	23878.360725
HLA B*1509	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.547283	0.289937	-4.257346	35260.019945
HLA B*0803	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.482587	0.225172	-4.257415	30379.955586
HLA A*2601	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.394796	0.137191	-4.257605	24819.685725
HLA B*1502	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.600837	0.343210	-4.257627	39887.490592

HLA B*4001	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.398804	0.141148	-4.257656	25049.813650
HLA B*4601	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.414962	0.157255	-4.257707	25999.315117
HLA B*5801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.355480	0.097746	-4.257734	22671.486477
HLA B*4601	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.403320	0.145582	-4.257738	25311.635605
HLA B*1509	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.561123	0.303325	-4.257798	36401.842794
HLA A*0202	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.449140	0.191274	-4.257866	28128.065591
HLA A*0301	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.349463	0.091584	-4.257879	22359.545163
HLA A*2601	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.397740	0.139834	-4.257906	24988.499740
HLA B*1501	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.355743	0.097746	-4.257997	22685.227466
HLA B*5101	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.492765	0.234640	-4.258125	31100.337617
HLA A*3001	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.283839	0.025675	-4.258165	19223.811499
HLA B*1501	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.393878	0.135619	-4.258258	24767.240958
HLA B*1517	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.444218	0.185815	-4.258403	27811.069798
HLA A*2603	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.633260	0.374749	-4.258510	42979.326710
HLA B*0702	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.406262	0.147675	-4.258587	25483.657810
HLA A*2301	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.540286	0.281539	-4.258747	34696.509557
HLA A*0203	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.400007	0.141148	-4.258859	25119.294390
HLA A*0202	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.528672	0.269777	-4.258895	33780.982990
HLA B*5701	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.406579	0.147675	-4.258904	25502.276216
HLA B*4601	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.400090	0.141148	-4.258941	25124.051081
HLA A*3002	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.537163	0.278063	-4.259100	34447.945210
HLA A*3002	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.534485	0.275316	-4.259169	34236.149079
HLA A*0201	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.397294	0.137730	-4.259564	24962.827783
HLA B*0802	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.459778	0.200115	-4.259663	28825.598565
HLA A*3002	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.530662	0.270903	-4.259759	33936.128584
HLA B*1502	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.514221	0.254355	-4.259866	32675.376520
HLA A*0301	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.359432	0.099536	-4.259896	22878.725611
HLA A*3301	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.604091	0.344171	-4.259920	40187.477905
HLA B*3501	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.407711	0.147675	-4.260037	25568.861875
HLA A*2501	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.494041	0.233980	-4.260061	31191.831348
HLA B*3801	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.562023	0.301939	-4.260084	36477.345152
HLA A*2301	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.529969	0.269777	-4.260192	33882.012524
HLA A*0212	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.414671	0.154429	-4.260242	25981.879943
HLA B*4501	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.637160	0.376904	-4.260256	43367.037237
HLA A*2403	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.359963	0.099536	-4.260427	22906.715048
HLA B*5101	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.485604	0.225172	-4.260432	30591.718432
HLA B*4402	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.415140	0.154429	-4.260712	26010.006974
HLA A*2402	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.551300	0.290570	-4.260730	35587.720659
HLA A*2601	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.396417	0.135619	-4.260798	24912.506365
HLA A*2301	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.533350	0.272539	-4.260811	34146.807602
HLA B*4403	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.645296	0.384476	-4.260820	44187.152878
HLA B*4801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.404199	0.143276	-4.260923	25362.900444
HLA A*0219	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.397717	0.136752	-4.260965	24987.147926
HLA B*4402	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.404288	0.143276	-4.261012	25368.114979
HLA B*5101	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.447030	0.185815	-4.261215	27991.748573
HLA A*0219	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.418517	0.157255	-4.261262	26212.997048
HLA A*2403	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.363456	0.101982	-4.261474	23091.731420
HLA B*5301	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.593419	0.331684	-4.261735	39212.035813
HLA A*0216	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.468958	0.207166	-4.261792	29441.353518
HLA A*3002	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.516469	0.254455	-4.262014	32844.984240
HLA A*0202	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.470694	0.208642	-4.262052	29559.292942
HLA B*5401	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.349099	0.086816	-4.262282	22340.803809
HLA B*4501	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.606560	0.344171	-4.262389	40416.626433
HLA A*0201	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.358151	0.095477	-4.262674	22811.369560
HLA B*4501	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.341101	0.078424	-4.262678	21933.157021
HLA B*5801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.354042	0.091322	-4.262721	22596.548660
HLA B*4601	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.399669	0.136752	-4.262917	25099.733476
HLA A*6802	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.399711	0.136752	-4.262959	25102.177757
HLA B*0802	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.473976	0.210953	-4.263023	29783.537009
HLA A*0101	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.409199	0.146138	-4.263060	25656.571508
HLA B*0801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.376849	0.113627	-4.263222	23814.889025
HLA B*4403	1:366-374	9	DLKFTLVEP	0.557720	-0.145809	-4.675142	0.411911	-4.263230	47330.547414
HLA A*2902	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.344437	0.081144	-4.263293	22102.297307
HLA A*3001	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.302854	0.039331	-4.263523	20084.169661
HLA A*3301	1:217-225	9	EQVRTQIGD	1.151480	-0.807324	-4.607801	0.344156	-4.263644	40532.238392

HLA B*0702	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.420908	0.157255	-4.263654	26357.757276
HLA A*0203	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.416289	0.152623	-4.263666	26078.905871
HLA A*2902	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.416501	0.152623	-4.263878	26091.606522
HLA B*5401	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.533674	0.269777	-4.263897	34172.309922
HLA B*5301	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.565858	0.301939	-4.263919	36800.827311
HLA B*5401	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.545473	0.281539	-4.263934	35113.445788
HLA A*2603	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.608228	0.344171	-4.264057	40572.166080
HLA B*4001	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.421324	0.157255	-4.264070	26383.008244
HLA B*4801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.411788	0.147675	-4.264113	25809.985084
HLA A*2902	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.377476	0.113362	-4.264114	23849.313069
HLA A*2902	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.471291	0.207166	-4.264125	29599.938636
HLA A*2301	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.539520	0.275316	-4.264204	34635.371893
HLA B*0801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.330510	0.066046	-4.264463	21404.725830
HLA A*2301	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.542614	0.278063	-4.264551	34883.024013
HLA A*0216	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.421940	0.157255	-4.264685	26420.429796
HLA B*4403	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.641791	0.376904	-4.264887	43831.929393
HLA A*2603	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.608315	0.343210	-4.265105	40580.288057
HLA B*4601	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.346254	0.081144	-4.265109	22194.919203
HLA A*6801	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.615544	0.350403	-4.265141	41261.450485
HLA A*0216	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.487333	0.222188	-4.265145	30713.767636
HLA B*5301	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.601842	0.336669	-4.265173	39979.954392
HLA B*0802	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.458237	0.192958	-4.265279	28723.481074
HLA A*8001	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.367512	0.101982	-4.265529	23308.359543
HLA A*2902	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.305156	0.039331	-4.265826	20190.932492
HLA A*0206	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.363602	0.097746	-4.265856	23099.477989
HLA A*3101	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.392830	0.126963	-4.265867	24707.554333
HLA A*2601	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.392999	0.126963	-4.266036	24717.180097
HLA A*6802	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.393088	0.126963	-4.266125	24722.261873
HLA A*0219	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.473311	0.207166	-4.266145	29737.973343
HLA A*2501	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.462071	0.195916	-4.266155	28978.201740
HLA A*0202	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.393119	0.126963	-4.266156	24724.000615
HLA B*1502	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.544235	0.278063	-4.266172	35013.479517
HLA B*4402	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.403910	0.137730	-4.266180	25346.029169
HLA A*0216	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.401805	0.135619	-4.266185	25223.467643
HLA B*7301	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.611684	0.345470	-4.266215	40896.325335
HLA B*1517	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.452744	0.186500	-4.266244	28362.465205
HLA A*0201	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.364016	0.097746	-4.266269	23121.482411
HLA A*0101	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.379948	0.113627	-4.266321	23985.431331
HLA A*0301	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.361882	0.095477	-4.266405	23008.184041
HLA B*1801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.501127	0.234640	-4.266487	31704.938913
HLA A*3001	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.298618	0.032127	-4.266491	19889.220382
HLA B*4601	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.402113	0.135619	-4.266493	25241.349736
HLA A*1101	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.473668	0.207166	-4.266502	29762.437029
HLA A*1101	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.477996	0.211398	-4.266598	30060.502833
HLA A*0202	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.521062	0.254455	-4.266607	33194.207234
HLA A*0212	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.379985	0.113362	-4.266624	23987.507557
HLA A*6802	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.419720	0.153079	-4.266641	26285.704113
HLA B*5401	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.537574	0.270903	-4.266672	34480.573576
HLA A*2403	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.414403	0.147675	-4.266728	25965.861147
HLA B*2705	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.477717	0.210953	-4.266763	30041.156806
HLA B*4403	1:450-458	9	LLADVRSVG	0.971141	-0.567162	-4.670797	0.403979	-4.266818	46859.465408
HLA A*6901	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.347327	0.080331	-4.266996	22249.860019
HLA A*0212	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.406849	0.139834	-4.267015	25518.147069
HLA A*0219	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.380406	0.113362	-4.267044	24010.747594
HLA A*3002	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.569734	0.302627	-4.267107	37130.793665
HLA B*4001	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.404901	0.137730	-4.267171	25403.959577
HLA B*5701	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.380894	0.113627	-4.267268	24037.781061
HLA B*4801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.424607	0.157255	-4.267352	26583.156235
HLA B*0702	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.460366	0.192958	-4.267408	28864.610764
HLA A*2601	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.369415	0.101982	-4.267433	23410.721124
HLA A*2602	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.553711	0.286262	-4.267448	35785.801168
HLA A*0101	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.365197	0.097746	-4.267451	23184.485676
HLA B*4403	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.674956	0.407463	-4.267493	47310.323548
HLA B*4601	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.381120	0.113627	-4.267493	24050.268310
HLA A*6802	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.413080	0.145582	-4.267498	25886.895485

HLA B*1517	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.476161	0.208642	-4.267519	29933.761436
HLA B*1502	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.540258	0.272539	-4.267719	34694.257179
HLA B*3801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.554028	0.286262	-4.267766	35811.946339
HLA A*0212	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.415453	0.147675	-4.267778	26028.728306
HLA A*0202	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.193868	-0.073933	-4.267801	15626.737635
HLA A*0212	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.403569	0.135619	-4.267950	25326.154680
HLA B*1503	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.475186	0.207166	-4.268020	29866.632413
HLA B*4002	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.346474	0.078424	-4.268051	22206.208846
HLA A*3101	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.405282	0.137191	-4.268091	25426.233418
HLA A*6901	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.287617	0.019419	-4.268199	19391.770880
HLA B*0801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.405954	0.137730	-4.268224	25465.604055
HLA B*4601	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.414367	0.146138	-4.268229	25963.754146
HLA B*3501	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.454739	0.186500	-4.268239	28493.033512
HLA A*2501	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.459614	0.191274	-4.268340	28814.684601
HLA B*7301	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.502328	0.233980	-4.268348	31792.706997
HLA B*3901	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.493651	0.225172	-4.268479	31163.832360
HLA A*0219	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.455129	0.186500	-4.268629	28518.632934
HLA B*4801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.389590	0.120764	-4.268826	24523.915963
HLA B*4002	1:190-198	9	QVLSRFLHD	1.113387	-0.736483	-4.645731	0.376904	-4.268827	44231.398822
HLA A*0101	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.364408	0.095477	-4.268931	23142.380988
HLA A*0206	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.494107	0.225172	-4.268934	31196.556548
HLA B*3501	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.351791	0.082695	-4.269096	22479.741069
HLA A*2602	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.611611	0.342132	-4.269480	40889.467328
HLA A*2402	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.555814	0.286262	-4.269551	35959.490828
HLA B*5301	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.572267	0.302627	-4.269640	37347.967924
HLA B*3501	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.396603	0.126963	-4.269640	24923.155778
HLA A*2403	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.422335	0.152623	-4.269711	26444.453219
HLA A*0211	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.539567	0.269777	-4.269790	34639.119566
HLA A*0206	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.524145	0.254355	-4.269790	33430.650351
HLA A*0201	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.383603	0.113627	-4.269977	24188.187778
HLA B*3901	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.424440	0.154429	-4.270011	26572.947549
HLA B*0803	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.524547	0.254455	-4.270092	33461.591056
HLA B*4001	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.382447	0.112320	-4.270128	24123.892518
HLA B*0702	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.351279	0.081144	-4.270135	22453.245082
HLA B*5801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.352454	0.082233	-4.270221	22514.062082
HLA B*5801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.357042	0.086816	-4.270226	22753.195769
HLA A*0250	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.573594	0.303325	-4.270269	37462.299894
HLA B*1503	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.524887	0.254455	-4.270432	33487.849761
HLA B*2705	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.383796	0.113362	-4.270434	24198.920302
HLA B*0802	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.479110	0.208642	-4.270468	30137.685520
HLA B*5701	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.423547	0.153079	-4.270468	26518.376114
HLA A*3201	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.561076	0.290570	-4.270507	36397.904408
HLA A*6801	1:229-237	9	ICGLSGGVD	1.181577	-0.774114	-4.678055	0.407463	-4.270592	47649.120493
HLA A*0202	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.498989	0.228245	-4.270744	31549.239096
HLA A*6801	1:507-515	9	VNRVVLDIT	0.782056	-0.397580	-4.655232	0.384476	-4.270756	45209.738138
HLA B*1517	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.423864	0.153079	-4.270785	26537.750488
HLA B*5801	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.351159	0.080331	-4.270828	22447.050989
HLA B*0803	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.504924	0.233980	-4.270944	31983.330695
HLA A*0202	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.532267	0.261282	-4.270985	34061.752973
HLA A*0101	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.351455	0.080331	-4.271124	22462.357148
HLA B*1502	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.370676	0.099536	-4.271140	23478.830740
HLA A*2902	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.414466	0.143276	-4.271190	25969.654179
HLA A*0206	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.543758	0.272539	-4.271220	34975.048558
HLA B*3501	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.428575	0.157255	-4.271320	26827.167687
HLA B*1801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.525822	0.254455	-4.271367	33560.031332
HLA B*0802	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.462642	0.191274	-4.271369	29016.321624
HLA B*5101	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.462673	0.191274	-4.271399	29018.362372
HLA B*5801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.354256	0.082695	-4.271561	22607.675678
HLA B*4403	1:351-359	9	TANIKSHHN	0.984366	-0.609617	-4.646551	0.374749	-4.271801	44314.988859
HLA B*4001	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.392590	0.120764	-4.271827	24693.924251
HLA B*1509	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.497356	0.225172	-4.272184	31430.840687
HLA A*1101	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.483182	0.210953	-4.272228	30421.565159
HLA B*1517	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.483804	0.211398	-4.272406	30465.209420
HLA A*1101	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.458951	0.186500	-4.272452	28770.758758
HLA A*2602	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.429771	0.157255	-4.272516	26901.141679

HLA A*2403	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.408456	0.135619	-4.272837	25612.748428
HLA A*0212	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.425607	0.152623	-4.272984	26644.490765
HLA B*0702	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.427417	0.154429	-4.272988	26755.712940
HLA B*4801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.419137	0.146138	-4.272999	26250.461479
HLA B*5701	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.408623	0.135619	-4.273004	25622.588229
HLA B*4601	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.410740	0.137730	-4.273010	25747.785547
HLA B*5801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.351632	0.078424	-4.273208	22471.472912
HLA B*5401	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.141212	-0.132020	-4.273231	13842.408542
HLA A*6801	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.615582	0.342132	-4.273450	41265.022157
HLA B*0803	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.508150	0.234640	-4.273509	32221.780247
HLA B*4402	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.419668	0.146138	-4.273530	26282.575839
HLA B*4002	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.646755	0.373125	-4.273630	44335.851076
HLA B*1509	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.460201	0.186500	-4.273702	28853.682029
HLA A*3201	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.546526	0.272539	-4.273987	35198.651011
HLA A*6802	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.355184	0.081144	-4.274040	22656.037815
HLA B*1502	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.306251	0.032127	-4.274124	20241.898216
HLA A*6801	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.647298	0.373125	-4.274173	44391.291532
HLA A*2603	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.642867	0.368545	-4.274322	43940.667702
HLA B*1801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.293783	0.019419	-4.274364	19669.010847
HLA A*0203	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.428814	0.154429	-4.274386	26841.975237
HLA A*2301	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.545300	0.270903	-4.274397	35099.391572
HLA A*2501	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.420103	0.145582	-4.274520	26308.893383
HLA B*1509	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.460345	0.185815	-4.274530	28863.205409
HLA B*0802	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.485982	0.211398	-4.274584	30618.375186
HLA A*1101	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.401579	0.126963	-4.274616	25210.371252
HLA B*1501	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.376625	0.101982	-4.274643	23802.652758
HLA B*1501	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.387196	0.112320	-4.274876	24389.095487
HLA A*0212	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.421075	0.146138	-4.274937	26367.883292
HLA B*4601	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.402028	0.126963	-4.275065	25236.434310
HLA B*3501	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.388695	0.113627	-4.275068	24473.420116
HLA B*4001	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.357790	0.082695	-4.275095	22792.372799
HLA A*2501	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.497361	0.222188	-4.275173	31431.180763
HLA B*5301	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.574391	0.299099	-4.275292	37531.067008
HLA A*0206	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.428432	0.153079	-4.275353	26818.316096
HLA A*6901	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.370848	0.095477	-4.275370	23488.104876
HLA A*0211	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.486781	0.211398	-4.275383	30674.745298
HLA B*3501	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.482557	0.207166	-4.275390	30377.819082
HLA A*0203	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.356554	0.081144	-4.275410	22727.606977
HLA B*4002	1:159-167	9	AGAPVAAFE	1.069234	-0.700689	-4.643964	0.368545	-4.275419	44051.820556
HLA A*2301	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.536757	0.261282	-4.275475	34415.720087
HLA A*2603	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.548107	0.272539	-4.275568	35327.037787
HLA B*4501	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.648806	0.373125	-4.275681	44545.737145
HLA A*0216	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.462210	0.186500	-4.275710	28987.452579
HLA B*1501	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.402780	0.126963	-4.275817	25280.160568
HLA A*2603	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.357047	0.081144	-4.275903	22753.441955
HLA B*4601	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.332067	0.055954	-4.276114	21481.637218
HLA B*0803	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.469078	0.192958	-4.276120	29449.477637
HLA B*5401	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.537419	0.261282	-4.276137	34468.264392
HLA A*6802	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.423888	0.147675	-4.276213	26539.186189
HLA A*6802	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.430692	0.154429	-4.276263	26958.250832
HLA A*3101	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.388678	0.112320	-4.276359	24472.493345
HLA B*1501	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.422544	0.146138	-4.276405	26457.188764
HLA A*1101	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.390001	0.113362	-4.276639	24547.144499
HLA A*2902	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.388970	0.112320	-4.276650	24488.915643
HLA A*6901	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.332685	0.055954	-4.276732	21512.223063
HLA A*0301	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.368174	0.091322	-4.276853	23343.945652
HLA A*8001	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.389230	0.112320	-4.276911	24503.625597
HLA B*3801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.566870	0.289937	-4.276934	36886.734524
HLA A*3201	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.627487	0.350403	-4.277084	42411.821328
HLA B*1517	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.413963	0.136752	-4.277211	25939.606085
HLA A*0211	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.486060	0.208642	-4.277417	30623.841861
HLA A*6801	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.666864	0.389429	-4.277435	46437.014630
HLA B*0801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.423582	0.146138	-4.277444	26520.528124
HLA B*5701	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.414283	0.136752	-4.277531	25958.698041
HLA B*4601	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.379602	0.101982	-4.277620	23966.364410

HLA A*2601	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.368999	0.091322	-4.277677	23388.314908
HLA B*4801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.430328	0.152623	-4.277704	26935.654929
HLA A*0201	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.390036	0.112320	-4.277717	24549.136540
HLA B*1502	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.580453	0.302627	-4.277826	38058.580224
HLA A*0301	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.360581	0.082695	-4.277886	22939.329938
HLA A*0203	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.390222	0.112320	-4.277902	24559.630622
HLA A*2501	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.390337	0.112320	-4.278017	24566.141864
HLA B*1502	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.623502	0.345470	-4.278033	42024.465319
HLA A*0206	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.486774	0.208642	-4.278132	30674.247461
HLA B*1801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.512130	0.233980	-4.278150	32518.429211
HLA A*0301	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.364984	0.086816	-4.278167	23173.074765
HLA B*5701	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.415982	0.137730	-4.278252	26060.430416
HLA A*2902	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.464766	0.186500	-4.278267	29158.574663
HLA A*0203	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.405247	0.126963	-4.278284	25424.170205
HLA B*4601	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.391749	0.113362	-4.278387	24646.144815
HLA A*3301	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.620530	0.342132	-4.278398	41737.852318
HLA B*4403	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.667896	0.389429	-4.278466	46547.430879
HLA B*4002	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.513170	0.234640	-4.278530	32596.455719
HLA A*6901	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.361227	0.082695	-4.278532	22973.482625
HLA A*2902	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.380725	0.101982	-4.278743	24028.419880
HLA B*0702	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.415735	0.136752	-4.278983	26045.631296
HLA A*2501	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.465492	0.186500	-4.278993	29207.358525
HLA B*0803	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.506498	0.227420	-4.279078	32099.468649
HLA B*1502	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.475003	0.195916	-4.279087	29854.032208
HLA A*0203	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.415951	0.136752	-4.279199	26058.597688
HLA B*4501	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.624705	0.345470	-4.279235	42141.028699
HLA A*2501	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.479483	0.200115	-4.279368	30163.620277
HLA A*2403	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.416193	0.136752	-4.279441	26073.122069
HLA B*2705	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.420608	0.141148	-4.279459	26339.511748
HLA B*5401	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.416682	0.137191	-4.279491	26102.477544
HLA A*2902	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.425915	0.146138	-4.279777	26663.380288
HLA A*3301	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.630201	0.350403	-4.279797	42677.657948
HLA A*2602	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.419684	0.139834	-4.279850	26283.571158
HLA B*4002	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.624108	0.344171	-4.279937	42083.161979
HLA B*0802	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.487112	0.207166	-4.279946	30698.152748
HLA B*5801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.351484	0.071401	-4.280082	22463.815422
HLA A*3002	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.361234	0.081144	-4.280090	22973.855480
HLA B*1509	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.502678	0.222188	-4.280490	31818.344587
HLA B*3801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.515144	0.234640	-4.280504	32744.921097
HLA A*0101	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.380147	0.099536	-4.280611	23996.463342
HLA B*5701	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.423982	0.143276	-4.280705	26544.929773
HLA B*4002	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.071531	-0.209501	-4.281032	11790.456941
HLA A*3101	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.416679	0.135619	-4.281060	26102.336333
HLA B*4801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.422281	0.141148	-4.281132	26441.163008
HLA B*4601	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.332641	0.051389	-4.281252	21510.011981
HLA A*3301	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.626768	0.345470	-4.281298	42341.669774
HLA A*3101	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.379172	0.097746	-4.281426	23942.649218
HLA A*3002	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.566985	0.285427	-4.281559	36896.513924
HLA B*4402	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.418841	0.137191	-4.281650	26232.574053
HLA B*0801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.417309	0.135619	-4.281690	26140.208260
HLA A*1101	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.474754	0.192958	-4.281796	29836.917373
HLA B*1502	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.585135	0.303325	-4.281810	38471.144493
HLA B*3801	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.536560	0.254355	-4.282204	34400.084081
HLA A*0216	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.419534	0.137191	-4.282343	26274.472496
HLA B*1509	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.543725	0.261282	-4.282443	34972.399702
HLA B*4402	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.422290	0.139834	-4.282456	26441.735189
HLA B*2705	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.489941	0.207166	-4.282775	30898.757978
HLA A*3101	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.334335	0.051389	-4.282946	21594.076270
HLA A*0206	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.107778	-0.175217	-4.282995	12816.767058
HLA B*3901	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.491656	0.208642	-4.283014	31021.025214
HLA B*3801	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.564554	0.281539	-4.283015	36690.498963
HLA B*5701	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.429508	0.146138	-4.283369	26884.847010
HLA A*0301	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.365613	0.082233	-4.283381	23206.696621
HLA B*4801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.396772	0.113362	-4.283411	24932.865538
HLA A*3002	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.585354	0.301939	-4.283415	38490.504953

HLA B*5701	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.410402	0.126963	-4.283439	25727.735214
HLA A*2403	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.429599	0.146138	-4.283461	26890.519926
HLA A*8001	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.423516	0.139834	-4.283682	26516.511181
HLA A*2402	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.511448	0.227657	-4.283791	32467.452092
HLA B*2705	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.404690	0.120764	-4.283926	25391.593653
HLA B*0702	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.419633	0.135619	-4.284013	26280.443138
HLA A*1101	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.492690	0.208642	-4.284048	31094.954103
HLA A*1101	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.438501	0.154429	-4.284072	27447.411790
HLA A*1101	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.431803	0.147675	-4.284128	27027.322030
HLA B*4501	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.634549	0.350403	-4.284146	43107.166312
HLA B*7301	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.582238	0.298081	-4.284158	38215.380799
HLA B*4001	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.419915	0.135619	-4.284295	26297.509591
HLA B*3901	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.419917	0.135619	-4.284298	26297.651858
HLA A*1101	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.405066	0.120764	-4.284302	25413.581681
HLA B*4001	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.376045	0.091584	-4.284461	23770.867880
HLA A*2301	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.506712	0.222188	-4.284524	32115.275105
HLA B*5701	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.365672	0.081144	-4.284528	23209.835475
HLA B*4001	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.421289	0.136752	-4.284537	26380.867394
HLA A*2402	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.574475	0.289937	-4.284539	37538.377121
HLA B*0801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.367272	0.082695	-4.284577	23295.501336
HLA A*2603	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.657882	0.373125	-4.284757	45486.467499
HLA A*0203	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.420481	0.135619	-4.284862	26331.818205
HLA B*3901	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.398344	0.113362	-4.284982	25023.266451
HLA A*0211	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.513260	0.228245	-4.285015	32603.157449
HLA B*1509	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.539525	0.254455	-4.285070	34635.746642
HLA A*6801	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.629251	0.344171	-4.285080	42584.483721
HLA A*2301	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.512802	0.227657	-4.285144	32568.781589
HLA B*1501	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.384686	0.099536	-4.285150	24248.587410
HLA A*8001	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.438351	0.153079	-4.285272	27437.910238
HLA A*0212	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.164199	-0.121106	-4.285305	14594.829439
HLA B*4002	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.644591	0.359286	-4.285305	44115.496762
HLA A*0211	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.481250	0.195916	-4.285334	30286.582973
HLA B*4801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.380812	0.095477	-4.285335	24033.230032
HLA B*4801	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.365773	0.080331	-4.285442	23215.235296
HLA A*2601	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.380984	0.095477	-4.285506	24042.723155
HLA A*0301	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.365846	0.080331	-4.285515	23219.128970
HLA B*0802	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.481455	0.195916	-4.285538	30300.841022
HLA B*1502	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.624959	0.339229	-4.285730	42165.657549
HLA B*0702	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.427008	0.141148	-4.285859	26730.539083
HLA B*4402	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.443231	0.157255	-4.285976	27747.950516
HLA A*2501	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.406823	0.120764	-4.286060	25516.628560
HLA A*2603	1:124-132	9	GGKLHSDLP	0.519330	-0.129901	-4.675494	0.389429	-4.286065	47368.970954
HLA B*1503	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.477414	0.191274	-4.286140	30020.199127
HLA B*3901	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.438769	0.152623	-4.286146	27464.344581
HLA A*2301	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.540594	0.254355	-4.286239	34721.107532
HLA B*4001	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.399627	0.113362	-4.286265	25097.289433
HLA A*0212	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.413331	0.126963	-4.286369	25901.884663
HLA B*1502	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.479418	0.192958	-4.286460	30159.051532
HLA A*0219	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.439105	0.152623	-4.286482	27485.599607
HLA A*6901	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.352541	0.066046	-4.286494	22518.569080
HLA A*3101	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.373317	0.086816	-4.286501	23622.033775
HLA A*6802	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.429968	0.143276	-4.286692	26913.369161
HLA A*0101	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.378183	0.091322	-4.286861	23888.180369
HLA A*3002	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.439624	0.152623	-4.287001	27518.480643
HLA A*0203	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.433253	0.146138	-4.287114	27117.687303
HLA B*0803	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.494283	0.207166	-4.287117	31209.216860
HLA A*6801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.368313	0.081144	-4.287169	23351.397843
HLA A*2402	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.589829	0.302627	-4.287202	38889.232978
HLA A*2403	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.444523	0.157255	-4.287268	27830.635803
HLA B*5801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.330573	0.043160	-4.287413	21407.852582
HLA A*0206	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.514836	0.227420	-4.287416	32721.723141
HLA A*0101	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.370230	0.082695	-4.287535	23454.709743
HLA B*4002	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.633090	0.345470	-4.287621	42962.589006
HLA B*4002	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.626876	0.339229	-4.287647	42352.208017
HLA A*2402	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.589665	0.301939	-4.287726	38874.508715

HLA B*3801	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.560383	0.272539	-4.287845	36339.862690
HLA A*0212	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.401485	0.113627	-4.287859	25204.916430
HLA A*0202	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.560552	0.272539	-4.288014	36354.020261
HLA A*0206	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.484025	0.195916	-4.288109	30480.705820
HLA B*5101	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.474636	0.186500	-4.288137	29828.847744
HLA B*2705	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.383648	0.095477	-4.288170	24190.674159
HLA B*4801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.366661	0.078424	-4.288238	23262.757589
HLA A*3101	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.401654	0.113362	-4.288293	25214.735960
HLA A*0219	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.441417	0.153079	-4.288338	27632.304682
HLA A*8001	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.409229	0.120764	-4.288466	25658.375962
HLA B*5101	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.409267	0.120764	-4.288503	25660.597001
HLA B*4402	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.401913	0.113362	-4.288551	25229.745407
HLA A*8001	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.424287	0.135619	-4.288668	26563.605006
HLA A*0250	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.590647	0.301939	-4.288708	38962.516420
HLA A*0201	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.380326	0.091584	-4.288742	24006.331554
HLA A*2902	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.428601	0.139834	-4.288766	26828.764187
HLA A*3101	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.402514	0.113627	-4.288888	25264.711087
HLA B*0801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.344842	0.055954	-4.288888	22122.873086
HLA B*5301	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.570441	0.281539	-4.288902	37191.305837
HLA B*4001	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.428775	0.139834	-4.288940	26839.506744
HLA B*4001	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.415977	0.126963	-4.289014	26060.148450
HLA A*0212	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.446412	0.157255	-4.289157	27951.950209
HLA B*4002	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.639594	0.350403	-4.289191	43610.776490
HLA B*0802	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.441821	0.152623	-4.289198	27658.028534
HLA A*0219	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.427055	0.137730	-4.289325	26733.431425
HLA A*0202	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.402728	0.113362	-4.289367	25277.151964
HLA B*2705	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.475870	0.186500	-4.289370	29913.687817
HLA B*5301	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.559314	0.269777	-4.289537	36250.522135
HLA A*0211	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.523604	0.233980	-4.289624	33389.079313
HLA B*3901	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.501024	0.211398	-4.289625	31697.392922
HLA A*0301	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.368050	0.078424	-4.289626	23337.253339
HLA A*0216	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.429754	0.139834	-4.289920	26900.122973
HLA B*4402	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.435520	0.145582	-4.289938	27259.626534
HLA A*2602	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.568075	0.278063	-4.290013	36989.247472
HLA A*3201	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.575481	0.285427	-4.290054	37625.395405
HLA A*0101	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.392167	0.101982	-4.290185	24669.889504
HLA B*5801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.356239	0.066046	-4.290193	22711.137134
HLA A*2501	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.497772	0.207166	-4.290606	31460.951714
HLA B*4601	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.256550	-0.034103	-4.290654	18053.035286
HLA A*6901	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.342180	0.051389	-4.290791	21987.687777
HLA B*4402	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.404439	0.113627	-4.290812	25376.899776
HLA A*2301	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.545276	0.254455	-4.290821	35097.492785
HLA A*2601	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.404486	0.113627	-4.290859	25379.645648
HLA B*4801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.443973	0.153079	-4.290895	27795.426900
HLA A*2902	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.445360	0.154429	-4.290931	27884.287043
HLA A*0219	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.426695	0.135619	-4.291076	26711.312970
HLA B*4001	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.087291	-0.203931	-4.291222	12226.185533
HLA B*3901	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.498540	0.207166	-4.291374	31516.656457
HLA B*4001	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.405136	0.113627	-4.291510	25417.706555
HLA B*2705	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.434801	0.143276	-4.291525	27214.537568
HLA A*6802	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.405172	0.113627	-4.291545	25419.769244
HLA A*2603	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.391117	0.099536	-4.291581	24610.304347
HLA A*0216	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.446013	0.154429	-4.291584	27926.255145
HLA B*3801	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.582158	0.290570	-4.291588	38208.352252
HLA A*3301	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.484619	0.192958	-4.291661	30522.453385
HLA A*2602	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.628594	0.336669	-4.291924	42520.026898
HLA A*6801	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.628723	0.336669	-4.292053	42532.680355
HLA B*1501	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.372455	0.080331	-4.292124	23575.180424
HLA A*2402	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.577675	0.285427	-4.292249	37815.991494
HLA A*0219	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.439942	0.147675	-4.292267	27538.585695
HLA B*3801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.546761	0.254455	-4.292306	35217.698243
HLA A*3101	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.430088	0.137730	-4.292358	26920.795701
HLA B*5101	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.501056	0.208642	-4.292414	31699.793725
HLA B*4801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.430205	0.137730	-4.292475	26928.078612
HLA A*0206	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.503523	0.210953	-4.292570	31880.373108

HLA B*3901	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.483891	0.191274	-4.292618	30471.308126
HLA B*4403	1:13-21	9	PARPVLVVD	1.322529	-0.949404	-4.665849	0.373125	-4.292724	46328.614696
HLA B*0801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.341355	0.048624	-4.292731	21945.975608
HLA A*6901	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.390501	0.097746	-4.292755	24575.446633
HLA A*6901	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.379572	0.086816	-4.292755	23964.678949
HLA A*0202	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.478626	0.185815	-4.292811	30104.117671
HLA B*1503	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.438567	0.145582	-4.292985	27451.569754
HLA A*0211	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.547438	0.254355	-4.293083	35272.611878
HLA B*3901	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.413886	0.120764	-4.293122	25934.975595
HLA A*0202	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.574710	0.281539	-4.293171	37558.690461
HLA A*2601	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.344628	0.051389	-4.293239	22111.984678
HLA A*2601	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.374429	0.081144	-4.293285	23682.557070
HLA A*0301	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.344785	0.051389	-4.293396	22120.000898
HLA B*4002	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.635651	0.342132	-4.293520	43216.678323
HLA B*1801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.375782	0.082233	-4.293549	23756.469293
HLA B*1503	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.395555	0.101982	-4.293573	24863.093414
HLA A*6901	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.375852	0.082233	-4.293620	23760.325202
HLA B*1801	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.430386	0.136752	-4.293634	26939.298148
HLA B*1801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.515872	0.222188	-4.293684	32799.882553
HLA B*4402	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.430757	0.136752	-4.294005	26962.334694
HLA A*2402	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.597345	0.303325	-4.294020	39568.116714
HLA A*3101	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.365442	0.071401	-4.294041	23197.533598
HLA A*1101	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.435419	0.141148	-4.294270	27253.285994
HLA B*2705	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.441950	0.147675	-4.294276	27666.259236
HLA A*0301	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.360353	0.066046	-4.294306	22927.295470
HLA A*2402	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.565280	0.270903	-4.294377	36751.884140
HLA A*6802	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.429996	0.135619	-4.294377	26915.116398
HLA A*0301	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.326607	0.032127	-4.294480	21213.248271
HLA A*2902	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.392254	0.097746	-4.294508	24674.828069
HLA A*0201	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.396507	0.101982	-4.294524	24917.628299
HLA A*3301	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.597320	0.302627	-4.294693	39565.762133
HLA B*3801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.516899	0.222188	-4.294711	32877.517195
HLA A*8001	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.431965	0.137191	-4.294774	27037.412736
HLA A*3201	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.570112	0.275316	-4.294796	37163.148383
HLA A*8001	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.447519	0.152623	-4.294895	28023.264211
HLA A*0219	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.449335	0.154429	-4.294906	28140.698514
HLA B*4501	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.654196	0.359286	-4.294910	45102.007064
HLA B*5101	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.517122	0.222188	-4.294934	32894.418592
HLA B*5801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.350950	0.055954	-4.294996	22436.245781
HLA A*3201	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.523306	0.228245	-4.295061	33366.147028
HLA A*2902	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.327225	0.032127	-4.295098	21243.451981
HLA A*0219	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.422114	0.126963	-4.295151	26431.008851
HLA B*5801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.353612	0.058419	-4.295193	22574.188927
HLA B*1502	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.376456	0.081144	-4.295312	23793.383144
HLA B*5101	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.491616	0.195916	-4.295700	31018.172400
HLA A*0301	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.367187	0.071401	-4.295786	23290.964839
HLA A*2501	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.439131	0.143276	-4.295855	27487.235290
HLA A*3002	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.487185	0.191274	-4.295912	30703.301461
HLA B*7301	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.585948	0.289937	-4.296011	38543.223052
HLA A*0250	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.568614	0.272539	-4.296075	37035.100539
HLA A*3002	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.439357	0.143276	-4.296080	27501.514476
HLA A*0250	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.571412	0.275316	-4.296096	37274.494684
HLA B*5101	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.433300	0.137191	-4.296109	27120.621535
HLA B*5301	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.586679	0.290570	-4.296109	38608.125665
HLA A*0216	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.449295	0.153079	-4.296216	28138.110586
HLA A*1101	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.439559	0.143276	-4.296282	27514.312545
HLA B*4801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.398332	0.101982	-4.296350	25022.589595
HLA B*5401	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.550722	0.254355	-4.296367	35540.390857
HLA A*8001	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.439711	0.143276	-4.296435	27523.989456
HLA B*3501	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.442162	0.145582	-4.296580	27679.732941
HLA A*2501	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.453836	0.157255	-4.296582	28433.903596
HLA A*0219	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.437787	0.141148	-4.296639	27402.308702
HLA B*5301	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.227616	-0.069030	-4.296646	16889.481737
HLA B*5301	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.567556	0.270903	-4.296653	36945.050090
HLA A*6802	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.442817	0.146138	-4.296679	27721.543143

HLA B*1503	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.508178	0.211398	-4.296779	32223.872110
HLA B*0801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.070121	-0.226766	-4.296887	11752.247947
HLA A*8001	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.394691	0.097746	-4.296944	24813.644232
HLA A*6802	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.438095	0.141148	-4.296946	27421.735477
HLA A*2603	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.647669	0.350403	-4.297266	44429.251763
HLA A*2501	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.450387	0.153079	-4.297309	28208.983880
HLA B*5101	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.504475	0.207166	-4.297309	31950.299745
HLA B*4601	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.409645	0.112320	-4.297325	25682.956916
HLA A*0101	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.368842	0.071401	-4.297440	23379.839056
HLA B*2705	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.450066	0.152623	-4.297442	28188.084402
HLA A*0219	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.437298	0.139834	-4.297464	27371.491406
HLA A*3101	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.389064	0.091584	-4.297480	24494.215509
HLA B*4501	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.636878	0.339229	-4.297649	43338.893070
HLA B*5701	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.418719	0.120764	-4.297955	26225.195495
HLA A*3002	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.570545	0.272539	-4.298006	37200.159728
HLA A*3301	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.601335	0.303325	-4.298010	39933.263659
HLA A*2402	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.559519	0.261282	-4.298237	36267.587835
HLA A*6901	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.376750	0.078424	-4.298326	23809.478532
HLA A*8001	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.411717	0.113362	-4.298356	25805.796549
HLA B*3501	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.410681	0.112320	-4.298362	25744.303466
HLA A*6901	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.330507	0.032127	-4.298380	21404.610033
HLA B*4601	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.396380	0.097746	-4.298633	24910.350076
HLA A*2403	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.385457	0.086816	-4.298641	24291.653359
HLA B*3501	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.439831	0.141148	-4.298683	27531.584492
HLA B*0702	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.444833	0.146138	-4.298695	27850.516907
HLA A*0219	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.379858	0.081144	-4.298714	23980.501014
HLA B*1517	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.434345	0.135619	-4.298726	27185.990391
HLA B*1501	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.359573	0.060842	-4.298731	22886.153099
HLA B*4002	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.646139	0.347374	-4.298766	44273.054356
HLA B*3801	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.569741	0.270903	-4.298838	37131.396291
HLA B*0801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.370411	0.071401	-4.299010	23464.482107
HLA B*0803	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.499212	0.200115	-4.299097	31565.457663
HLA A*0101	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.381470	0.082233	-4.299237	24069.662409
HLA B*1501	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.381970	0.082695	-4.299275	24097.414021
HLA B*0801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.426246	0.126963	-4.299284	26683.726723
HLA A*2601	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.390870	0.091584	-4.299287	24596.328720
HLA A*2403	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.437026	0.137730	-4.299296	27354.319893
HLA B*5301	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.602744	0.303325	-4.299420	40063.094974
HLA A*6802	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.379764	0.080331	-4.299433	23975.312301
HLA A*0201	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.398985	0.099536	-4.299449	25060.250611
HLA B*4801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.439331	0.139834	-4.299496	27499.877943
HLA B*1503	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.527162	0.227420	-4.299742	33663.678002
HLA B*1501	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.266970	-0.032788	-4.299758	18491.417192
HLA B*0702	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.391199	0.091322	-4.299878	24614.964654
HLA B*0802	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.485794	0.185815	-4.299979	30605.126692
HLA B*4601	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.399521	0.099536	-4.299985	25091.180367
HLA B*1502	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.601948	0.301939	-4.300009	39989.688497
HLA B*3901	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.486548	0.186500	-4.300049	30658.320947
HLA A*0250	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.527718	0.227657	-4.300061	33706.867357
HLA A*0203	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.437392	0.137191	-4.300202	27377.415116
HLA B*1509	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.534396	0.233980	-4.300416	34229.111679
HLA B*1801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.493449	0.192958	-4.300491	31149.336745
HLA B*4801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.436126	0.135619	-4.300507	27297.700761
HLA A*0219	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.412876	0.112320	-4.300556	25874.714416
HLA B*4402	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.453665	0.153079	-4.300586	28422.676642
HLA B*1801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.509399	0.208642	-4.300757	32314.650075
HLA B*7301	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.604142	0.303325	-4.300817	40192.261205
HLA B*0803	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.509550	0.208642	-4.300907	32325.840408
HLA A*0201	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.392275	0.091322	-4.300954	24676.029491
HLA A*0212	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.392639	0.091584	-4.301056	24696.729829
HLA B*4501	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.643212	0.342132	-4.301080	43975.625579
HLA B*5701	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.413468	0.112320	-4.301148	25910.013265
HLA A*3101	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.367216	0.066046	-4.301169	23292.476906
HLA B*4501	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.648545	0.347374	-4.301172	44518.995562
HLA A*6802	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.400733	0.099536	-4.301197	25161.320320

HLA A*0219	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.438546	0.137191	-4.301355	27450.233197
HLA A*0212	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.382563	0.081144	-4.301418	24130.288237
HLA B*4801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.438609	0.137191	-4.301419	27454.243063
HLA B*4501	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.604866	0.303325	-4.301541	40259.287219
HLA A*0101	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.388432	0.086816	-4.301615	24458.595977
HLA B*5301	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.587102	0.285427	-4.301675	38645.739798
HLA B*4002	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.644946	0.343210	-4.301736	44151.549138
HLA B*1509	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.367817	0.066046	-4.301771	23324.757742
HLA A*6801	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.647270	0.345470	-4.301800	44388.409801
HLA A*2601	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.380394	0.078424	-4.301970	24010.098125
HLA A*2902	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.439288	0.137191	-4.302098	27497.200190
HLA B*4002	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.638786	0.336669	-4.302116	43529.692226
HLA B*4402	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.401687	0.099536	-4.302151	25216.645757
HLA B*4403	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.573120	0.270903	-4.302217	37421.383543
HLA B*3901	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.339503	0.037065	-4.302439	21852.619205
HLA B*1801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.448094	0.145582	-4.302512	28060.431511
HLA B*4001	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.400280	0.097746	-4.302534	25135.062879
HLA A*3301	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.580678	0.278063	-4.302615	38078.351056
HLA A*2601	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.400402	0.097746	-4.302656	25142.134724
HLA A*0250	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.588103	0.285427	-4.302676	38734.905971
HLA B*3901	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.502849	0.200115	-4.302734	31830.912830
HLA A*0216	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.416376	0.113627	-4.302750	26084.126501
HLA B*1517	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.394451	0.091584	-4.302867	24799.955624
HLA B*4403	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.580995	0.278063	-4.302932	38106.171168
HLA B*0802	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.448520	0.145582	-4.302937	28087.921460
HLA B*1502	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.588370	0.285427	-4.302944	38758.802215
HLA B*1503	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.416313	0.113362	-4.302951	26080.316749
HLA B*5801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.351601	0.048624	-4.302977	22469.892581
HLA A*0202	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.530451	0.227420	-4.303031	33919.609444
HLA B*4801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.430158	0.126963	-4.303196	26925.165211
HLA B*1517	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.440459	0.137191	-4.303268	27571.380960
HLA A*0203	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.417027	0.113627	-4.303401	26123.243892
HLA B*5401	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.538136	0.234640	-4.303496	34525.184533
HLA B*1501	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.374936	0.071401	-4.303535	23710.247167
HLA B*4402	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.424440	0.120764	-4.303676	26572.947549
HLA A*2601	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.359758	0.055954	-4.303805	22895.936302
HLA B*4601	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.399368	0.095477	-4.303891	25082.358785
HLA A*8001	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.440710	0.136752	-4.303958	27587.345498
HLA A*0206	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.359921	0.055954	-4.303967	22904.484546
HLA B*1503	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.504153	0.200115	-4.304038	31926.628399
HLA A*3201	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.495350	0.191274	-4.304076	31285.963705
HLA B*4001	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.355492	0.051389	-4.304103	22672.099737
HLA B*5301	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.602204	0.298081	-4.304123	40013.276487
HLA B*0802	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.406161	0.101982	-4.304178	25477.730358
HLA B*1503	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.343559	0.039331	-4.304228	22057.622971
HLA A*0212	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.384576	0.080331	-4.304245	24242.422632
HLA B*1517	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.445439	0.141148	-4.304291	27889.416445
HLA B*5701	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.406288	0.101982	-4.304305	25485.174357
HLA B*3901	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.450566	0.146138	-4.304428	28220.584433
HLA B*4402	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.384834	0.080331	-4.304503	24256.853295
HLA B*4601	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.384914	0.080331	-4.304583	24261.315420
HLA B*5401	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.445907	0.141148	-4.304758	27919.457465
HLA B*2705	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.457840	0.153079	-4.304761	28697.232022
HLA A*6901	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.376188	0.071401	-4.304787	23778.713638
HLA A*0202	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.594815	0.289937	-4.304878	39338.245353
HLA B*5801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.356276	0.051389	-4.304888	22713.103055
HLA A*1101	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.396483	0.091584	-4.304899	24916.280320
HLA A*2402	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.577523	0.272539	-4.304984	37802.696111
HLA A*0201	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.385436	0.080331	-4.305105	24290.470652
HLA A*0212	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.361133	0.055954	-4.305179	22968.511803
HLA B*4501	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.595142	0.289937	-4.305205	39367.837839
HLA A*2403	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.402961	0.097746	-4.305214	25290.693502
HLA B*5801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.366086	0.060842	-4.305244	23231.945023
HLA B*3801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.566673	0.261282	-4.305391	36869.975868
HLA B*0702	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.371696	0.066046	-4.305650	23534.021261

HLA A*0301	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.366532	0.060842	-4.305690	23255.836927
HLA A*0250	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.591998	0.286262	-4.305736	39083.905288
HLA B*1501	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.130597	-0.175217	-4.305813	13508.175348
HLA A*1101	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.458451	0.152623	-4.305828	28737.625122
HLA B*5701	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.386228	0.080331	-4.305896	24334.795795
HLA A*3002	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.595882	0.289937	-4.305945	39434.982360
HLA A*3001	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.302880	-0.003120	-4.305999	20085.364881
HLA A*2403	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.364535	0.058419	-4.306116	23149.142652
HLA B*1801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.502064	0.195916	-4.306148	31773.449390
HLA A*0216	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.452429	0.146138	-4.306291	28341.911992
HLA B*4403	1:106-114	9	IVAHTGTRE	0.973291	-0.614005	-4.665605	0.359286	-4.306319	46302.556230
HLA A*3002	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.463622	0.157255	-4.306367	29081.854124
HLA B*4501	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.649607	0.343210	-4.306398	44627.989728
HLA A*0101	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.372504	0.066046	-4.306458	23577.858897
HLA A*0203	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.444300	0.137730	-4.306570	27816.336215
HLA A*2402	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.584700	0.278063	-4.306638	38432.660698
HLA B*4403	1:34-42	9	VREARVFSE	0.911057	-0.566886	-4.650843	0.344171	-4.306672	44755.164068
HLA B*5301	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.540664	0.233980	-4.306684	34726.743109
HLA A*0101	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.365143	0.058419	-4.306725	23181.601069
HLA A*0219	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.420392	0.113627	-4.306765	26326.405577
HLA A*6802	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.185669	-0.121106	-4.306774	15334.464625
HLA A*1101	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.446741	0.139834	-4.306907	27973.128601
HLA A*6801	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.646144	0.339229	-4.306915	44273.533383
HLA A*3101	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.387273	0.080331	-4.306942	24393.449972
HLA B*5301	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.593520	0.286262	-4.307258	39221.158583
HLA A*2301	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.534708	0.227420	-4.307288	34253.748910
HLA A*2501	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.405108	0.097746	-4.307362	25416.056525
HLA A*0250	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.597303	0.289937	-4.307367	39564.263837
HLA B*1509	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.516041	0.208642	-4.307399	32812.660990
HLA A*2402	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.588981	0.281539	-4.307442	38813.357588
HLA A*6802	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.399035	0.091584	-4.307451	25063.097810
HLA A*0203	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.399129	0.091584	-4.307545	25068.521940
HLA B*0702	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.460211	0.152623	-4.307587	28854.306417
HLA A*2301	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.542948	0.235291	-4.307657	34909.831596
HLA A*2601	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.390039	0.082233	-4.307806	24549.269348
HLA B*1501	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.340110	0.032127	-4.307983	21883.141325
HLA B*3901	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.503960	0.195916	-4.308044	31912.468540
HLA A*0219	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.388462	0.080331	-4.308131	24460.316175
HLA B*2705	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.504068	0.195916	-4.308152	31920.411102
HLA A*0101	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.364159	0.055954	-4.308205	23129.113834
HLA A*2603	1:251-259	9	DRLTCVFVD	1.180954	-0.841725	-4.647455	0.339229	-4.308227	44407.384630
HLA A*8001	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.449436	0.141148	-4.308287	28147.245512
HLA B*7301	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.515513	0.207166	-4.308347	32772.744895
HLA B*5301	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.543667	0.235291	-4.308376	34967.670102
HLA A*0201	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.391093	0.082695	-4.308398	24608.972993
HLA A*0101	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.369257	0.060842	-4.308416	23402.237151
HLA A*6802	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.406189	0.097746	-4.308443	25479.384392
HLA A*0202	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.504581	0.195916	-4.308664	31958.078833
HLA B*1517	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.446424	0.137730	-4.308694	27952.706304
HLA A*0201	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.395543	0.086816	-4.308727	24862.420890
HLA A*2603	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.645435	0.336669	-4.308765	44201.258938
HLA B*0801	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.345911	0.037065	-4.308846	22177.395605
HLA B*1517	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.466131	0.157255	-4.308877	29250.368493
HLA A*2403	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.435882	0.126963	-4.308919	27282.346617
HLA A*1101	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.462010	0.153079	-4.308932	28974.126037
HLA B*5401	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.448787	0.139834	-4.308953	28105.249392
HLA A*6901	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.369936	0.060842	-4.309095	23438.854182
HLA A*0250	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.500481	0.191274	-4.309207	31657.805926
HLA B*4403	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.579041	0.269777	-4.309263	37935.039656
HLA B*1503	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.328764	0.019419	-4.309345	21318.861199
HLA A*3101	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.188333	-0.121106	-4.309439	15428.827872
HLA A*2602	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.563987	0.254355	-4.309632	36642.693675
HLA A*2301	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.543683	0.233980	-4.309703	34968.994326
HLA B*3501	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.453071	0.143276	-4.309794	28383.801080
HLA B*5701	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.401384	0.091584	-4.309800	25199.053812

HLA A*0301	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.368235	0.058419	-4.309817	23347.229375
HLA B*0803	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.495639	0.185815	-4.309823	31306.788825
HLA A*0219	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.456022	0.146138	-4.309883	28577.320641
HLA B*4501	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.643990	0.334057	-4.309932	44054.442104
HLA A*0216	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.423371	0.113362	-4.310009	26507.618686
HLA B*1503	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.347163	0.037065	-4.310098	22241.435764
HLA A*3002	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.521126	0.210953	-4.310172	33199.056167
HLA B*0702	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.423566	0.113362	-4.310204	26519.523831
HLA A*0216	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.422560	0.112320	-4.310241	26458.190696
HLA B*3501	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.450089	0.139834	-4.310255	28189.609387
HLA A*2403	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.391514	0.081144	-4.310370	24632.815130
HLA A*2501	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.412373	0.101982	-4.310391	25844.776172
HLA B*0803	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.521812	0.211398	-4.310413	33251.541750
HLA A*0212	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.448289	0.137730	-4.310559	28073.034058
HLA B*1801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.463251	0.152623	-4.310628	29057.006667
HLA A*0203	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.366682	0.055954	-4.310729	23263.890257
HLA B*5801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.350088	0.039331	-4.310757	22391.744393
HLA B*5701	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.408553	0.097746	-4.310806	25618.430105
HLA A*0212	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.423232	0.112320	-4.310912	26499.159243
HLA A*3301	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.565277	0.254355	-4.310922	36751.685317
HLA A*3002	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.437977	0.126963	-4.311015	27414.319053
HLA A*0202	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.431834	0.120764	-4.311070	27029.222890
HLA A*8001	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.465676	0.154429	-4.311247	29219.685794
HLA B*1502	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.581026	0.269777	-4.311249	38108.851214
HLA A*0101	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.392430	0.081144	-4.311286	24684.841707
HLA A*8001	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.457462	0.146138	-4.311323	28672.247840
HLA B*5101	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.398198	0.086816	-4.311382	25014.874727
HLA B*4402	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.423735	0.112320	-4.311415	26529.855516
HLA A*0301	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.367422	0.055954	-4.311469	23303.568402
HLA B*5101	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.377586	0.066046	-4.311540	23855.377880
HLA A*2601	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.398473	0.086816	-4.311657	25030.713079
HLA A*0250	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.589907	0.278063	-4.311844	38896.176350
HLA B*1502	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.587325	0.275316	-4.312009	38665.606474
HLA A*3201	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.614642	0.302627	-4.312015	41175.823025
HLA A*0201	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.394329	0.082233	-4.312096	24792.980025
HLA B*4403	1:110-118	9	TGTREYGRT	0.808206	-0.457803	-4.662567	0.350403	-4.312164	45979.800618
HLA B*1509	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.505156	0.192958	-4.312198	32000.464884
HLA B*3501	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.399030	0.086816	-4.312214	25062.826634
HLA B*3801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.537530	0.225172	-4.312358	34477.029573
HLA B*4501	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.361013	0.048624	-4.312389	22962.175565
HLA A*0201	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.393570	0.081144	-4.312426	24749.694745
HLA B*4402	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.407904	0.095477	-4.312427	25580.207017
HLA B*4801	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.449250	0.136752	-4.312498	28135.218477
HLA B*4501	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.649194	0.336669	-4.312525	44585.517834
HLA B*3901	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.458108	0.145582	-4.312526	28714.935848
HLA B*5301	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.232433	-0.080273	-4.312706	17077.833200
HLA A*0202	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.368743	0.055954	-4.312789	23374.527401
HLA A*0101	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.391300	0.078424	-4.312877	24620.691382
HLA A*2602	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.615739	0.302627	-4.313113	41279.981894
HLA A*2601	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.393549	0.080331	-4.313217	24748.489736
HLA A*3201	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.513351	0.200115	-4.313236	32610.036974
HLA B*1509	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.547952	0.234640	-4.313312	35314.426425
HLA A*0216	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.465965	0.152623	-4.313341	29239.135522
HLA A*2402	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.567782	0.254355	-4.313427	36964.242461
HLA B*5801	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.350520	0.037065	-4.313455	22414.044671
HLA A*0211	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.450796	0.137191	-4.313605	28235.550082
HLA B*1517	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.415655	0.101982	-4.313673	26040.841001
HLA A*0211	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.450683	0.136752	-4.313931	28228.218977
HLA B*0702	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.453827	0.139834	-4.313993	28433.288306
HLA A*6802	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.245003	-0.069030	-4.314032	17579.337829
HLA B*5101	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.333536	0.019419	-4.314117	21554.393447
HLA A*2902	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.450893	0.136752	-4.314140	28241.813576
HLA B*1503	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.460281	0.146138	-4.314143	28858.989755
HLA B*4601	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.405846	0.091584	-4.314262	25459.267603
HLA B*5101	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.514378	0.200115	-4.314263	32687.222268

HLA B*4002	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.648400	0.334057	-4.314342	44504.065811
HLA A*2501	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.466970	0.152623	-4.314347	29306.915207
HLA B*0803	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.505633	0.191274	-4.314360	32035.627338
HLA A*2902	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.452197	0.137730	-4.314466	28326.736722
HLA A*0202	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.549782	0.235291	-4.314492	35463.566180
HLA B*4403	1:117-125	9	RTELKVLGG	0.929797	-0.584327	-4.659985	0.345470	-4.314515	45707.240230
HLA B*4801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.414151	0.099536	-4.314615	25950.834946
HLA A*0201	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.393060	0.078424	-4.314636	24720.656989
HLA A*2601	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.397338	0.082695	-4.314643	24965.393792
HLA A*2301	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.543131	0.228245	-4.314886	34924.565653
HLA B*3501	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.139802	-0.175217	-4.315019	13797.549848
HLA A*0211	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.468222	0.153079	-4.315144	29391.542797
HLA A*0250	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.586047	0.270903	-4.315144	38551.981659
HLA B*1517	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.427478	0.112320	-4.315158	26759.476586
HLA A*6802	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.410648	0.095477	-4.315171	25742.353706
HLA B*0803	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.511145	0.195916	-4.315229	32444.801751
HLA A*2402	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.585128	0.269777	-4.315351	38470.520124
HLA A*2301	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.540537	0.225172	-4.315365	34716.599728
HLA A*2601	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.347581	0.032127	-4.315454	22262.863699
HLA A*6901	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.241624	-0.073933	-4.315556	17443.111335
HLA A*0250	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.550910	0.235291	-4.315620	35555.775752
HLA A*3002	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.452814	0.137191	-4.315624	28367.068713
HLA B*1502	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.550391	0.234640	-4.315751	35513.291184
HLA B*3501	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.470238	0.154429	-4.315809	29528.286191
HLA A*0206	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.194719	-0.121106	-4.315825	15657.370709
HLA B*4501	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.614959	0.299099	-4.315861	41205.906156
HLA A*2402	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.591199	0.275316	-4.315883	39012.081901
HLA B*5301	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.543317	0.227420	-4.315897	34939.494948
HLA B*5301	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.605886	0.289937	-4.315949	40353.922727
HLA A*2501	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.415533	0.099536	-4.315997	26033.516372
HLA A*2301	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.501888	0.185815	-4.316073	31760.560192
HLA B*0803	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.469247	0.153079	-4.316168	29460.950796
HLA B*0801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.359695	0.043160	-4.316535	22892.592205
HLA B*1501	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.407942	0.091322	-4.316620	25582.421290
HLA B*1801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.453862	0.137191	-4.316672	28435.595714
HLA B*0801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.403503	0.086816	-4.316687	25322.318644
HLA B*0702	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.453928	0.137191	-4.316737	28439.903376
HLA B*0702	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.403689	0.086816	-4.316873	25333.143240
HLA B*5701	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.412401	0.095477	-4.316923	25846.454034
HLA A*3101	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.316385	-0.000735	-4.317119	20719.752603
HLA B*1501	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.395703	0.078424	-4.317280	24871.568772
HLA B*0801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.375730	0.058419	-4.317311	23753.642025
HLA A*6802	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.336731	0.019419	-4.317312	21713.563628
HLA B*4402	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.399594	0.082233	-4.317361	25095.388675
HLA B*5701	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.404269	0.086816	-4.317453	25367.017093
HLA B*4403	1:282-290	9	NLVTVDAAE	0.886481	-0.552424	-4.651522	0.334057	-4.317465	44825.191614
HLA B*2705	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.397839	0.080331	-4.317508	24994.178155
HLA B*1801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.455312	0.137730	-4.317582	28530.669519
HLA B*2705	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.369051	0.051389	-4.317662	23391.098694
HLA B*5301	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.595750	0.278063	-4.317687	39423.037192
HLA B*2705	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.457537	0.139834	-4.317703	28677.211907
HLA A*3101	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.400451	0.082695	-4.317756	25144.991226
HLA A*3301	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.615852	0.298081	-4.317772	41290.702652
HLA B*3901	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.470964	0.153079	-4.317886	29577.688601
HLA B*4501	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.587703	0.269777	-4.317926	38699.298584
HLA B*0801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.417488	0.099536	-4.317951	26150.958058
HLA B*5401	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.509237	0.191274	-4.317964	32302.589838
HLA B*1801	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.355205	0.037065	-4.318140	22657.140941
HLA B*4002	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.617410	0.299099	-4.318311	41439.068265
HLA A*2601	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.384433	0.066046	-4.318386	24234.423873
HLA B*5801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.350624	0.032127	-4.318497	22419.380636
HLA A*2403	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.409955	0.091322	-4.318634	25701.303803
HLA A*8001	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.432287	0.113627	-4.318660	27057.459072
HLA B*4801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.410106	0.091322	-4.318784	25710.203981
HLA A*3201	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.620805	0.301939	-4.318866	41764.278948

HLA A*0301	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.355931	0.037065	-4.318866	22695.047556
HLA B*5301	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.594357	0.275316	-4.319041	39296.768203
HLA B*5101	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.459036	0.139834	-4.319202	28776.362581
HLA A*1101	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.476493	0.157255	-4.319238	29956.603451
HLA B*0702	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.318565	-0.000735	-4.319300	20824.035124
HLA B*3501	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.071357	-0.247969	-4.319326	11785.737791
HLA A*0216	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.467111	0.147675	-4.319436	29316.429581
HLA B*4801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.358842	0.039331	-4.319511	22847.680080
HLA B*5101	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.457450	0.137730	-4.319720	28671.472282
HLA A*2602	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.595038	0.275316	-4.319722	39358.468026
HLA B*4601	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.402451	0.082695	-4.319756	25261.021015
HLA B*4403	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.264886	-0.055017	-4.319903	18402.897355
HLA B*1501	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.378514	0.058419	-4.320096	23906.409090
HLA A*0212	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.422158	0.101982	-4.320176	26433.725779
HLA A*8001	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.371581	0.051389	-4.320192	23527.783582
HLA A*2603	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.618291	0.298081	-4.320210	41523.221384
HLA A*2603	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.589989	0.269777	-4.320212	38903.541887
HLA A*0301	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.368856	0.048624	-4.320232	23380.597962
HLA B*3501	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.239965	-0.080273	-4.320239	17376.616499
HLA A*0202	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.472863	0.152623	-4.320239	29707.261297
HLA A*0216	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.352449	0.032127	-4.320322	22513.818486
HLA A*3002	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.590154	0.269777	-4.320376	38918.277147
HLA A*2403	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.400738	0.080331	-4.320407	25161.592561
HLA A*8001	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.402665	0.082233	-4.320432	25273.460075
HLA B*7301	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.574809	0.254355	-4.320454	37567.225341
HLA A*0301	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.363644	0.043160	-4.320484	23101.727479
HLA A*2301	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.511794	0.191274	-4.320520	32493.282223
HLA A*0206	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.542764	0.222188	-4.320576	34895.103755
HLA A*0250	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.401788	0.081144	-4.320644	25222.512468
HLA A*3101	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.402933	0.082233	-4.320700	25289.051717
HLA A*0216	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.461869	0.141148	-4.320721	28964.722754
HLA A*2402	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.548173	0.227420	-4.320753	35332.389422
HLA A*3301	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.542978	0.222188	-4.320790	34912.286841
HLA B*0803	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.531947	0.210953	-4.320994	34036.701428
HLA B*4501	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.591942	0.270903	-4.321039	39078.831067
HLA A*6901	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.358130	0.037065	-4.321065	22810.258924
HLA A*2603	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.620222	0.299099	-4.321124	41708.283370
HLA B*1517	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.448200	0.126963	-4.321237	28067.263515
HLA B*3501	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.412843	0.091584	-4.321259	25872.754780
HLA A*0216	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.459083	0.137730	-4.321353	28779.476289
HLA B*3801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.549726	0.228245	-4.321481	35458.961984
HLA B*1502	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.607763	0.286262	-4.321501	40528.730146
HLA A*0211	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.532509	0.210953	-4.321556	34080.738104
HLA B*1517	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.465011	0.143276	-4.321734	29174.984723
HLA A*3201	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.576245	0.254355	-4.321890	37691.607091
HLA B*5701	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.321178	-0.000735	-4.321912	20949.685852
HLA B*4403	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.625271	0.303325	-4.321946	42196.007300
HLA A*2501	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.469674	0.147675	-4.322000	29489.972328
HLA B*4001	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.404319	0.082233	-4.322086	25369.899144
HLA B*4801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.435753	0.113627	-4.322126	27274.230128
HLA B*5301	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.515128	0.192958	-4.322169	32743.681096
HLA B*3801	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.557569	0.235291	-4.322278	36105.103888
HLA A*0250	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.583584	0.261282	-4.322302	38334.027176
HLA B*4403	1:33-41	9	RVREARVFS	1.063374	-0.731690	-4.654149	0.331684	-4.322465	45097.127391
HLA B*1517	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.365674	0.043160	-4.322514	23209.961038
HLA B*0801	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.402965	0.080331	-4.322634	25290.967143
HLA B*4403	1:513-521	9	DITSKPPAT	0.730601	-0.383227	-4.670090	0.347374	-4.322716	46783.222642
HLA B*0702	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.449770	0.126963	-4.322807	28168.876653
HLA B*4002	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.626181	0.303325	-4.322856	42284.442547
HLA A*3101	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.414205	0.091322	-4.322884	25954.064143
HLA A*8001	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.404201	0.081144	-4.323057	25363.037655
HLA A*0219	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.414666	0.091584	-4.323082	25981.598826
HLA B*1503	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.534175	0.210953	-4.323221	34211.709589
HLA B*5701	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.422769	0.099536	-4.323233	26470.932857
HLA A*2301	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.531959	0.208642	-4.323317	34037.622115

HLA B*7301	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.436951	0.113627	-4.323324	27349.584820
HLA A*6801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.423039	0.099536	-4.323503	26487.406534
HLA A*3101	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.191599	-0.132020	-4.323618	15545.286056
HLA A*0211	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.546009	0.222188	-4.323821	35156.783355
HLA B*4601	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.415173	0.091322	-4.323852	26011.977007
HLA A*0201	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.395261	0.071401	-4.323860	24846.285775
HLA A*6901	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.382318	0.058419	-4.323899	24116.715669
HLA B*1503	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.519852	0.195916	-4.323936	33101.853801
HLA A*0211	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.531315	0.207166	-4.324149	33987.205196
HLA A*2902	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.459832	0.135619	-4.324213	28829.185484
HLA A*0216	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.405409	0.081144	-4.324265	25433.662370
HLA A*2902	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.415871	0.091584	-4.324287	26053.805009
HLA B*4001	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.361396	0.037065	-4.324331	22982.432816
HLA A*0101	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.356580	0.032127	-4.324453	22728.959510
HLA B*5401	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.533101	0.208642	-4.324459	34127.231789
HLA A*2301	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.535866	0.211398	-4.324468	34345.228176
HLA A*0250	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.594345	0.269777	-4.324568	39295.705262
HLA B*1501	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.411398	0.086816	-4.324581	25786.817048
HLA B*4403	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.614788	0.289937	-4.324851	41189.636253
HLA A*0250	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.533569	0.208642	-4.324926	34163.991856
HLA A*8001	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.424503	0.099536	-4.324967	26576.829263
HLA A*2602	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.560280	0.235291	-4.324989	36331.213556
HLA B*1801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.525141	0.200115	-4.325026	33507.421357
HLA A*3101	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.383577	0.058419	-4.325159	24186.748411
HLA A*3301	1:478-486	9	EDAMTADWT	0.800588	-0.498649	-4.627130	0.301939	-4.325191	42376.960289
HLA A*2301	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.536186	0.210953	-4.325233	34370.506801
HLA B*1801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.478342	0.153079	-4.325263	30084.418067
HLA A*2902	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.405745	0.080331	-4.325414	25453.345824
HLA A*3101	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.403868	0.078424	-4.325444	25343.561144
HLA B*5301	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.598121	0.272539	-4.325582	39638.819317
HLA B*5401	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.550840	0.225172	-4.325667	35550.005636
HLA B*4601	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.412570	0.086816	-4.325754	25856.523500
HLA A*0216	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.452826	0.126963	-4.325863	28367.836037
HLA A*8001	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.463641	0.137730	-4.325911	29083.112788
HLA A*2602	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.616548	0.290570	-4.325978	41356.875545
HLA B*0702	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.423772	0.097746	-4.326026	26532.151993
HLA A*0202	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.560132	0.233980	-4.326152	36318.833152
HLA A*6801	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.628812	0.302627	-4.326185	42541.424943
HLA B*0802	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.479352	0.153079	-4.326273	30154.483478
HLA A*6802	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.428262	0.101982	-4.326280	26807.872073
HLA B*2705	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.463538	0.137191	-4.326347	29076.190810
HLA A*2403	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.417950	0.091584	-4.326367	26178.843250
HLA A*3201	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.596178	0.269777	-4.326401	39461.872223
HLA A*3101	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.387555	0.060842	-4.326713	24409.291016
HLA B*4001	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.358875	0.032127	-4.326748	22849.410594
HLA B*0801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.422231	0.095477	-4.326754	26438.159260
HLA A*6801	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.548967	0.222188	-4.326779	35397.055303
HLA A*2402	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.581263	0.254455	-4.326808	38129.679535
HLA A*2601	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.398219	0.071401	-4.326818	25016.092706
HLA A*0202	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.581216	0.254355	-4.326861	38125.554211
HLA A*2602	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.555193	0.228245	-4.326949	35908.169755
HLA B*7301	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.191993	-0.135106	-4.327100	15559.420989
HLA B*1503	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.479730	0.152623	-4.327107	30180.759238
HLA A*2402	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.535801	0.208642	-4.327158	34340.026061
HLA A*0202	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.552513	0.225172	-4.327340	35687.202669
HLA A*0250	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.554937	0.227420	-4.327517	35887.001742
HLA A*3101	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.427057	0.099536	-4.327521	26733.576050
HLA A*0250	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.562446	0.234640	-4.327806	36512.883363
HLA B*5101	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.480898	0.153079	-4.327819	30262.015884
HLA A*0216	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.410575	0.082695	-4.327880	25738.036906
HLA B*0802	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.482467	0.154429	-4.328038	30371.574780
HLA B*4801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.440397	0.112320	-4.328078	27567.503122
HLA A*0201	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.388965	0.060842	-4.328123	24488.650680
HLA B*4403	1:141-149	9	HGDAVTAAP	0.506674	-0.164542	-4.670323	0.342132	-4.328191	46808.285466
HLA B*3501	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.409450	0.081144	-4.328306	25671.427323

HLA B*5101	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.442056	0.113627	-4.328430	27672.995269
HLA B*4402	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.420072	0.091584	-4.328488	26307.043182
HLA A*0211	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.481142	0.152623	-4.328519	30279.046946
HLA B*0803	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.482984	0.154429	-4.328555	30407.743807
HLA A*2603	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.603922	0.275316	-4.328606	40171.827448
HLA A*0206	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.515153	0.186500	-4.328654	32745.629690
HLA A*1101	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.474808	0.146138	-4.328670	29840.630136
HLA A*0212	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.411402	0.082695	-4.328707	25787.096057
HLA B*4403	1:471-479	9	VLRPVSSED	1.064752	-0.728083	-4.665650	0.336669	-4.328980	46307.315817
HLA A*0250	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.583380	0.254355	-4.329025	38315.989114
HLA B*5101	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.431016	0.101982	-4.329034	26978.384425
HLA B*1517	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.483525	0.154429	-4.329096	30445.602936
HLA B*4403	1:495-503	9	RISTRITNE	0.934031	-0.590821	-4.672386	0.343210	-4.329176	47031.148196
HLA A*2902	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.395252	0.066046	-4.329206	24845.748118
HLA B*0802	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.472557	0.143276	-4.329281	29686.375954
HLA B*5701	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.400832	0.071401	-4.329431	25167.038007
HLA B*5301	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.590734	0.261282	-4.329452	38970.316168
HLA B*5101	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.409842	0.080331	-4.329511	25694.630692
HLA B*5701	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.412248	0.082695	-4.329553	25837.366913
HLA A*0301	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.368938	0.039331	-4.329607	23385.025407
HLA B*5801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.355306	0.025675	-4.329632	22662.412177
HLA A*0203	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.431629	0.101982	-4.329647	27016.504299
HLA A*0201	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.385617	0.055954	-4.329663	24300.591233
HLA B*4001	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.410829	0.081144	-4.329685	25753.079212
HLA B*0801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.421409	0.091584	-4.329825	26388.146994
HLA A*2602	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.555085	0.225172	-4.329913	35899.234942
HLA B*5101	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.482843	0.152623	-4.330220	30397.875258
HLA A*2602	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.600000	0.269777	-4.330223	39810.744382
HLA A*2403	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.391176	0.060842	-4.330334	24613.633047
HLA B*4002	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.632966	0.302627	-4.330339	42950.272361
HLA A*0201	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.396392	0.066046	-4.330345	24911.023896
HLA B*4002	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.601363	0.270903	-4.330460	39935.856157
HLA B*3501	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.476608	0.146138	-4.330469	29964.545537
HLA B*0801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.250209	-0.080273	-4.330482	17791.352768
HLA B*0802	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.467391	0.136752	-4.330638	29335.308895
HLA A*6802	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.413743	0.082695	-4.331048	25926.418381
HLA B*4402	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.417868	0.086816	-4.331052	26173.886857
HLA A*1101	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.468307	0.137191	-4.331116	29397.267534
HLA B*0802	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.478917	0.147675	-4.331242	30124.319079
HLA A*6802	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.422602	0.091322	-4.331281	26460.767267
HLA B*1502	1:290-298	9	ETFLEALSG	0.858728	-0.587825	-4.602286	0.270903	-4.331383	40020.853563
HLA A*0219	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.383002	0.051389	-4.331613	24154.711978
HLA A*2602	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.522895	0.191274	-4.331621	33334.573223
HLA A*0211	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.412124	0.080331	-4.331793	25829.959779
HLA A*0219	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.414523	0.082695	-4.331828	25973.026229
HLA B*1502	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.622034	0.289937	-4.332097	41882.612957
HLA B*1501	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.210991	-0.121106	-4.332097	16255.164443
HLA B*4001	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.329022	-0.003120	-4.332142	21331.551569
HLA B*1509	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.560602	0.228245	-4.332357	36358.150591
HLA B*4601	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.375615	0.043160	-4.332455	23747.346135
HLA B*4402	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.434526	0.101982	-4.332544	27197.317386
HLA B*4501	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.618867	0.286262	-4.332604	41578.293699
HLA B*4801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.388622	0.055954	-4.332668	24469.316107
HLA A*1101	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.469491	0.136752	-4.332739	29477.531030
HLA B*1502	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.568132	0.235291	-4.332841	36994.050369
HLA A*0212	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.432444	0.099536	-4.332908	27067.268166
HLA A*2501	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.414158	0.081144	-4.333014	25951.256123
HLA A*2902	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.446807	0.113627	-4.333180	27977.366205
HLA A*6801	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.602961	0.269777	-4.333183	40083.039732
HLA A*0250	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.567265	0.233980	-4.333285	36920.274691
HLA A*2603	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.623885	0.290570	-4.333315	42061.539338
HLA B*0802	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.473213	0.139834	-4.333378	29731.217187
HLA A*0216	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.413801	0.080331	-4.333470	25929.925095
HLA A*0101	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.382165	0.048624	-4.333542	24108.236690
HLA B*4001	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.420441	0.086816	-4.333625	26329.396629

HLA B*0802	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.490958	0.157255	-4.333704	30971.222603
HLA A*0219	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.429329	0.095477	-4.333852	26873.795535
HLA A*1101	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.446250	0.112320	-4.333930	27941.518186
HLA A*2301	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.534184	0.200115	-4.334069	34212.449923
HLA B*4001	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.414436	0.080331	-4.334104	25967.827835
HLA B*5801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.353770	0.019419	-4.334351	22582.372709
HLA B*5701	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.416797	0.082233	-4.334564	26109.397825
HLA A*2602	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.331534	-0.003120	-4.334654	21455.272996
HLA A*0203	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.434225	0.099536	-4.334689	27178.490693
HLA B*1509	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.482376	0.147675	-4.334701	30365.167489
HLA B*0803	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.482390	0.147675	-4.334715	30366.153138
HLA A*2601	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.395710	0.060842	-4.334868	24871.972433
HLA B*1509	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.481008	0.146138	-4.334870	30269.711428
HLA A*3002	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.570261	0.235291	-4.334970	37175.816599
HLA B*0702	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.426582	0.091584	-4.334999	26704.377619
HLA B*3901	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.471869	0.136752	-4.335117	29639.357427
HLA B*5401	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.557357	0.222188	-4.335169	36087.528952
HLA B*0801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.426559	0.091322	-4.335237	26702.932981
HLA A*2403	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.447570	0.112320	-4.335251	28026.599670
HLA A*2301	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.542440	0.207166	-4.335274	34869.062024
HLA A*3301	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.605061	0.269777	-4.335284	40277.368536
HLA B*2705	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.492556	0.157255	-4.335301	31085.367026
HLA A*6901	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.360980	0.025675	-4.335306	22960.436512
HLA A*3201	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.448982	0.113362	-4.335621	28117.872068
HLA A*0201	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.394040	0.058419	-4.335621	24776.487858
HLA B*1509	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.472433	0.136752	-4.335680	29677.865374
HLA A*3002	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.597324	0.261282	-4.336042	39566.190228
HLA A*6801	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.614186	0.278063	-4.336124	41132.630907
HLA B*5701	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.427543	0.091322	-4.336222	26763.530335
HLA B*4402	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.375582	0.039331	-4.336252	23745.547616
HLA A*3001	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.204544	-0.132020	-4.336564	16015.643036
HLA A*2603	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.639345	0.302627	-4.336718	43585.775136
HLA B*5701	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.402867	0.066046	-4.336820	25285.221300
HLA A*2403	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.402897	0.066046	-4.336851	25286.999636
HLA B*7301	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.522796	0.185815	-4.336981	33326.999957
HLA B*0803	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.449513	0.112320	-4.337194	28152.270985
HLA B*0803	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.439209	0.101982	-4.337226	27492.142924
HLA A*0202	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.559467	0.222188	-4.337279	36263.271612
HLA B*2705	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.474108	0.136752	-4.337356	29792.561412
HLA A*2301	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.530418	0.192958	-4.337460	33917.040522
HLA A*0202	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.483153	0.145582	-4.337571	30419.590296
HLA B*5401	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.533590	0.195916	-4.337674	34165.655307
HLA B*4002	1:508-516	9	NRVVLDITS	1.086398	-0.816621	-4.607519	0.269777	-4.337741	40505.933942
HLA A*6901	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.380960	0.043160	-4.337800	24041.422506
HLA B*0803	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.481130	0.143276	-4.337854	30278.227926
HLA A*3301	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.495145	0.157255	-4.337890	31271.242107
HLA A*0301	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.363586	0.025675	-4.337911	23098.603246
HLA B*5101	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.451283	0.113362	-4.337921	28267.187291
HLA B*3501	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.473882	0.135619	-4.338263	29777.092681
HLA A*0216	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.429867	0.091584	-4.338283	26907.109160
HLA B*4501	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.623833	0.285427	-4.338407	42056.533574
HLA A*3002	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.538528	0.200115	-4.338413	34556.390457
HLA B*4002	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.623859	0.285427	-4.338433	42059.036381
HLA A*2403	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.357999	0.019419	-4.338580	22803.349516
HLA B*4801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.430170	0.091584	-4.338586	26925.893532
HLA A*6801	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.624912	0.286262	-4.338650	42161.095565
HLA B*0801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.305936	-0.032788	-4.338725	20227.229673
HLA B*3801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.572709	0.233980	-4.338729	37385.972339
HLA B*3901	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.495989	0.157255	-4.338734	31332.034571
HLA A*2301	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.525244	0.186500	-4.338745	33515.398250
HLA A*2403	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.410214	0.071401	-4.338812	25716.602888
HLA B*1517	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.304750	-0.034103	-4.338853	20172.044420
HLA B*1517	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.421580	0.082695	-4.338885	26398.570310
HLA B*3501	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.419243	0.080331	-4.338911	26256.852801
HLA B*0802	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.452295	0.113362	-4.338934	28333.173723

HLA B*4402	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.420446	0.081144	-4.339302	26329.681508
HLA A*2603	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.625673	0.286262	-4.339411	42235.060509
HLA A*3301	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.624980	0.285427	-4.339553	42167.710602
HLA B*1501	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.347583	0.007934	-4.339650	22262.984139
HLA A*0250	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.551364	0.211398	-4.339965	35592.919231
HLA B*0802	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.486137	0.146138	-4.339999	30629.309511
HLA B*1509	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.483402	0.143276	-4.340126	30437.039359
HLA B*1501	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.388967	0.048624	-4.340343	24488.783161
HLA B*5101	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.488374	0.147675	-4.340699	30787.463939
HLA B*4001	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.412110	0.071401	-4.340708	25829.121369
HLA B*4801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.412166	0.071401	-4.340765	25832.475171
HLA B*1502	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.569036	0.228245	-4.340792	37071.182145
HLA B*3801	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.493583	0.152623	-4.340959	31158.943550
HLA A*8001	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.427792	0.086816	-4.340976	26778.882236
HLA A*3201	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.630959	0.289937	-4.341023	42752.297833
HLA A*2603	1:476-484	9	SSEDAMTAD	1.094329	-0.791004	-4.644387	0.303325	-4.341062	44094.738232
HLA B*1517	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.438950	0.097746	-4.341204	27475.787551
HLA B*4501	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.644032	0.302627	-4.341405	44058.732246
HLA A*0203	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.421785	0.080331	-4.341454	26410.997994
HLA A*2501	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.481379	0.139834	-4.341545	30295.595902
HLA A*2602	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.626975	0.285427	-4.341548	42361.832182
HLA B*4002	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.432975	0.091322	-4.341654	27100.381793
HLA B*3801	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.569332	0.227657	-4.341675	37096.460184
HLA B*1517	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.437160	0.095477	-4.341682	27362.756273
HLA B*1509	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.552670	0.210953	-4.341717	35700.140289
HLA B*0801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.402707	0.060842	-4.341865	25275.921274
HLA A*3002	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.488085	0.146138	-4.341947	30766.984271
HLA A*3002	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.553356	0.211398	-4.341958	35756.579925
HLA A*0202	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.483163	0.141148	-4.342014	30420.248569
HLA A*1101	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.444119	0.101982	-4.342137	27804.751415
HLA B*4601	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.403045	0.060842	-4.342203	25295.619496
HLA A*0212	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.403059	0.060842	-4.342218	25296.440589
HLA B*3801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.553231	0.210953	-4.342278	35746.329121
HLA A*3201	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.482174	0.139834	-4.342339	30351.043366
HLA A*6802	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.424616	0.082233	-4.342383	26583.731489
HLA A*0206	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.479650	0.137191	-4.342459	30175.208413
HLA B*3801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.569892	0.227420	-4.342472	37144.254628
HLA B*0801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.424787	0.082233	-4.342555	26594.232060
HLA A*8001	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.438057	0.095477	-4.342580	27419.362003
HLA A*1101	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.478304	0.135619	-4.342685	30081.814126
HLA B*7301	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.535648	0.192958	-4.342690	34327.952762
HLA A*2602	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.604060	0.261282	-4.342778	40184.651677
HLA A*3301	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.629101	0.286262	-4.342839	42569.742124
HLA B*3501	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.221747	-0.121106	-4.342853	16662.774219
HLA B*4601	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.421287	0.078424	-4.342863	26380.724677
HLA B*3901	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.469841	0.126963	-4.342878	29501.301665
HLA B*5701	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.421416	0.078424	-4.342992	26388.575268
HLA B*4403	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.629334	0.286262	-4.343071	42592.547691
HLA B*7301	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.438579	0.095477	-4.343101	27452.312313
HLA A*6901	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.391810	0.048624	-4.343186	24649.611715
HLA A*2602	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.551913	0.208642	-4.343271	35638.005339
HLA A*0203	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.425967	0.082695	-4.343272	26666.553887
HLA B*0802	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.478945	0.135619	-4.343326	30126.274773
HLA A*6801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.470821	0.126963	-4.343858	29567.929478
HLA A*2501	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.485071	0.141148	-4.343922	30554.173489
HLA B*1801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.479634	0.135619	-4.344015	30174.065723
HLA B*1501	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.426256	0.082233	-4.344023	26684.304154
HLA B*3801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.552919	0.208642	-4.344277	35720.618343
HLA B*7301	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.598769	0.254455	-4.344314	39698.049412
HLA B*0803	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.496957	0.152623	-4.344333	31401.947623
HLA A*0211	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.501602	0.157255	-4.344347	31739.604933
HLA B*5701	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.387522	0.043160	-4.344362	24407.442365
HLA A*2601	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.387536	0.043160	-4.344376	24408.234627
HLA A*2601	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.402860	0.058419	-4.344441	25284.810933
HLA A*0301	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.363886	0.019419	-4.344468	23114.603778

HLA B*2705	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.436081	0.091584	-4.344498	27294.895032
HLA A*0203	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.431333	0.086816	-4.344517	26998.094882
HLA A*8001	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.435868	0.091322	-4.344546	27281.461064
HLA B*1801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.492225	0.147675	-4.344550	31061.664325
HLA B*1517	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.490737	0.146138	-4.344599	30955.476824
HLA A*6901	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.383939	0.039331	-4.344609	24206.907342
HLA B*1801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.501891	0.157255	-4.344636	31760.732014
HLA B*0803	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.490378	0.145582	-4.344796	30929.865174
HLA A*3002	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.484655	0.139834	-4.344820	30524.930332
HLA A*0206	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.047749	-0.297084	-4.344833	11162.183284
HLA A*0219	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.444382	0.099536	-4.344846	27821.603629
HLA B*0803	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.502201	0.157255	-4.344946	31783.420623
HLA A*3301	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.540887	0.195916	-4.344971	34744.595140
HLA B*4002	1:455-463	9	RSVGVQGDG	0.714164	-0.427902	-4.631425	0.286262	-4.345162	42798.116837
HLA B*4001	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.401311	0.055954	-4.345358	25194.828120
HLA A*0101	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.388587	0.043160	-4.345426	24467.330544
HLA B*4601	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.416839	0.071401	-4.345438	26111.940430
HLA A*3201	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.443198	0.097746	-4.345452	27745.849009
HLA B*4601	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.411511	0.066046	-4.345464	25793.514101
HLA A*3301	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.426681	0.081144	-4.345537	26710.445953
HLA A*2601	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.382769	0.037065	-4.345704	24141.778685
HLA A*0203	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.437035	0.091322	-4.345714	27354.911835
HLA A*2403	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.401814	0.055954	-4.345860	25224.013473
HLA B*0702	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.424372	0.078424	-4.345948	26568.778931
HLA A*0101	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.371642	0.025675	-4.345968	23531.093165
HLA A*3002	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.493693	0.147675	-4.346018	31166.867180
HLA A*3001	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.210930	-0.135106	-4.346036	16252.878199
HLA B*5301	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.573728	0.227657	-4.346071	37473.853688
HLA B*4501	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.621439	0.275316	-4.346123	41825.327355
HLA B*4601	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.428380	0.082233	-4.346147	26815.124435
HLA B*0801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.378533	0.032127	-4.346406	23907.443761
HLA B*3801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.546531	0.200115	-4.346416	35199.031855
HLA A*2403	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.372100	0.025675	-4.346426	23555.929882
HLA A*0206	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.458782	0.112320	-4.346463	28759.554384
HLA B*4801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.428735	0.082233	-4.346502	26837.038479
HLA B*3901	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.489793	0.143276	-4.346517	30888.228765
HLA A*2403	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.429294	0.082695	-4.346599	26871.614859
HLA A*0250	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.489903	0.143276	-4.346627	30896.083553
HLA A*2902	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.442176	0.095477	-4.346698	27680.631422
HLA B*5101	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.501313	0.154429	-4.346884	31718.491905
HLA A*2602	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.636859	0.289937	-4.346922	43337.017442
HLA B*5101	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.428110	0.081144	-4.346966	26798.446935
HLA A*2601	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.386348	0.039331	-4.347017	24341.510797
HLA A*2501	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.484314	0.137191	-4.347123	30500.994930
HLA A*0206	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.554352	0.207166	-4.347186	35838.692256
HLA A*2601	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.395849	0.048624	-4.347225	24879.912422
HLA A*3201	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.581263	0.233980	-4.347283	38129.679535
HLA A*6802	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.434101	0.086816	-4.347284	27170.699081
HLA A*2603	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.601668	0.254355	-4.347313	39963.952348
HLA A*0250	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.572495	0.225172	-4.347323	37367.571758
HLA A*0206	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.495044	0.147675	-4.347369	31263.968473
HLA A*0212	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.434249	0.086816	-4.347432	27179.961059
HLA A*0212	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.438765	0.091322	-4.347443	27464.047424
HLA B*5301	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.601917	0.254355	-4.347562	39986.876179
HLA A*3301	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.538928	0.191274	-4.347654	34588.185937
HLA B*4002	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.638285	0.290570	-4.347715	43479.561573
HLA B*4001	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.413883	0.066046	-4.347837	25934.835290
HLA B*5801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.355800	0.007934	-4.347866	22688.173046
HLA B*4801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.414163	0.066046	-4.348117	25951.536911
HLA A*2402	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.582175	0.233980	-4.348195	38209.799200
HLA B*1801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.491494	0.143276	-4.348218	31009.447774
HLA A*3301	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.623556	0.275316	-4.348240	42029.694642
HLA B*1501	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.367662	0.019419	-4.348243	23316.431062
HLA A*2402	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.534844	0.186500	-4.348345	34264.498517
HLA B*0702	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.486135	0.137730	-4.348405	30629.143811

HLA B*5101	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.484166	0.135619	-4.348547	30490.601260
HLA B*4801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.429764	0.081144	-4.348620	26900.705086
HLA A*0250	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.534483	0.185815	-4.348668	34235.963866
HLA A*2602	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.494259	0.145582	-4.348677	31207.528521
HLA B*3901	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.486490	0.137730	-4.348760	30654.174774
HLA B*4801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.446678	0.097746	-4.348931	27969.042949
HLA B*0802	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.490232	0.141148	-4.349084	30919.492630
HLA B*4601	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.407530	0.058419	-4.349112	25558.213090
HLA B*4403	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.496971	0.147675	-4.349296	31402.966926
HLA A*2501	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.495476	0.146138	-4.349338	31295.104734
HLA B*0802	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.470125	0.120764	-4.349362	29520.619438
HLA A*0201	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.392571	0.043160	-4.349411	24692.855543
HLA A*0201	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.398057	0.048624	-4.349433	25006.756382
HLA B*4001	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.398062	0.048624	-4.349438	25007.026951
HLA B*4403	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.634979	0.285427	-4.349553	43149.863958
HLA A*3002	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.576985	0.227420	-4.349565	37755.892686
HLA A*2902	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.432271	0.082695	-4.349576	27056.434447
HLA A*2301	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.545570	0.195916	-4.349654	35121.235005
HLA B*7301	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.536207	0.186500	-4.349707	34372.180308
HLA A*2402	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.577974	0.228245	-4.349729	37841.982123
HLA A*6801	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.635167	0.285427	-4.349741	43168.542878
HLA B*0802	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.487627	0.137730	-4.349897	30734.544420
HLA B*4501	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.640491	0.290570	-4.349921	43700.994736
HLA B*5101	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.493289	0.143276	-4.350013	31137.879869
HLA A*6802	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.410881	0.060842	-4.350039	25756.144464
HLA A*3001	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.295098	-0.055017	-4.350115	19728.689214
HLA B*5101	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.495765	0.145582	-4.350183	31315.935939
HLA A*2402	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.572518	0.222188	-4.350330	37369.593357
HLA B*4002	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.648463	0.298081	-4.350382	44510.566861
HLA A*3002	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.442030	0.091584	-4.350447	27671.348531
HLA A*3301	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.578261	0.227657	-4.350603	37866.966320
HLA B*0702	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.433004	0.082233	-4.350771	27102.141171
HLA B*1509	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.550964	0.200115	-4.350849	35560.200142
HLA A*6802	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.376524	0.025675	-4.350850	23797.116305
HLA A*0101	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.388077	0.037065	-4.351012	24438.624073
HLA A*0212	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.433309	0.082233	-4.351076	27121.208420
HLA B*1502	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.612528	0.261282	-4.351246	40975.829321
HLA B*2705	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.463610	0.112320	-4.351291	29081.067487
HLA B*3501	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.442681	0.091322	-4.351360	27712.846220
HLA B*0702	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.465036	0.113627	-4.351410	29176.720942
HLA A*0203	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.412354	0.060842	-4.351512	25843.657657
HLA B*1503	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.504604	0.153079	-4.351525	31959.807776
HLA A*2402	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.586820	0.235291	-4.351529	38620.659640
HLA B*0802	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.478696	0.126963	-4.351734	30109.003866
HLA A*2403	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.403132	0.051389	-4.351743	25300.683323
HLA B*5101	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.478776	0.126963	-4.351814	30114.542512
HLA A*0219	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.443158	0.091322	-4.351836	27743.297393
HLA A*1101	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.434538	0.082695	-4.351843	27198.053068
HLA B*5801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.351166	-0.000735	-4.351901	22447.415300
HLA B*1501	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.417969	0.066046	-4.351923	26179.976272
HLA B*5401	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.559303	0.207166	-4.352136	36249.541592
HLA B*5401	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.505001	0.152623	-4.352378	31989.041071
HLA A*2402	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.543657	0.191274	-4.352384	34966.913426
HLA A*2602	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.587228	0.234640	-4.352588	38657.031182
HLA B*0802	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.489781	0.137191	-4.352590	30887.393267
HLA A*0201	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.389677	0.037065	-4.352612	24528.825306
HLA B*3901	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.444164	0.091322	-4.352842	27807.609553
HLA A*6801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.544195	0.191274	-4.352922	35010.259542
HLA B*4402	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.413853	0.060842	-4.353011	25933.011395
HLA B*4402	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.450810	0.097746	-4.353064	28236.466605
HLA A*2402	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.578268	0.225172	-4.353095	37867.580893
HLA B*4501	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.587085	0.233980	-4.353105	38644.276342
HLA B*4501	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.580819	0.227657	-4.353162	38090.713042
HLA A*3301	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.587421	0.233980	-4.353441	38674.183667
HLA A*3002	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.467586	0.113627	-4.353959	29348.484017

HLA A*0211	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.540650	0.186500	-4.354150	34725.615921
HLA A*6901	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.285289	-0.069030	-4.354319	19288.085901
HLA B*1509	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.561582	0.207166	-4.354415	36440.264393
HLA B*1502	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.581867	0.227420	-4.354447	38182.729681
HLA B*0802	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.466850	0.112320	-4.354531	29298.830418
HLA A*2501	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.492403	0.137730	-4.354673	31074.438003
HLA B*5101	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.511946	0.157255	-4.354692	32504.710261
HLA B*1502	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.498021	0.143276	-4.354745	31478.998116
HLA A*0301	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.354037	-0.000735	-4.354772	22596.304172
HLA A*0101	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.394214	0.039331	-4.354883	24786.408659
HLA B*4801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.441824	0.086816	-4.355007	27658.178161
HLA A*3301	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.644948	0.289937	-4.355012	44151.787993
HLA B*4501	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.589778	0.234640	-4.355137	38884.604751
HLA B*0702	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.450644	0.095477	-4.355166	28225.623000
HLA A*2602	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.589211	0.233980	-4.355232	38833.940688
HLA B*7301	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.476023	0.120764	-4.355259	29924.208599
HLA A*0206	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.435703	0.080331	-4.355372	27271.131743
HLA B*0702	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.454952	0.099536	-4.355416	28507.064083
HLA A*0201	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.394921	0.039331	-4.355590	24826.803148
HLA A*1101	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.469270	0.113627	-4.355644	29462.544644
HLA A*3301	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.564354	0.208642	-4.355712	36673.631062
HLA A*0219	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.427198	0.071401	-4.355797	26742.254999
HLA B*5701	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.414234	0.058419	-4.355815	25955.749101
HLA A*8001	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.447498	0.091584	-4.355914	28021.899819
HLA B*4403	1:379-387	9	FKDEVRAVG	0.983022	-0.680395	-4.658589	0.302627	-4.355962	45560.596938
HLA A*0202	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.286922	-0.069085	-4.356007	19360.743159
HLA A*2501	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.492861	0.136752	-4.356109	31107.236606
HLA B*3801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.542013	0.185815	-4.356198	34834.746848
HLA B*1801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.322171	-0.034103	-4.356275	20997.681655
HLA A*0206	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.508958	0.152623	-4.356334	32281.800872
HLA A*2402	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.451889	0.095477	-4.356411	28306.668804
HLA B*1509	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.510868	0.154429	-4.356439	32424.096672
HLA A*2501	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.483419	0.126963	-4.356456	30438.192008
HLA A*2601	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.353373	-0.003120	-4.356492	22561.735730
HLA B*4001	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.415131	0.058419	-4.356712	26009.444135
HLA A*6901	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.364704	0.007934	-4.356770	23158.161277
HLA A*6802	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.428206	0.071401	-4.356805	26804.391636
HLA B*4402	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.364814	0.007934	-4.356881	23164.050331
HLA B*1503	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.514329	0.157255	-4.357074	32683.508959
HLA B*0702	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.440057	0.082695	-4.357362	27545.886716
HLA A*0206	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.514620	0.157255	-4.357365	32705.441271
HLA B*3801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.543927	0.186500	-4.357428	34988.674413
HLA B*1502	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.557585	0.200115	-4.357470	36106.471186
HLA B*2705	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.423533	0.066046	-4.357486	26517.515360
HLA B*2705	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.495505	0.137730	-4.357775	31297.136437
HLA B*5101	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.499024	0.141148	-4.357876	31551.799369
HLA A*3002	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.409318	0.051389	-4.357930	25663.651245
HLA B*4001	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.453616	0.095477	-4.358138	28419.447791
HLA B*2705	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.471777	0.113627	-4.358151	29633.104607
HLA A*3101	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.383843	0.025675	-4.358168	24201.538713
HLA A*2601	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.357444	-0.000735	-4.358179	22774.254286
HLA A*0203	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.401777	0.043160	-4.358616	25221.830222
HLA B*4601	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.395818	0.037065	-4.358754	24878.162715
HLA B*5801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.355640	-0.003120	-4.358759	22679.828227
HLA A*3301	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.471101	0.112320	-4.358781	29586.970754
HLA B*5701	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.419846	0.060842	-4.359005	26293.384183
HLA A*0203	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.437489	0.078424	-4.359065	27383.488250
HLA B*0803	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.500269	0.141148	-4.359121	31642.395808
HLA A*3101	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.407815	0.048624	-4.359191	25574.948886
HLA B*5301	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.584397	0.225172	-4.359225	38405.848835
HLA A*3301	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.620551	0.261282	-4.359269	41739.884542
HLA A*0301	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.367333	0.007934	-4.359400	23298.778244
HLA B*1801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.499238	0.139834	-4.359404	31567.336141
HLA B*5401	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.559540	0.200115	-4.359425	36269.353710
HLA A*3301	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.499344	0.139834	-4.359509	31575.021987

HLA A*0101	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.378951	0.019419	-4.359533	23930.476768
HLA A*2501	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.513969	0.154429	-4.359540	32656.467585
HLA B*1502	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.545375	0.185815	-4.359560	35105.468380
HLA A*0250	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.552614	0.192958	-4.359656	35695.505378
HLA A*0211	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.514138	0.154429	-4.359709	32669.190150
HLA B*0802	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.451379	0.091584	-4.359795	28273.457803
HLA B*0801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.367763	0.007934	-4.359829	23321.855683
HLA B*3901	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.497100	0.137191	-4.359909	31412.312078
HLA A*3002	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.501108	0.141148	-4.359960	31703.566781
HLA B*4801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.442667	0.082695	-4.359972	27711.946694
HLA B*2705	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.442794	0.082695	-4.360099	27720.043478
HLA B*4501	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.595428	0.235291	-4.360138	39393.829444
HLA B*4403	1:337-345	9	TLYPDVVES	1.208014	-0.908915	-4.659278	0.299099	-4.360179	45632.872194
HLA A*6802	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.418714	0.058419	-4.360295	26224.911745
HLA A*3001	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.286370	-0.073933	-4.360302	19336.145022
HLA B*4402	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.403534	0.043160	-4.360374	25324.099588
HLA A*3002	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.588713	0.228245	-4.360469	38789.427709
HLA B*5401	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.547052	0.186500	-4.360553	35241.331125
HLA B*1501	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.305546	-0.055017	-4.360563	20209.072933
HLA B*7301	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.588932	0.228245	-4.360687	38808.948344
HLA B*4002	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.636086	0.275316	-4.360770	43259.952501
HLA B*4601	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.360127	-0.000735	-4.360862	22915.391286
HLA A*6802	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.439429	0.078424	-4.361006	27506.127047
HLA A*0203	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.443252	0.082233	-4.361019	27749.301569
HLA A*3201	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.615594	0.254455	-4.361139	41266.138368
HLA B*4501	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.659254	0.298081	-4.361174	45630.403573
HLA A*0206	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.488393	0.126963	-4.361430	30788.796422
HLA A*2602	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.616285	0.254455	-4.361830	41331.824690
HLA A*6801	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.572831	0.210953	-4.361877	37396.491025
HLA A*8001	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.394066	0.032127	-4.361939	24777.962320
HLA A*0250	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.590264	0.228245	-4.362019	38928.173952
HLA B*7301	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.453364	0.091322	-4.362043	28403.001723
HLA B*1501	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.399117	0.037065	-4.362052	25067.843859
HLA A*3001	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.293094	-0.069085	-4.362179	19637.858243
HLA A*6901	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.361445	-0.000735	-4.362180	22985.043945
HLA A*0212	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.428253	0.066046	-4.362207	26807.291969
HLA A*0201	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.387962	0.025675	-4.362287	24432.146630
HLA A*8001	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.440736	0.078424	-4.362312	27588.987236
HLA B*7301	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.553652	0.191274	-4.362378	35780.961565
HLA B*5101	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.418427	0.055954	-4.362474	26207.608844
HLA A*2501	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.498115	0.135619	-4.362496	31485.810768
HLA A*2501	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.453989	0.091322	-4.362668	28443.903932
HLA B*7301	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.573627	0.210953	-4.362674	37465.137338
HLA B*3501	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.395165	0.032127	-4.363038	24840.775344
HLA A*0203	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.233835	-0.129234	-4.363069	17133.078708
HLA A*0203	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.429320	0.066046	-4.363273	26873.214004
HLA B*4402	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.445992	0.082695	-4.363297	27924.895476
HLA B*5701	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.419567	0.055954	-4.363613	26276.462559
HLA A*1101	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.443945	0.080331	-4.363614	27793.622516
HLA B*1502	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.550158	0.186500	-4.363659	35494.276103
HLA B*4001	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.406849	0.043160	-4.363689	25518.147069
HLA B*0803	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.509827	0.146138	-4.363689	32346.482743
HLA A*0212	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.442141	0.078424	-4.363717	27678.385276
HLA B*3801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.575211	0.211398	-4.363812	37601.994525
HLA A*3201	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.591253	0.227420	-4.363833	39016.936376
HLA B*5101	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.510043	0.146138	-4.363905	32362.585911
HLA B*3501	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.461653	0.097746	-4.363907	28950.310315
HLA B*0803	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.499548	0.135619	-4.363929	31589.886596
HLA A*0216	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.450817	0.086816	-4.364001	28236.924877
HLA B*5401	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.521572	0.157255	-4.364317	33233.198321
HLA A*2403	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.442883	0.078424	-4.364460	27725.742634
HLA A*2902	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.446760	0.082233	-4.364527	27974.339280
HLA B*4403	1:195-203	9	FLHDFAGLG	0.857921	-0.567351	-4.655159	0.290570	-4.364589	45202.156804
HLA A*3201	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.589771	0.225172	-4.364598	38883.973672
HLA B*1502	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.571943	0.207166	-4.364777	37320.095655

HLA A*3201	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.189653	-0.175217	-4.364870	15475.808410
HLA A*3101	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.404213	0.039331	-4.364882	25363.723721
HLA B*3501	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.436382	0.071401	-4.364981	27313.802359
HLA B*4002	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.646522	0.281539	-4.364983	44312.112082
HLA A*3101	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.397132	0.032127	-4.365005	24953.511339
HLA A*0203	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.423526	0.058419	-4.365107	26517.084993
HLA A*2602	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.576567	0.211398	-4.365168	37719.552762
HLA B*1502	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.599211	0.233980	-4.365231	39738.445216
HLA A*0219	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.467254	0.101982	-4.365272	29326.105694
HLA B*1801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.446537	0.081144	-4.365393	27959.965857
HLA B*2705	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.463209	0.097746	-4.365462	29054.177291
HLA B*0702	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.416860	0.051389	-4.365471	26113.211825
HLA B*4001	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.426364	0.060842	-4.365522	26690.945500
HLA B*4801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.416971	0.051389	-4.365582	26119.852340
HLA B*0702	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.437035	0.071401	-4.365634	27354.911835
HLA A*1101	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.426514	0.060842	-4.365673	26700.188383
HLA A*3101	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.402810	0.037065	-4.365746	25281.938547
HLA B*7301	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.577180	0.211398	-4.365781	37772.849674
HLA A*3002	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.465368	0.099536	-4.365831	29198.985271
HLA A*2601	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.391512	0.025675	-4.365837	24632.681869
HLA A*8001	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.424416	0.058419	-4.365997	26571.510020
HLA B*1502	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.557388	0.191274	-4.366114	36090.067026
HLA B*1502	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.577133	0.210953	-4.366179	37768.762957
HLA A*2902	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.457629	0.091322	-4.366307	28683.263027
HLA A*2301	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.511895	0.145582	-4.366312	32500.841859
HLA A*0206	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.520783	0.154429	-4.366354	33172.844451
HLA A*8001	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.446689	0.080331	-4.366358	27969.799506
HLA A*0211	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.479834	0.113362	-4.366472	30187.944174
HLA B*3901	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.424961	0.058419	-4.366542	26604.880708
HLA A*2403	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.448877	0.082233	-4.366644	28111.027745
HLA B*1517	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.453587	0.086816	-4.366771	28417.602898
HLA A*6801	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.552590	0.185815	-4.366775	35693.574343
HLA A*2602	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.589094	0.222188	-4.366906	38823.437743
HLA B*0801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.445458	0.078424	-4.367035	27890.623501
HLA B*0803	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.462600	0.095477	-4.367123	29013.496210
HLA B*4403	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.601979	0.234640	-4.367338	39992.501013
HLA B*5301	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.601986	0.234640	-4.367345	39993.150083
HLA A*0203	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.438772	0.071401	-4.367370	27464.493160
HLA B*0802	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.433650	0.066046	-4.367603	27142.491563
HLA A*3101	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.423942	0.055954	-4.367988	26542.488598
HLA B*3801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.514253	0.146138	-4.368115	32677.851396
HLA A*1101	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.465993	0.097746	-4.368246	29241.033749
HLA B*5401	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.506131	0.137730	-4.368401	32072.389965
HLA A*2402	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.554326	0.185815	-4.368511	35836.559603
HLA A*0202	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.579496	0.210953	-4.368543	37974.874082
HLA A*0250	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.590790	0.222188	-4.368602	38975.376298
HLA B*5401	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.482033	0.113362	-4.368671	30341.193218
HLA B*2705	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.495693	0.126963	-4.368730	31310.684491
HLA A*0101	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.376708	0.007934	-4.368774	23807.160125
HLA A*6802	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.400919	0.032127	-4.368792	25172.076094
HLA B*4501	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.516636	0.147675	-4.368961	32857.602492
HLA B*4402	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.440571	0.071401	-4.369170	27578.541479
HLA B*3901	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.464762	0.095477	-4.369284	29158.259175
HLA A*0212	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.440696	0.071401	-4.369295	27586.450046
HLA B*5401	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.522434	0.153079	-4.369356	33299.246032
HLA A*3201	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.580323	0.210953	-4.369370	38047.257810
HLA A*1101	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.464884	0.095477	-4.369406	29166.462962
HLA B*4601	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.401556	0.032127	-4.369429	25209.007436
HLA B*0802	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.483118	0.113627	-4.369492	30417.121897
HLA B*4501	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.623904	0.254355	-4.369549	42063.359763
HLA B*4001	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.395233	0.025675	-4.369559	24844.672839
HLA B*3501	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.465173	0.095477	-4.369695	29185.877263
HLA A*2402	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.565620	0.195916	-4.369704	36780.724875
HLA B*1502	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.624379	0.254455	-4.369924	42109.351628
HLA A*2403	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.418622	0.048624	-4.369999	26219.379248

HLA B*5701	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.421418	0.051389	-4.370029	26388.718028
HLA A*2402	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.580988	0.210953	-4.370035	38105.552723
HLA A*2301	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.497025	0.126963	-4.370062	31406.874560
HLA B*5301	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.522773	0.152623	-4.370149	33325.197052
HLA B*1801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.511411	0.141148	-4.370262	32464.641889
HLA A*2601	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.389728	0.019419	-4.370310	24531.744841
HLA B*3501	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.431371	0.060842	-4.370529	27000.431890
HLA A*2602	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.598264	0.227657	-4.370607	39651.902415
HLA B*1801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.497840	0.126963	-4.370877	31465.887909
HLA A*3101	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.414241	0.043160	-4.371080	25956.170358
HLA B*1502	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.582485	0.211398	-4.371086	38237.094768
HLA B*3901	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.511063	0.139834	-4.371229	32438.659035
HLA B*0802	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.452420	0.081144	-4.371276	28341.298692
HLA A*0301	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.368228	-0.003120	-4.371348	23346.850461
HLA A*2402	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.498373	0.126963	-4.371411	31504.553167
HLA B*1801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.517646	0.146138	-4.371508	32934.126539
HLA B*0702	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.429933	0.058419	-4.371514	26911.185274
HLA A*6802	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.242303	-0.129234	-4.371537	17470.404236
HLA A*2603	1:354-362	9	IKSHHNVGG	0.800003	-0.514576	-4.656992	0.285427	-4.371565	45393.299957
HLA B*4501	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.653282	0.281539	-4.371743	45007.192088
HLA A*2602	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.582901	0.210953	-4.371947	38273.726248
HLA A*2603	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.661902	0.289937	-4.371966	45909.459467
HLA B*1801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.526447	0.154429	-4.372018	33608.360006
HLA A*1101	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.509822	0.137730	-4.372092	32346.132763
HLA A*2501	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.467574	0.095477	-4.372096	29347.690167
HLA B*4402	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.438461	0.066046	-4.372415	27444.887619
HLA B*0801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.398217	0.025675	-4.372543	25015.957372
HLA B*5401	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.527039	0.154429	-4.372610	33654.209262
HLA B*1503	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.510541	0.137730	-4.372811	32399.723740
HLA A*0212	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.431232	0.058419	-4.372813	26991.815174
HLA B*0702	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.453317	0.080331	-4.372986	28399.928748
HLA B*5301	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.459818	0.086816	-4.373002	28828.249723
HLA B*4403	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.600698	0.227657	-4.373041	39874.761196
HLA A*6801	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.584562	0.211398	-4.373163	38420.395586
HLA B*4403	1:43-51	9	VIPHTASIE	0.972611	-0.674530	-4.671357	0.298081	-4.373276	46919.838340
HLA B*5701	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.421959	0.048624	-4.373335	26421.573273
HLA B*4501	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.595687	0.222188	-4.373499	39417.279208
HLA A*2402	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.573703	0.200115	-4.373587	37471.623731
HLA B*4403	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.648952	0.275316	-4.373636	44560.680876
HLA B*0803	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.510396	0.136752	-4.373643	32388.858270
HLA B*4601	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.422269	0.048624	-4.373645	26440.447799
HLA A*2301	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.510978	0.137191	-4.373788	32432.342026
HLA A*2603	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.602211	0.228245	-4.373966	40013.925894
HLA B*1509	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.511286	0.137191	-4.374095	32455.334827
HLA B*0702	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.430111	0.055954	-4.374158	26922.252126
HLA A*2902	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.417365	0.043160	-4.374205	26143.602456
HLA B*4601	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.382205	0.007934	-4.374272	24110.453981
HLA B*0803	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.514141	0.139834	-4.374306	32669.366887
HLA A*3001	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.305391	-0.069030	-4.374421	20201.858518
HLA A*2402	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.585826	0.211398	-4.374427	38532.381820
HLA A*6802	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.411536	0.037065	-4.374472	25795.049087
HLA A*0201	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.393908	0.019419	-4.374489	24768.982864
HLA B*3801	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.565768	0.191274	-4.374495	36793.262729
HLA B*3801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.581714	0.207166	-4.374548	38169.305360
HLA A*0250	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.486910	0.112320	-4.374591	30683.873740
HLA A*2501	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.461416	0.086816	-4.374600	28934.496221
HLA A*3201	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.527281	0.152623	-4.374658	33672.967238
HLA B*7301	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.602110	0.227420	-4.374690	40004.618728
HLA B*7301	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.515882	0.141148	-4.374733	32800.592336
HLA B*0802	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.474418	0.099536	-4.374882	29813.844038
HLA B*7301	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.512780	0.137730	-4.375050	32567.195886
HLA B*0803	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.512517	0.137191	-4.375326	32547.469152
HLA A*2501	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.431347	0.055954	-4.375393	26998.971236
HLA A*2902	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.433983	0.058419	-4.375565	27163.350551
HLA B*4002	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.603261	0.227657	-4.375604	40110.805479

HLA B*3901	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.458303	0.082695	-4.375608	28727.832347
HLA B*1801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.431925	0.055954	-4.375971	27034.926270
HLA A*0206	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.517303	0.141148	-4.376155	32908.123993
HLA B*1503	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.467912	0.091584	-4.376328	29370.561631
HLA B*5701	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.413407	0.037065	-4.376342	25906.369093
HLA A*0250	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.529450	0.153079	-4.376371	33841.527887
HLA B*0802	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.413458	0.037065	-4.376393	25909.452590
HLA B*3501	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.342306	-0.034103	-4.376410	21994.112066
HLA A*2601	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.343747	-0.032788	-4.376535	22067.171380
HLA B*3801	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.569795	0.192958	-4.376837	37136.016743
HLA A*2902	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.463686	0.086816	-4.376869	29086.102334
HLA A*0206	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.514761	0.137730	-4.377031	32716.058962
HLA B*4402	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.414201	0.037065	-4.377136	25953.783327
HLA B*5401	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.490850	0.113627	-4.377224	30963.516222
HLA B*1509	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.498042	0.120764	-4.377278	31480.530834
HLA A*8001	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.343343	-0.034103	-4.377446	22046.647407
HLA B*5701	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.409697	0.032127	-4.377570	25686.013821
HLA B*0803	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.458761	0.081144	-4.377617	28758.154144
HLA B*4002	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.650162	0.272539	-4.377623	44685.004180
HLA A*0219	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.414750	0.037065	-4.377686	25986.659391
HLA B*0803	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.504700	0.126963	-4.377738	31966.897422
HLA B*4801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.436206	0.058419	-4.377787	27302.722259
HLA A*8001	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.443992	0.066046	-4.377946	27796.629887
HLA B*5101	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.490397	0.112320	-4.378077	30931.203820
HLA A*3001	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.299076	-0.079025	-4.378101	19910.213156
HLA B*1503	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.505076	0.126963	-4.378114	31994.579380
HLA B*0803	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.429519	0.051389	-4.378130	26885.574240
HLA A*0202	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.473701	0.095477	-4.378224	29764.691275
HLA A*2902	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.449680	0.071401	-4.378279	28163.086409
HLA B*0801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.377810	-0.000735	-4.378544	23867.641251
HLA B*7301	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.574485	0.195916	-4.378569	37539.189444
HLA A*8001	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.434841	0.055954	-4.378887	27217.040553
HLA A*2403	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.415965	0.037065	-4.378900	26059.443547
HLA A*3301	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.579109	0.200115	-4.378994	37940.991630
HLA B*1801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.445129	0.066046	-4.379083	27869.507573
HLA A*0219	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.461421	0.082233	-4.379188	28934.809287
HLA A*0203	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.204004	-0.175217	-4.379221	15995.727572
HLA A*0202	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.586437	0.207166	-4.379271	38586.618492
HLA A*2301	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.526976	0.147675	-4.379301	33649.293851
HLA B*1509	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.575272	0.195916	-4.379356	37607.283885
HLA A*6801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.517148	0.137730	-4.379418	32896.376157
HLA A*2603	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.575476	0.195916	-4.379560	37624.988309
HLA A*2501	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.493101	0.113362	-4.379740	31124.406587
HLA B*4601	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.405430	0.025675	-4.379756	25434.900740
HLA B*5301	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.565721	0.185815	-4.379906	36789.281995
HLA B*5801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.345918	-0.034103	-4.380021	22177.755539
HLA A*6801	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.607462	0.227420	-4.380042	40500.675100
HLA B*5401	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.431458	0.051389	-4.380069	27005.836997
HLA A*2501	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.493731	0.113627	-4.380104	31169.565045
HLA A*0219	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.446386	0.066046	-4.380340	27950.286872
HLA A*2603	1:193-201	9	SRFLHDFAG	0.701505	-0.423442	-4.658458	0.278063	-4.380395	45546.796273
HLA B*7301	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.419868	0.039331	-4.380537	26294.664413
HLA B*5301	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.571924	0.191274	-4.380650	37318.480509
HLA A*0216	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.480238	0.099536	-4.380701	30216.047157
HLA B*4002	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.635163	0.254455	-4.380708	43168.075806
HLA B*4403	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.616134	0.235291	-4.380844	41317.516730
HLA A*1101	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.446938	0.066046	-4.380892	27985.843338
HLA A*2301	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.538176	0.157255	-4.380921	34528.359895
HLA A*3002	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.589811	0.208642	-4.381168	38887.549923
HLA A*8001	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.463873	0.082695	-4.381178	29098.693265
HLA B*4002	1:167-175	9	EAFDRRLAG	0.903409	-0.668118	-4.616545	0.235291	-4.381255	41356.651809
HLA A*0219	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.468103	0.086816	-4.381286	29383.434661
HLA A*0212	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.424501	0.043160	-4.381340	26576.685486
HLA A*3301	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.635860	0.254455	-4.381405	43237.491306
HLA A*0206	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.464266	0.082695	-4.381571	29124.994402

HLA A*3301	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.609004	0.227420	-4.381584	40644.662778
HLA B*5101	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.477080	0.095477	-4.381602	29997.146338
HLA A*0250	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.592557	0.210953	-4.381604	39134.260322
HLA B*1502	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.527234	0.145582	-4.381652	33669.324095
HLA B*3501	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.424867	0.043160	-4.381707	26599.124153
HLA A*0202	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.529537	0.147675	-4.381862	33848.302485
HLA B*0802	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.464099	0.082233	-4.381866	29113.809578
HLA B*4601	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.421280	0.039331	-4.381949	26380.296530
HLA A*0250	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.589256	0.207166	-4.382090	38837.932553
HLA B*4501	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.654645	0.272539	-4.382106	45148.634550
HLA A*2403	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.414262	0.032127	-4.382135	25957.434168
HLA A*2402	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.575225	0.192958	-4.382267	37603.215080
HLA B*4001	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.401748	0.019419	-4.382330	25220.192907
HLA B*1509	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.573778	0.191274	-4.382504	37478.111247
HLA A*0219	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.421851	0.039331	-4.382520	26414.998953
HLA A*0201	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.390457	0.007934	-4.382523	24572.920705
HLA B*1517	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.419597	0.037065	-4.382533	26278.310610
HLA B*4402	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.441076	0.058419	-4.382658	27610.637464
HLA B*4002	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.637023	0.254355	-4.382668	43353.431942
HLA B*5701	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.402113	0.019419	-4.382694	25241.349736
HLA A*2501	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.464933	0.082233	-4.382701	29169.776685
HLA A*2301	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.478201	0.095477	-4.382723	30074.654450
HLA B*1801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.313727	-0.069030	-4.382757	20593.364097
HLA B*4402	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.414985	0.032127	-4.382859	26000.721689
HLA A*2602	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.530535	0.147675	-4.382861	33926.216135
HLA B*3801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.524044	0.141148	-4.382895	33422.874443
HLA A*3201	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.605287	0.222188	-4.383099	40298.291994
HLA A*0201	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.415263	0.032127	-4.383136	26017.324989
HLA A*3201	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.444164	0.060842	-4.383322	27807.609553
HLA A*0219	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.439335	0.055954	-4.383382	27500.175487
HLA B*4403	1:323-331	9	DVLDGKTAE	0.971511	-0.689972	-4.664945	0.281539	-4.383406	46232.221538
HLA A*2501	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.449537	0.066046	-4.383491	28153.794033
HLA A*0212	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.382870	-0.000735	-4.383605	24147.395325
HLA A*0211	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.497525	0.113627	-4.383899	31443.085762
HLA A*8001	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.421009	0.037065	-4.383945	26363.889469
HLA A*0212	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.421080	0.037065	-4.384015	26368.168588
HLA A*0203	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.383293	-0.000735	-4.384028	24170.921029
HLA B*3801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.538467	0.154429	-4.384038	34551.530197
HLA B*0801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.349975	-0.034103	-4.384079	22385.930579
HLA B*4601	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.403501	0.019419	-4.384082	25322.181653
HLA B*0803	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.497497	0.113362	-4.384135	31441.044584
HLA B*4801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.432799	0.048624	-4.384175	27089.388269
HLA A*2902	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.383453	-0.000735	-4.384188	24179.814481
HLA B*3901	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.496592	0.112320	-4.384273	31375.627096
HLA A*3001	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.271035	-0.113369	-4.384404	18665.292757
HLA A*3201	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.612126	0.227657	-4.384469	40937.940476
HLA B*1801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.482300	0.097746	-4.384554	30359.911234
HLA B*0802	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.471408	0.086816	-4.384592	29607.946338
HLA B*3801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.486772	0.101982	-4.384789	30674.081518
HLA A*1101	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.456292	0.071401	-4.384891	28595.105189
HLA A*2301	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.539409	0.154429	-4.384980	34626.566457
HLA A*6802	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.428222	0.043160	-4.385062	26805.406717
HLA A*6801	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.646365	0.261282	-4.385083	44296.053510
HLA B*4501	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.639650	0.254455	-4.385195	43616.439165
HLA B*5301	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.607418	0.222188	-4.385230	40496.512335
HLA B*1509	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.538355	0.153079	-4.385276	34542.559204
HLA A*3301	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.620034	0.234640	-4.385394	41690.236301
HLA B*1503	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.522719	0.137191	-4.385528	33321.050741
HLA A*0301	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.352757	-0.032788	-4.385545	22529.779582
HLA B*1801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.497878	0.112320	-4.385558	31468.611658
HLA A*0211	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.521215	0.135619	-4.385596	33205.881791
HLA A*0212	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.411370	0.025675	-4.385695	25785.143056
HLA B*2705	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.477122	0.091322	-4.385801	30000.067542
HLA B*3901	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.499466	0.113627	-4.385839	31583.905739
HLA A*0211	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.533648	0.147675	-4.385974	34170.276430

HLA B*3501	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.468229	0.082233	-4.385997	29392.019816
HLA B*1502	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.611179	0.225172	-4.386007	40848.785402
HLA A*3001	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.306012	-0.080273	-4.386285	20230.731642
HLA A*0216	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.488315	0.101982	-4.386333	30783.300302
HLA B*5701	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.425704	0.039331	-4.386373	26650.401314
HLA A*2902	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.442329	0.055954	-4.386375	27690.366828
HLA B*1501	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.412239	0.025675	-4.386564	25836.807810
HLA B*1503	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.385939	-0.000735	-4.386673	24318.608409
HLA B*0702	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.426030	0.039331	-4.386700	26670.449276
HLA A*2603	1:505-513	9	AEVNRVVLD	0.992362	-0.731080	-4.648108	0.261282	-4.386826	44474.221326
HLA A*0250	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.582929	0.195916	-4.387013	38276.211008
HLA A*8001	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.426470	0.039331	-4.387139	26697.444068
HLA B*3801	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.583084	0.195916	-4.387168	38289.880072
HLA B*2705	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.468323	0.081144	-4.387179	29398.380807
HLA A*0212	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.435818	0.048624	-4.387194	27278.361857
HLA A*0216	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.443276	0.055954	-4.387322	27750.802816
HLA A*2301	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.540023	0.152623	-4.387399	34675.493047
HLA B*4601	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.313575	-0.073933	-4.387507	20586.123862
HLA A*2501	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.439007	0.051389	-4.387618	27479.355166
HLA A*0206	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.501343	0.113627	-4.387717	31720.722700
HLA A*2902	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.466228	0.078424	-4.387804	29256.857104
HLA A*0206	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.534022	0.146138	-4.387884	34199.681403
HLA B*4002	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.616294	0.228245	-4.388049	41332.719102
HLA A*3301	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.613249	0.225172	-4.388077	41043.939997
HLA B*4002	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.610425	0.222188	-4.388237	40777.910004
HLA B*1517	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.468594	0.080331	-4.388262	29416.676325
HLA A*0211	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.529471	0.141148	-4.388323	33843.175637
HLA A*2402	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.595604	0.207166	-4.388438	39409.816405
HLA A*0216	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.479824	0.091322	-4.388503	30187.290927
HLA B*0803	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.471202	0.082695	-4.388507	29593.854231
HLA A*2403	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.431782	0.043160	-4.388621	27026.006129
HLA B*3901	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.469773	0.081144	-4.388629	29496.673664
HLA A*2301	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.541710	0.153079	-4.388631	34810.445006
HLA B*0803	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.526424	0.137730	-4.388694	33606.541880
HLA A*6901	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.385680	-0.003120	-4.388800	24304.141007
HLA A*2601	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.396749	0.007934	-4.388815	24931.516734
HLA A*0101	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.354759	-0.034103	-4.388862	22633.864108
HLA B*4801	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.426014	0.037065	-4.388949	26669.439305
HLA B*2705	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.488505	0.099536	-4.388969	30796.792531
HLA B*5301	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.597693	0.208642	-4.389051	39599.810150
HLA A*0203	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.421334	0.032127	-4.389207	26383.579167
HLA A*2902	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.450143	0.060842	-4.389301	28193.117167
HLA B*1501	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.257293	-0.132020	-4.389312	18083.923795
HLA A*2602	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.527079	0.137730	-4.389349	33657.304519
HLA A*3101	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.397468	0.007934	-4.389534	24972.823197
HLA B*4002	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.623559	0.233980	-4.389579	42029.922018
HLA B*1501	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.428946	0.039331	-4.389615	26850.108347
HLA B*7301	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.537485	0.147675	-4.389810	34473.485934
HLA B*1517	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.455862	0.066046	-4.389815	28566.809765
HLA B*1517	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.489372	0.099536	-4.389836	30858.332004
HLA A*0202	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.576456	0.186500	-4.389956	37709.963227
HLA A*2603	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.598717	0.208642	-4.390075	39693.324928
HLA A*3301	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.601509	0.211398	-4.390110	39949.253414
HLA B*0802	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.485637	0.095477	-4.390159	30594.035490
HLA A*0301	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.356131	-0.034103	-4.390234	22705.486059
HLA A*8001	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.451078	0.060842	-4.390236	28253.886177
HLA B*3801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.537972	0.147675	-4.390297	34512.112589
HLA B*4001	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.389844	-0.000735	-4.390578	24538.248690
HLA B*1517	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.481920	0.091322	-4.390598	30333.315402
HLA A*2902	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.427792	0.037065	-4.390728	26778.882236
HLA B*4501	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.619005	0.228245	-4.390761	41591.566921
HLA B*0803	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.511761	0.120764	-4.390997	32490.821325
HLA A*2301	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.534382	0.143276	-4.391105	34228.000643
HLA B*1502	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.599897	0.208642	-4.391255	39801.269154
HLA A*2301	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.537412	0.146138	-4.391274	34467.704988

HLA A*0206	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.526917	0.135619	-4.391298	33644.743185
HLA A*0219	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.452157	0.060842	-4.391315	28324.131686
HLA B*1517	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.447453	0.055954	-4.391499	28019.019655
HLA B*5101	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.311514	-0.080273	-4.391787	20488.684888
HLA B*0702	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.357794	-0.034103	-4.391898	22792.619409
HLA A*0202	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.527559	0.135619	-4.391939	33694.469809
HLA B*5801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.359164	-0.032788	-4.391952	22864.620025
HLA B*1517	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.443426	0.051389	-4.392037	27760.412721
HLA A*2602	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.619701	0.227420	-4.392281	41658.221982
HLA A*0202	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.546792	0.154429	-4.392363	35220.175140
HLA B*1509	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.411940	0.019419	-4.392522	25819.062575
HLA B*3901	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.479357	0.086816	-4.392540	30154.809745
HLA A*2402	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.549797	0.157255	-4.392542	35464.717322
HLA A*0216	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.453395	0.060842	-4.392553	28404.999336
HLA B*1502	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.448764	0.055954	-4.392810	28103.728971
HLA B*1503	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.444229	0.051389	-4.392841	27811.822083
HLA A*6801	1:430-438	9	VREELTAAG	0.822860	-0.547544	-4.668218	0.275316	-4.392902	46581.942519
HLA B*5401	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.538636	0.145582	-4.393054	34564.991054
HLA B*1517	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.453921	0.060842	-4.393079	28439.441809
HLA A*0203	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.418895	0.025675	-4.393220	26235.838309
HLA B*0802	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.484784	0.091322	-4.393462	30534.014190
HLA B*3901	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.473922	0.080331	-4.393591	29779.831350
HLA A*0202	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.530355	0.136752	-4.393602	33912.086724
HLA B*1509	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.539205	0.145582	-4.393623	34610.272939
HLA B*3901	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.493183	0.099536	-4.393647	31130.300430
HLA A*0203	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.413082	0.019419	-4.393663	25887.035530
HLA A*0219	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.452135	0.058419	-4.393717	28322.752646
HLA B*5301	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.605150	0.211398	-4.393752	40285.649439
HLA A*2603	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.628500	0.234640	-4.393859	42510.826748
HLA A*3201	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.589869	0.195916	-4.393953	38892.809712
HLA A*0219	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.437212	0.043160	-4.394051	27366.013115
HLA A*3301	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.496090	0.101982	-4.394107	31339.324041
HLA A*6801	1:461-469	9	GDGRTYGHP	0.549544	-0.259607	-4.684135	0.289937	-4.394199	48320.937985
HLA B*1801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.465647	0.071401	-4.394246	29217.788953
HLA B*5101	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.485656	0.091322	-4.394334	30595.359601
HLA A*6801	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.594465	0.200115	-4.394350	39306.548614
HLA B*4801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.437773	0.043160	-4.394613	27401.419256
HLA B*0802	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.492399	0.097746	-4.394652	31074.101786
HLA B*2705	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.426839	0.032127	-4.394712	26720.129244
HLA A*3001	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.265659	-0.129234	-4.394893	18435.680983
HLA B*3801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.530639	0.135619	-4.395020	33934.292727
HLA A*2301	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.536179	0.141148	-4.395030	34369.948984
HLA A*0203	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.432097	0.037065	-4.395032	27045.605063
HLA A*0101	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.392022	-0.003120	-4.395141	24661.616287
HLA B*1502	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.617396	0.222188	-4.395208	41437.723202
HLA A*3201	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.516004	0.120764	-4.395240	32809.820907
HLA A*3201	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.581082	0.185815	-4.395267	38113.799487
HLA B*4403	1:515-523	9	TSKPPATIE	0.921461	-0.667106	-4.649628	0.254355	-4.395273	44630.162673
HLA A*2501	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.486868	0.091584	-4.395284	30680.885951
HLA B*5701	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.421458	0.025675	-4.395784	26391.145060
HLA A*0216	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.098827	-0.297084	-4.395911	12555.295923
HLA A*8001	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.421630	0.025675	-4.395955	26401.569560
HLA B*4403	1:453-461	9	DVRSVGVQG	0.867050	-0.594511	-4.668551	0.272539	-4.396012	46617.740714
HLA A*0201	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.395301	-0.000735	-4.396036	24848.570946
HLA B*1503	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.439359	0.043160	-4.396199	27501.663256
HLA B*2705	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.474707	0.078424	-4.396283	29833.689259
HLA A*2501	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.395555	-0.000735	-4.396290	24863.093414
HLA A*0203	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.363508	-0.032788	-4.396296	23094.479905
HLA B*2705	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.467738	0.071401	-4.396337	29358.806014
HLA A*3002	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.603785	0.207166	-4.396619	40159.224567
HLA A*2402	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.542426	0.145582	-4.396844	34867.930216
HLA A*0202	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.549970	0.153079	-4.396892	35478.917819
HLA A*0203	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.404831	0.007934	-4.396897	25399.836933
HLA A*6802	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.445569	0.048624	-4.396945	27897.716006
HLA A*2501	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.477362	0.080331	-4.397031	30016.626408

HLA A*0216	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.436481	0.039331	-4.397150	27320.009179
HLA A*0211	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.524204	0.126963	-4.397241	33435.172060
HLA B*4403	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.625488	0.228245	-4.397243	42217.013893
HLA B*4501	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.608259	0.210953	-4.397305	40575.019563
HLA B*7301	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.605961	0.208642	-4.397319	40360.909259
HLA B*0702	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.445977	0.048624	-4.397354	27923.989067
HLA B*5401	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.524403	0.126963	-4.397441	33450.550444
HLA B*3801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.550628	0.153079	-4.397550	35532.700906
HLA B*1801	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.477914	0.080331	-4.397583	30054.811532
HLA B*1509	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.554932	0.157255	-4.397678	35886.613454
HLA B*4403	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.608679	0.210953	-4.397726	40614.330231
HLA A*8001	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.469289	0.071401	-4.397888	29463.819785
HLA A*3002	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.584414	0.186500	-4.397914	38407.303262
HLA A*0212	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.437399	0.039331	-4.398069	27377.859446
HLA B*0802	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.449497	0.051389	-4.398108	28151.204901
HLA A*2501	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.417535	0.019419	-4.398116	26153.787687
HLA A*3301	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.324227	-0.073933	-4.398160	21097.313018
HLA A*0219	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.476706	0.078424	-4.398283	29971.354715
HLA B*1503	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.194357	-0.203931	-4.398288	15644.331627
HLA A*0216	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.480548	0.082233	-4.398315	30237.632304
HLA A*0201	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.395273	-0.003120	-4.398393	24846.957862
HLA B*3801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.519194	0.120764	-4.398431	33051.750098
HLA A*0219	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.430760	0.032127	-4.398633	26962.480558
HLA B*0802	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.481363	0.082695	-4.398668	30294.448653
HLA B*4402	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.450136	0.051389	-4.398747	28192.659605
HLA A*6901	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.364718	-0.034103	-4.398822	23158.912988
HLA B*3901	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.490437	0.091584	-4.398853	30934.048635
HLA A*0216	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.442183	0.043160	-4.399023	27681.080673
HLA B*1502	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.546716	0.147675	-4.399042	35214.078476
HLA A*6901	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.366309	-0.032788	-4.399097	23243.887905
HLA B*3501	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.477578	0.078424	-4.399154	30031.569696
HLA A*0211	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.545490	0.146138	-4.399352	35114.775532
HLA A*3301	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.552017	0.152623	-4.399393	35646.489446
HLA A*1101	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.478022	0.078424	-4.399598	30062.291750
HLA B*7301	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.419062	0.019419	-4.399643	26245.917486
HLA A*0211	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.482425	0.082695	-4.399730	30368.617401
HLA B*0702	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.460702	0.060842	-4.399860	28886.949474
HLA A*0216	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.471272	0.071401	-4.399871	29598.657604
HLA B*4801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.419374	0.019419	-4.399955	26264.808619
HLA B*4501	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.344994	-0.055017	-4.400011	22130.653803
HLA B*3801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.545800	0.145582	-4.400218	35139.860137
HLA B*3901	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.497995	0.097746	-4.400249	31477.124895
HLA B*7301	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.545887	0.145582	-4.400305	35146.894642
HLA A*6801	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.654880	0.254455	-4.400425	45173.066068
HLA A*0202	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.461367	0.060842	-4.400525	28931.209227
HLA A*0212	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.419950	0.019419	-4.400531	26299.643677
HLA A*3101	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.366600	-0.034103	-4.400704	23259.485747
HLA A*2301	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.540718	0.139834	-4.400884	34731.064338
HLA A*2403	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.440240	0.039331	-4.400909	27557.512744
HLA B*4002	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.528073	0.126963	-4.401110	33734.413520
HLA A*0216	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.459663	0.058419	-4.401244	28817.958356
HLA B*4001	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.409246	0.007934	-4.401312	25659.347643
HLA A*2603	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.612883	0.211398	-4.401484	41009.315875
HLA B*5301	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.608752	0.207166	-4.401586	40621.142092
HLA B*1801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.515144	0.113362	-4.401782	32744.921097
HLA A*3201	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.549529	0.147675	-4.401854	35442.852004
HLA B*5401	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.548157	0.146138	-4.402018	35331.051437
HLA B*2705	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.421555	0.019419	-4.402136	26396.999410
HLA B*4001	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.441760	0.039331	-4.402429	27654.138509
HLA A*3002	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.538206	0.135619	-4.402587	34530.788311
HLA A*3301	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.613569	0.210953	-4.402615	41074.148979
HLA B*0802	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.482968	0.080331	-4.402637	30406.592311
HLA A*0202	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.516401	0.113627	-4.402774	32839.831701
HLA A*3301	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.631084	0.228245	-4.402839	42764.557706
HLA A*2402	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.540276	0.137191	-4.403086	34695.758748

HLA A*2402	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.484234	0.081144	-4.403090	30495.385208
HLA B*4402	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.422527	0.019419	-4.403108	26456.186870
HLA A*2603	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.657793	0.254455	-4.403338	45477.117543
HLA A*8001	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.446560	0.043160	-4.403400	27961.478501
HLA A*3201	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.596413	0.192958	-4.403455	39483.226434
HLA B*3901	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.334544	-0.069030	-4.403574	21604.475893
HLA B*2705	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.490425	0.086816	-4.403609	30933.211897
HLA B*1801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.486313	0.082695	-4.403618	30641.739621
HLA B*7301	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.540908	0.137191	-4.403718	34746.286861
HLA A*2603	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.629070	0.225172	-4.403898	42566.748360
HLA B*5101	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.503559	0.099536	-4.404022	31882.960252
HLA B*5101	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.501785	0.097746	-4.404038	31753.000963
HLA A*3201	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.590600	0.186500	-4.404100	38958.300990
HLA A*0250	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.561384	0.157255	-4.404129	36423.708581
HLA A*0101	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.403492	-0.000735	-4.404226	25321.633698
HLA A*0203	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.443839	0.039331	-4.404509	27786.857121
HLA A*0203	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.453228	0.048624	-4.404604	28394.091010
HLA A*0212	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.412662	0.007934	-4.404728	25861.979432
HLA A*1101	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.463324	0.058419	-4.404905	29061.880126
HLA B*1509	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.532016	0.126963	-4.405053	34042.041756
HLA B*5301	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.601041	0.195916	-4.405125	39906.268471
HLA B*1517	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.437256	0.032127	-4.405129	27368.826155
HLA A*6802	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.444518	0.039331	-4.405188	27830.334683
HLA A*1101	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.492006	0.086816	-4.405190	31046.040521
HLA A*3201	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.517533	0.112320	-4.405214	32925.575491
HLA A*3201	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.612417	0.207166	-4.405251	40965.411935
HLA B*5101	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.487977	0.082695	-4.405282	30759.328709
HLA A*2301	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.541019	0.135619	-4.405400	34755.122742
HLA B*3901	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.487676	0.082233	-4.405444	30738.036299
HLA A*8001	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.425208	0.019419	-4.405789	26619.997594
HLA B*5801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.230612	-0.175217	-4.405829	17006.381473
HLA B*0801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.402947	-0.003120	-4.406066	25289.872596
HLA B*1503	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.492911	0.086816	-4.406094	31110.770828
HLA B*4403	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.454732	0.048624	-4.406108	28492.571083
HLA A*0250	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.592656	0.186500	-4.406156	39143.153237
HLA B*0803	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.519812	0.113627	-4.406186	33098.809626
HLA A*1101	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.505727	0.099536	-4.406191	32042.560456
HLA A*2601	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.332262	-0.073933	-4.406195	21491.285086
HLA A*2301	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.527176	0.120764	-4.406412	33664.770720
HLA B*7301	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.488654	0.082233	-4.406421	30807.290576
HLA B*2705	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.445787	0.039331	-4.406456	27911.755427
HLA B*5301	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.519972	0.113362	-4.406611	33110.988007
HLA B*1517	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.485045	0.078424	-4.406621	30552.355301
HLA B*5401	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.554298	0.147675	-4.406623	35834.233217
HLA A*2602	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.613794	0.207166	-4.406628	41095.486352
HLA A*2301	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.543493	0.136752	-4.406741	34953.674234
HLA A*3001	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.292016	-0.114983	-4.406999	19589.155202
HLA A*2301	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.545043	0.137730	-4.407313	35078.700337
HLA A*0216	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.473419	0.066046	-4.407373	29745.374704
HLA A*6801	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.641368	0.233980	-4.407388	43789.267510
HLA B*1503	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.439547	0.032127	-4.407420	27513.568308
HLA A*2602	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.593478	0.185815	-4.407663	39217.339491
HLA A*0211	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.545403	0.137730	-4.407673	35107.747455
HLA B*4402	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.407016	-0.000735	-4.407751	25527.950526
HLA B*5701	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.415824	0.007934	-4.407891	26050.986197
HLA B*0802	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.463906	0.055954	-4.407953	29100.897238
HLA B*0801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.353109	-0.055017	-4.408126	22548.069544
HLA B*0802	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.479575	0.071401	-4.408174	30169.985040
HLA A*0211	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.520531	0.112320	-4.408212	33153.647636
HLA A*2301	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.507917	0.099536	-4.408381	32204.527558
HLA A*6801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.440592	0.032127	-4.408466	27579.884283
HLA A*6802	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.416543	0.007934	-4.408609	26094.147394
HLA B*7301	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.608891	0.200115	-4.408776	40634.109758
HLA B*0802	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.487213	0.078424	-4.408790	30705.294743
HLA B*4801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.440992	0.032127	-4.408865	27605.260650

HLA B*0802	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.428354	0.019419	-4.408935	26813.528747
HLA B*5301	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.609199	0.200115	-4.409083	40662.917175
HLA B*5401	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.552402	0.143276	-4.409126	35678.129823
HLA B*2705	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.469996	0.060842	-4.409154	29511.837065
HLA B*1801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.522784	0.113627	-4.409158	33326.098493
HLA A*3201	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.620641	0.211398	-4.409242	41748.466134
HLA A*0216	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.487733	0.078424	-4.409309	30742.027503
HLA A*6901	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.288304	-0.121106	-4.409409	19422.428028
HLA A*1101	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.460850	0.051389	-4.409461	28896.796490
HLA A*0206	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.496315	0.086816	-4.409499	31355.604326
HLA A*0250	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.441654	0.032127	-4.409528	27647.407066
HLA A*6801	1:57-65	9	QPVALVLSG	0.869043	-0.640798	-4.637782	0.228245	-4.409538	43429.253703
HLA B*1801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.458195	0.048624	-4.409571	28720.684175
HLA A*1101	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.500918	0.091322	-4.409596	31689.677290
HLA B*1503	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.522164	0.112320	-4.409845	33278.535774
HLA A*6801	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.618592	0.208642	-4.409949	41551.984753
HLA A*2501	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.442225	0.032127	-4.410098	27683.776332
HLA A*2603	1:96-104	9	FQAMAQALG	0.847247	-0.619590	-4.637764	0.227657	-4.410106	43427.374164
HLA A*2501	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.488628	0.078424	-4.410204	30805.457326
HLA B*5101	1:400-408	9	QPFGPGLG	0.498724	-0.625772	-4.283337	-0.127048	-4.410385	19201.568658
HLA B*3901	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.275381	-0.135106	-4.410487	18853.038452
HLA A*2902	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.289499	-0.121106	-4.410605	19475.983981
HLA B*5401	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.491947	0.081144	-4.410803	31041.841914
HLA A*2603	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.621991	0.210953	-4.411038	41878.534710
HLA B*1501	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.407967	-0.003120	-4.411087	25583.943714
HLA B*4801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.436923	0.025675	-4.411248	27347.809379
HLA A*0202	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.492436	0.081144	-4.411292	31076.791622
HLA B*3501	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.469768	0.058419	-4.411350	29496.354518
HLA B*4403	1:4-12	9	PADIDVPET	0.844779	-0.590324	-4.665805	0.254455	-4.411350	46323.852920
HLA A*2402	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.559032	0.147675	-4.411358	36226.996416
HLA A*0101	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.378648	-0.032788	-4.411436	23913.782095
HLA B*0803	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.502767	0.091322	-4.411445	31824.886341
HLA A*0206	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.503136	0.091584	-4.411552	31851.928373
HLA A*3001	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.275924	-0.135927	-4.411851	18876.613527
HLA B*7301	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.483308	0.071401	-4.411907	30430.453632
HLA B*4403	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.645987	0.233980	-4.412007	44257.488792
HLA B*1517	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.494311	0.082233	-4.412078	31211.242986
HLA B*5801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.357099	-0.055017	-4.412116	22756.150175
HLA B*7301	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.492568	0.080331	-4.412237	31086.207880
HLA A*8001	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.460890	0.048624	-4.412266	28899.454196
HLA B*0702	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.444758	0.032127	-4.412631	27845.695941
HLA B*0802	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.471140	0.058419	-4.412722	29589.691937
HLA B*4801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.412072	-0.000735	-4.412807	25826.885743
HLA B*2705	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.468845	0.055954	-4.412891	29433.709337
HLA B*4601	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.410056	-0.003120	-4.413176	25707.283271
HLA B*0803	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.500114	0.086816	-4.413298	31631.099822
HLA B*3901	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.298319	-0.114983	-4.413303	19875.560068
HLA B*5401	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.484706	0.071401	-4.413305	30528.563551
HLA A*6801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.526741	0.113362	-4.413379	33631.094880
HLA B*4002	1:135-143	9	QPVWMSHGD	1.072348	-0.861395	-4.624397	0.210953	-4.413444	42111.174122
HLA B*4403	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.641018	0.227420	-4.413598	43753.984365
HLA B*1509	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.553737	0.139834	-4.413902	35787.930801
HLA A*3001	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.116833	-0.297084	-4.413917	13086.798224
HLA B*1502	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.527364	0.113362	-4.414002	33679.343688
HLA A*6801	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.515994	0.101982	-4.414012	32809.110925
HLA B*4801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.422135	0.007934	-4.414201	26432.295782
HLA B*3901	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.475221	0.060842	-4.414380	29869.056138
HLA B*4002	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.562077	0.147675	-4.414403	36481.884217
HLA B*5301	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.600980	0.186500	-4.414480	39900.655765
HLA B*5101	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.506075	0.091584	-4.414491	32068.226041
HLA A*2403	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.422476	0.007934	-4.414542	26453.038306
HLA B*0801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.345525	-0.069030	-4.414555	22157.728061
HLA B*0803	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.512470	0.097746	-4.414724	32543.947778
HLA A*0219	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.464057	0.048624	-4.415433	29110.974671
HLA A*2902	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.434876	0.019419	-4.415457	27219.249260

HLA B*0801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.454898	0.039331	-4.415568	28503.517242
HLA B*4501	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.627254	0.211398	-4.415856	42389.112527
HLA B*1517	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.474343	0.058419	-4.415924	29808.683218
HLA A*2402	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.557106	0.141148	-4.415957	36066.645437
HLA B*5301	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.569260	0.153079	-4.416181	37090.239386
HLA A*2902	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.441967	0.025675	-4.416292	27667.306955
HLA A*2403	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.347325	-0.069085	-4.416410	22249.739650
HLA B*1503	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.496790	0.080331	-4.416459	31389.888384
HLA A*2501	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.499165	0.082695	-4.416470	31562.042535
HLA A*2602	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.569920	0.153079	-4.416841	37146.666062
HLA B*1801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.416522	-0.000735	-4.417257	26092.876927
HLA A*6801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.348711	-0.069030	-4.417741	22320.870597
HLA B*4403	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.640097	0.222188	-4.417909	43661.294633
HLA B*4002	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.645338	0.227420	-4.417918	44191.455945
HLA A*1101	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.474110	0.055954	-4.418156	29792.722587
HLA B*5301	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.303319	-0.114983	-4.418303	20105.694507
HLA B*0803	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.500608	0.082233	-4.418375	31667.055599
HLA B*3501	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.444330	0.025675	-4.418656	27818.292567
HLA A*0211	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.510349	0.091584	-4.418765	32385.354057
HLA A*2301	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.516847	0.097746	-4.419101	32873.604426
HLA A*0250	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.571764	0.152623	-4.419141	37304.754592
HLA A*1101	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.501385	0.082233	-4.419153	31723.811751
HLA B*1801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.505981	0.086816	-4.419165	32061.287370
HLA B*3801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.562484	0.143276	-4.419207	36516.043990
HLA B*4001	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.385333	-0.034103	-4.419436	24284.689355
HLA A*0101	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.350548	-0.069085	-4.419634	22415.499808
HLA A*2902	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.385692	-0.034103	-4.419795	24304.798430
HLA B*4402	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.445524	0.025675	-4.419850	27894.848606
HLA B*5301	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.565496	0.145582	-4.419914	36770.180466
HLA B*1509	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.532427	0.112320	-4.420107	34074.285659
HLA A*2301	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.533811	0.113627	-4.420184	34183.033972
HLA B*5801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.351300	-0.069030	-4.420330	22454.338335
HLA B*3801	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.577605	0.157255	-4.420350	37809.854583
HLA B*1503	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.307076	-0.113369	-4.420445	20280.371488
HLA A*2603	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.566158	0.145582	-4.420576	36826.319450
HLA B*3901	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.492046	0.071401	-4.420645	31048.895898
HLA B*3901	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.499069	0.078424	-4.420645	31555.042678
HLA A*0203	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.346829	-0.073933	-4.420762	22224.356360
HLA B*1502	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.517103	0.095477	-4.421626	32892.994981
HLA B*1801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.473046	0.051389	-4.421657	29719.799556
HLA A*2603	1:242-250	9	AALVQRAIG	0.678927	-0.444947	-4.655918	0.233980	-4.421938	45281.211840
HLA B*4001	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.366929	-0.055017	-4.421946	23277.108793
HLA B*1801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.513589	0.091584	-4.422005	32627.859928
HLA A*2402	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.574682	0.152623	-4.422059	37556.252280
HLA A*2402	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.561988	0.139834	-4.422154	36474.385196
HLA B*1503	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.522049	0.099536	-4.422513	33269.715317
HLA A*6801	1:56-64	9	RQPVALVLS	1.011755	-0.777115	-4.657184	0.234640	-4.422544	45413.441388
HLA A*2501	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.493966	0.071401	-4.422565	31186.431997
HLA A*3201	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.575836	0.153079	-4.422757	37656.143894
HLA B*5401	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.558595	0.135619	-4.422976	36190.561719
HLA B*5101	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.494614	0.071401	-4.423213	31233.032157
HLA B*2705	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.466484	0.043160	-4.423323	29274.114314
HLA A*3301	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.544364	0.120764	-4.423601	35023.899115
HLA B*4002	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.614950	0.191274	-4.423677	41205.014488
HLA A*0203	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.302588	-0.121106	-4.423694	20071.895609
HLA A*0301	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.368752	-0.055017	-4.423769	23375.033221
HLA A*6901	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.308843	-0.114983	-4.423826	20363.044892
HLA A*1101	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.467207	0.043160	-4.424047	29322.932846
HLA B*1517	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.443525	0.019419	-4.424106	27766.721029
HLA B*4501	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.617166	0.192958	-4.424208	41415.760023
HLA B*5701	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.390227	-0.034103	-4.424330	24559.896354
HLA B*5301	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.551758	0.126963	-4.424796	35625.282965
HLA A*6801	1:483-491	9	ADWTRVPYE	0.895434	-0.670262	-4.649983	0.225172	-4.424811	44666.635647
HLA A*0250	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.579339	0.154429	-4.424910	37961.112105
HLA A*6901	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.250117	-0.175217	-4.425334	17787.599443

HLA B*1801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.457525	0.032127	-4.425398	28676.436215
HLA B*5301	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.546432	0.120764	-4.425668	35191.035003
HLA B*1801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.345405	-0.080273	-4.425679	22151.615491
HLA B*0702	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.433819	0.007934	-4.425885	27153.065949
HLA B*5801	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.357143	-0.069085	-4.426229	22758.489352
HLA B*4002	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.619217	0.192958	-4.426259	41611.822371
HLA A*0202	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.572598	0.146138	-4.426460	37376.467611
HLA A*2603	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.547654	0.120764	-4.426890	35290.171772
HLA B*5301	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.584216	0.157255	-4.426962	38389.853770
HLA A*0211	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.459132	0.032127	-4.427005	28782.746044
HLA B*0803	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.507541	0.080331	-4.427210	32176.663951
HLA A*3101	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.394425	-0.032788	-4.427213	24798.479853
HLA A*3002	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.539628	0.112320	-4.427308	34643.992147
HLA B*2705	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.509557	0.082233	-4.427324	32326.365049
HLA B*4002	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.638974	0.211398	-4.427575	43548.535569
HLA A*0201	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.393647	-0.034103	-4.427751	24754.113612
HLA B*3801	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.540110	0.112320	-4.427790	34682.434593
HLA A*2902	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.476551	0.048624	-4.427927	29960.655273
HLA A*3001	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.300899	-0.127048	-4.427948	19993.973396
HLA A*2301	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.508321	0.080331	-4.427990	32234.507847
HLA B*5101	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.479404	0.051389	-4.428015	30158.072605
HLA A*2301	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.540345	0.112320	-4.428025	34701.202481
HLA B*1509	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.565768	0.137730	-4.428038	36793.262729
HLA A*3001	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.303418	-0.124898	-4.428315	20110.263349
HLA B*5701	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.425274	-0.003120	-4.428393	26624.030214
HLA A*6802	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.425481	-0.003120	-4.428600	26636.708140
HLA B*1509	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.542264	0.113627	-4.428637	34854.917062
HLA A*2601	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.394651	-0.034103	-4.428754	24811.362272
HLA B*3501	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.477599	0.048624	-4.428975	30033.031939
HLA A*0250	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.568964	0.139834	-4.429129	37064.965586
HLA A*3301	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.614964	0.185815	-4.429149	41206.351997
HLA A*0219	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.454837	0.025675	-4.429163	28499.508302
HLA B*4601	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.396434	-0.032788	-4.429222	24913.449800
HLA A*2601	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.360595	-0.069030	-4.429625	22940.074545
HLA A*0301	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.132702	-0.297084	-4.429786	13573.811945
HLA B*5801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.350931	-0.079025	-4.429957	22435.274781
HLA B*4501	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.657386	0.227420	-4.429966	45434.574928
HLA B*5301	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.569878	0.139834	-4.430043	37143.048969
HLA B*1501	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.361102	-0.069030	-4.430132	22966.896518
HLA B*1801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.438069	0.007934	-4.430135	27420.103692
HLA A*0211	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.491015	0.060842	-4.430173	30975.244085
HLA A*2402	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.529934	0.099536	-4.430398	33879.263166
HLA B*0801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.351429	-0.079025	-4.430455	22461.020480
HLA A*6802	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.397670	-0.032788	-4.430458	24984.444518
HLA B*3501	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.272491	-0.158117	-4.430608	18728.003711
HLA A*0212	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.462755	0.032127	-4.430628	29023.857406
HLA A*2501	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.491471	0.060842	-4.430629	31007.770242
HLA B*0702	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.397989	-0.032788	-4.430777	25002.833461
HLA A*3002	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.568668	0.137730	-4.430937	37039.709008
HLA A*2403	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.430342	-0.000735	-4.431076	26936.529257
HLA A*0212	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.362096	-0.069030	-4.431126	23019.513757
HLA B*5101	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.362174	-0.069030	-4.431204	23023.623713
HLA B*0803	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.489687	0.058419	-4.431268	30880.710095
HLA A*6801	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.578963	0.147675	-4.431288	37928.267857
HLA A*2602	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.631432	0.200115	-4.431317	42798.811442
HLA A*0201	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.398703	-0.032788	-4.431492	25043.987109
HLA B*0803	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.503021	0.071401	-4.431619	31843.486037
HLA B*1801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.310570	-0.121106	-4.431675	20444.175017
HLA A*2902	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.304637	-0.127048	-4.431686	20166.806931
HLA A*3002	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.568442	0.136752	-4.431690	37020.477454
HLA A*3201	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.588960	0.157255	-4.431705	38811.467851
HLA B*1501	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.276932	-0.154863	-4.431795	18920.474050
HLA B*5301	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.572944	0.141148	-4.431795	37406.203208
HLA A*2501	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.457739	0.025675	-4.432064	28690.557098
HLA B*0802	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.480766	0.048624	-4.432142	30252.849280

HLA A*2602	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.568900	0.136752	-4.432148	37059.552013
HLA A*2603	1:71-79	9	YADGAPKLD	1.058109	-0.830689	-4.659755	0.227420	-4.432335	45683.014084
HLA B*5101	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.510960	0.078424	-4.432536	32430.938414
HLA B*1503	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.493390	0.060842	-4.432548	31145.124168
HLA A*3301	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.639789	0.207166	-4.432623	43630.363033
HLA B*5301	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.570383	0.137730	-4.432653	37186.276156
HLA B*1503	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.524314	0.091322	-4.432992	33443.674527
HLA B*5301	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.545321	0.112320	-4.433001	35101.100568
HLA A*6801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.274926	-0.158117	-4.433042	18833.262219
HLA A*3301	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.570007	0.136752	-4.433255	37154.102302
HLA A*0211	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.520073	0.086816	-4.433257	33118.691354
HLA A*2603	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.515518	0.082233	-4.433285	32773.099491
HLA A*1101	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.481939	0.048624	-4.433315	30334.628229
HLA A*0216	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.470541	0.037065	-4.433477	29548.900457
HLA A*0216	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.459276	0.025675	-4.433601	28792.246010
HLA A*3002	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.535674	0.101982	-4.433692	34329.995637
HLA A*2402	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.586874	0.153079	-4.433795	38625.465409
HLA A*3001	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.278948	-0.154863	-4.433811	19008.501067
HLA A*0203	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.399930	-0.034103	-4.434033	25114.810335
HLA B*3501	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.441979	0.007934	-4.434045	27668.055351
HLA B*1801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.379052	-0.055017	-4.434069	23936.044248
HLA A*6901	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.365122	-0.069085	-4.434207	23180.472407
HLA B*4403	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.514542	0.080331	-4.434211	32699.603009
HLA B*5401	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.533815	0.099536	-4.434279	34183.403827
HLA B*0803	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.533853	0.099536	-4.434317	34186.362810
HLA A*3301	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.620934	0.186500	-4.434434	41776.707504
HLA B*3901	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.473871	0.039331	-4.434540	29776.287238
HLA B*1509	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.514890	0.080331	-4.434559	32725.794875
HLA A*0301	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.365548	-0.069030	-4.434577	23203.181609
HLA B*5101	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.493012	0.058419	-4.434593	31118.008820
HLA B*7301	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.591902	0.157255	-4.434647	39075.237226
HLA A*2301	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.548161	0.113362	-4.434800	35331.433713
HLA B*1509	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.548192	0.113362	-4.434830	35333.918610
HLA B*5701	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.259637	-0.175217	-4.434854	18181.824202
HLA A*3101	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.431789	-0.003120	-4.434909	27026.444756
HLA A*0219	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.454344	0.019419	-4.434925	28467.149058
HLA B*3501	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.474298	0.039331	-4.434967	29805.619403
HLA B*5801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.354836	-0.080273	-4.435110	22637.905210
HLA A*2403	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.321788	-0.113369	-4.435158	20979.173810
HLA A*0211	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.361516	-0.073933	-4.435448	22988.774644
HLA A*2603	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.635649	0.200115	-4.435534	43216.444527
HLA B*4501	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.621442	0.185815	-4.435627	41825.553626
HLA B*7301	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.549016	0.113362	-4.435655	35401.076908
HLA B*0801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.260453	-0.175217	-4.435669	18215.987752
HLA A*2603	1:310-318	9	GRQFIRAFE	0.898913	-0.676725	-4.657866	0.222188	-4.435678	45484.744994
HLA B*3801	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.573665	0.137730	-4.435935	37468.380394
HLA B*1801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.531428	0.095477	-4.435951	33996.031958
HLA B*5101	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.518210	0.082233	-4.435977	32976.915104
HLA A*6901	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.356970	-0.079025	-4.435995	22749.380229
HLA B*4403	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.563022	0.126963	-4.436059	36561.310458
HLA A*1101	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.473138	0.037065	-4.436073	29726.070669
HLA A*2402	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.590555	0.154429	-4.436126	38954.296754
HLA A*2301	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.522977	0.086816	-4.436161	33340.885593
HLA A*3001	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.307543	-0.128649	-4.436193	20302.216443
HLA B*5301	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.583942	0.147675	-4.436267	38365.562331
HLA B*5101	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.475781	0.039331	-4.436450	29907.538919
HLA B*5301	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.573724	0.137191	-4.436533	37473.448232
HLA B*0802	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.479707	0.043160	-4.436546	30179.126536
HLA B*0702	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.462292	0.025675	-4.436618	28992.941761
HLA B*4402	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.357625	-0.079025	-4.436650	22783.743139
HLA B*1509	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.492861	0.055954	-4.436908	31107.236606
HLA A*2301	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.538895	0.101982	-4.436913	34585.566380
HLA A*0250	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.574111	0.137191	-4.436921	37506.913153
HLA B*1501	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.363184	-0.073933	-4.437116	23077.244816
HLA B*1503	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.403135	-0.034103	-4.437238	25300.820198

HLA A*0206	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.528574	0.091322	-4.437252	33773.308305
HLA A*0216	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.486029	0.048624	-4.437405	30621.688206
HLA A*0301	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.368506	-0.069085	-4.437591	23361.759076
HLA B*1517	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.509169	0.071401	-4.437768	32297.522386
HLA B*5301	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.592224	0.154429	-4.437795	39104.208761
HLA A*0250	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.574586	0.136752	-4.437834	37547.923022
HLA A*0301	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.364006	-0.073933	-4.437939	23120.982078
HLA B*3801	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.574790	0.136752	-4.438038	37565.599500
HLA B*1517	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.477503	0.039331	-4.438172	30026.371187
HLA A*0202	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.309207	-0.129234	-4.438441	20380.127134
HLA B*5101	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.481654	0.043160	-4.438494	30314.777783
HLA A*0206	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.540481	0.101982	-4.438499	34712.092510
HLA A*0211	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.317496	-0.121106	-4.438602	20772.839806
HLA B*4002	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.579973	0.141148	-4.438825	38016.601282
HLA A*0250	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.586592	0.147675	-4.438917	38600.398408
HLA A*2602	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.591603	0.152623	-4.438980	39048.399573
HLA A*0211	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.538524	0.099536	-4.438987	34556.016567
HLA B*0702	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.435879	-0.003120	-4.438999	27282.199023
HLA A*6801	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.559871	0.120764	-4.439107	36297.030323
HLA B*1503	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.517545	0.078424	-4.439122	32926.466121
HLA B*3801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.576390	0.137191	-4.439200	37704.251471
HLA A*0250	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.585342	0.146138	-4.439204	38489.463821
HLA B*1503	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.536971	0.097746	-4.439224	34432.667114
HLA B*4501	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.639359	0.200115	-4.439244	43587.189924
HLA A*2402	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.582522	0.143276	-4.439246	38240.404646
HLA B*1503	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.505452	0.066046	-4.439406	32022.285310
HLA A*1101	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.471627	0.032127	-4.439500	29622.846427
HLA B*4801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.436427	-0.003120	-4.439546	27316.610031
HLA B*0802	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.500396	0.060842	-4.439554	31651.640978
HLA B*4801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.405472	-0.034103	-4.439576	25437.377661
HLA B*1801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.500429	0.060842	-4.439587	31654.038315
HLA A*2501	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.365879	-0.073933	-4.439811	23220.887617
HLA A*2603	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.647187	0.207166	-4.440021	44380.005824
HLA A*1101	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.264830	-0.175217	-4.440046	18400.508127
HLA A*2501	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.477172	0.037065	-4.440107	30003.475974
HLA A*3101	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.366797	-0.073933	-4.440730	23270.057973
HLA A*8001	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.440036	-0.000735	-4.440770	27544.545567
HLA B*3801	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.567808	0.126963	-4.440845	36966.442224
HLA B*3501	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.440242	-0.000735	-4.440977	27557.661828
HLA B*4002	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.649751	0.208642	-4.441108	44642.719539
HLA A*3301	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.584395	0.143276	-4.441119	38405.641064
HLA B*1509	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.540800	0.099536	-4.441264	34737.641153
HLA B*3801	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.581129	0.139834	-4.441295	38117.923539
HLA B*5801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.367392	-0.073933	-4.441324	23301.929553
HLA A*3002	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.596030	0.154429	-4.441601	39448.425000
HLA A*0202	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.533190	0.091584	-4.441607	34134.248242
HLA A*2603	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.632898	0.191274	-4.441624	42943.534559
HLA B*5401	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.537654	0.095477	-4.442177	34486.916386
HLA A*1101	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.321163	-0.121106	-4.442269	20949.005850
HLA B*5801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.310339	-0.132020	-4.442359	20433.339019
HLA A*2402	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.563214	0.120764	-4.442451	36577.533053
HLA B*0802	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.474608	0.032127	-4.442481	29826.911358
HLA A*3002	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.462015	0.019419	-4.442596	28974.439532
HLA B*7301	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.595731	0.153079	-4.442653	39421.331035
HLA B*4601	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.373651	-0.069030	-4.442681	23640.187293
HLA A*8001	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.439655	-0.003120	-4.442775	27520.416046
HLA A*2501	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.501519	0.058419	-4.443100	31733.595731
HLA B*0803	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.480235	0.037065	-4.443171	30215.883692
HLA A*0202	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.525992	0.082695	-4.443296	33573.105914
HLA A*2402	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.580077	0.136752	-4.443324	38025.651645
HLA A*2602	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.630036	0.186500	-4.443536	42661.499310
HLA A*0203	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.440543	-0.003120	-4.443663	27576.751175
HLA B*1502	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.579297	0.135619	-4.443677	37957.415708
HLA B*1502	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.601006	0.157255	-4.443751	39903.030275
HLA A*0219	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.451752	0.007934	-4.443819	28297.788313

HLA B*4002	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.644119	0.200115	-4.444004	44067.552185
HLA A*0206	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.543688	0.099536	-4.444152	34969.372685
HLA B*3801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.531008	0.086816	-4.444191	33963.127150
HLA B*4002	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.630013	0.185815	-4.444198	42659.191433
HLA A*2402	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.542090	0.097746	-4.444344	34840.966323
HLA B*0803	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.510400	0.066046	-4.444354	32389.208712
HLA A*2603	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.592303	0.147675	-4.444629	39111.402103
HLA B*4002	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.590800	0.146138	-4.444661	38976.219717
HLA A*6901	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.389726	-0.055017	-4.444743	24531.612127
HLA B*0803	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.500948	0.055954	-4.444995	31691.906057
HLA A*3101	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.269799	-0.175217	-4.445016	18612.254268
HLA B*0803	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.523473	0.078424	-4.445049	33378.965497
HLA A*2601	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.316018	-0.129234	-4.445252	20702.273695
HLA B*5101	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.506136	0.060842	-4.445294	32072.736983
HLA A*3002	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.558682	0.113362	-4.445321	36197.806561
HLA A*6802	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.316753	-0.128649	-4.445403	20737.358454
HLA B*7301	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.585246	0.139834	-4.445411	38480.927594
HLA B*5401	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.557752	0.112320	-4.445432	36120.342423
HLA A*3201	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.537027	0.091584	-4.445443	34437.138050
HLA A*2301	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.526595	0.081144	-4.445451	33619.816461
HLA B*4001	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.412683	-0.032788	-4.445471	25863.238656
HLA A*2603	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.631382	0.185815	-4.445567	42793.949444
HLA B*5401	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.506737	0.060842	-4.445896	32117.186303
HLA B*4403	1:227-235	9	HAICGLSGG	0.798230	-0.605272	-4.638868	0.192958	-4.445910	43537.935185
HLA B*0702	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.489213	0.043160	-4.446052	30846.982161
HLA B*7301	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.582826	0.136752	-4.446073	38267.101009
HLA A*0206	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.506944	0.060842	-4.446102	32132.479980
HLA B*1503	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.528339	0.082233	-4.446106	33755.042261
HLA A*2601	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.391213	-0.055017	-4.446230	24615.763652
HLA A*0250	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.582233	0.135619	-4.446614	38214.967319
HLA A*0212	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.443661	-0.003120	-4.446780	27775.434859
HLA A*0301	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.367855	-0.079025	-4.446880	23326.776779
HLA A*2402	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.582518	0.135619	-4.446898	38239.990895
HLA A*1101	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.486450	0.039331	-4.447119	30651.355697
HLA A*2501	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.495796	0.048624	-4.447172	31318.138421
HLA B*2705	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.455166	0.007934	-4.447233	28521.101563
HLA A*3301	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.592846	0.145582	-4.447264	39160.309565
HLA A*0211	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.503239	0.055954	-4.447285	31859.511153
HLA B*5401	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.545095	0.097746	-4.447349	35082.875567
HLA A*2301	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.538989	0.091584	-4.447405	34593.051353
HLA A*8001	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.368452	-0.079025	-4.447477	23358.852412
HLA B*7301	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.503761	0.055954	-4.447807	31897.797265
HLA A*2501	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.444857	-0.003120	-4.447976	27852.023629
HLA B*1502	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.600614	0.152623	-4.447990	39866.996103
HLA B*1502	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.584778	0.136752	-4.448026	38439.522553
HLA B*4002	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.528461	0.080331	-4.448130	33764.539370
HLA A*2402	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.585870	0.137730	-4.448140	38536.342686
HLA A*0216	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.447427	-0.000735	-4.448162	28017.352327
HLA A*2402	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.594317	0.146138	-4.448179	39293.154320
HLA B*5701	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.415392	-0.032788	-4.448180	26025.067437
HLA A*8001	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.456120	0.007934	-4.448187	28583.814585
HLA A*0201	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.327148	-0.121106	-4.448253	21239.659803
HLA B*1509	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.543803	0.095477	-4.448325	34978.643754
HLA B*4002	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.644319	0.195916	-4.448402	44087.820893
HLA B*4501	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.657062	0.208642	-4.448420	45400.667737
HLA B*4501	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.639789	0.191274	-4.448515	43630.363033
HLA A*0301	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.368254	-0.080273	-4.448527	23348.239845
HLA A*0101	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.393777	-0.055017	-4.448793	24761.480143
HLA A*0202	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.561410	0.112320	-4.449090	36425.876176
HLA B*0802	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.446210	-0.003120	-4.449330	27938.948576
HLA B*2705	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.448628	-0.000735	-4.449362	28094.912147
HLA B*1517	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.498016	0.048624	-4.449392	31478.657522
HLA B*1801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.475092	0.025675	-4.449418	29860.170105
HLA B*3501	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.320771	-0.128649	-4.449420	20930.087987
HLA A*6802	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.448769	-0.000735	-4.449503	28104.033048

HLA A*0201	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.394655	-0.055017	-4.449672	24811.630727
HLA A*0250	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.590941	0.141148	-4.449792	38988.873193
HLA B*5301	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.593222	0.143276	-4.449946	39194.220709
HLA A*0250	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.587872	0.137730	-4.450142	38714.375362
HLA A*0206	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.493381	0.043160	-4.450220	31144.450209
HLA A*2402	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.563910	0.113627	-4.450283	36636.152573
HLA B*3901	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.482573	0.032127	-4.450446	30378.969489
HLA A*2902	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.458512	0.007934	-4.450578	28741.667558
HLA B*0801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.376799	-0.073933	-4.450732	23812.183625
HLA A*2402	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.531095	0.080331	-4.450763	33969.926090
HLA A*3301	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.533042	0.082233	-4.450810	34122.616487
HLA B*4501	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.646861	0.195916	-4.450945	44346.645732
HLA B*2705	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.476634	0.025675	-4.450959	29966.328744
HLA B*4403	1:145-153	9	VTAAPDGFD	0.892882	-0.696966	-4.647044	0.195916	-4.451128	44365.362695
HLA A*3101	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.382443	-0.069030	-4.451473	24123.631504
HLA B*1503	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.534335	0.082695	-4.451640	34224.297450
HLA A*3002	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.510335	0.058419	-4.451916	32384.302867
HLA B*1501	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.317089	-0.135106	-4.452195	20753.407375
HLA A*6901	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.320205	-0.132020	-4.452225	20902.817469
HLA A*2902	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.383244	-0.069030	-4.452274	24168.175183
HLA A*2403	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.449389	-0.003120	-4.452509	28144.200207
HLA A*0212	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.418425	-0.034103	-4.452528	26207.467065
HLA B*7301	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.564859	0.112320	-4.452539	36716.311938
HLA B*2705	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.501475	0.048624	-4.452851	31730.334069
HLA A*3101	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.372622	-0.080273	-4.452895	23584.237440
HLA B*3901	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.496076	0.043160	-4.452915	31338.306803
HLA A*2501	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.492321	0.039331	-4.452990	31068.554736
HLA A*3002	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.452286	-0.000735	-4.453021	28332.560612
HLA B*0803	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.544717	0.091584	-4.453133	35052.331961
HLA B*1502	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.550945	0.097746	-4.453199	35558.661161
HLA A*2603	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.593215	0.139834	-4.453381	39193.584605
HLA B*1509	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.545142	0.091584	-4.453558	35086.671662
HLA B*4501	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.580622	0.126963	-4.453659	38073.407386
HLA A*3001	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.295566	-0.158117	-4.453683	19749.939926
HLA A*0211	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.555839	0.101982	-4.453857	35961.630797
HLA B*7301	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.606553	0.152623	-4.453930	40415.970490
HLA A*0211	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.525482	0.071401	-4.454081	33533.716027
HLA B*1503	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.525648	0.071401	-4.454247	33546.598873
HLA B*4501	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.597609	0.143276	-4.454332	39592.098600
HLA A*0202	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.592705	0.137730	-4.454975	39147.600452
HLA A*0206	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.533456	0.078424	-4.455032	34155.121484
HLA B*1509	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.541853	0.086816	-4.455037	34821.934461
HLA A*2301	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.546585	0.091322	-4.455263	35203.411853
HLA A*0101	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.386606	-0.069030	-4.455636	24356.000444
HLA B*5401	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.546991	0.091322	-4.455670	35236.374530
HLA B*4403	1:73-81	9	DGAPKLDPA	0.621654	-0.410256	-4.667104	0.211398	-4.455705	46462.646049
HLA A*0201	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.386679	-0.069085	-4.455764	24360.085448
HLA A*0212	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.280628	-0.175217	-4.455844	19082.169680
HLA B*7301	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.582870	0.126963	-4.455907	38271.034606
HLA B*1502	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.593114	0.137191	-4.455923	39184.468248
HLA B*1801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.495312	0.039331	-4.455981	31283.255764
HLA A*2501	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.297885	-0.158117	-4.456002	19855.677972
HLA A*0101	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.382191	-0.073933	-4.456124	24109.671385
HLA A*0250	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.583178	0.126963	-4.456215	38298.166728
HLA A*2301	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.527650	0.071401	-4.456249	33701.579610
HLA A*0202	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.555792	0.099536	-4.456256	35957.740039
HLA A*2403	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.341275	-0.114983	-4.456258	21941.939319
HLA A*2403	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.423483	-0.032788	-4.456272	26514.502937
HLA A*3002	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.543098	0.086816	-4.456282	34921.920621
HLA A*6901	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.327079	-0.129234	-4.456313	21236.327843
HLA A*3201	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.593643	0.137191	-4.456452	39232.193605
HLA A*1101	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.475886	0.019419	-4.456468	29914.820646
HLA A*0301	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.281363	-0.175217	-4.456580	19114.508800
HLA B*5401	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.548206	0.091584	-4.456622	35335.065544
HLA A*0206	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.522669	0.066046	-4.456623	33317.265429

HLA A*0219	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.382758	-0.073933	-4.456690	24141.125672
HLA B*1509	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.535126	0.078424	-4.456703	34286.749796
HLA B*4501	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.602874	0.146138	-4.456735	40075.017277
HLA A*0101	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.377732	-0.079025	-4.456757	23863.380629
HLA B*3801	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.570352	0.113362	-4.456991	37183.660991
HLA A*2601	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.387964	-0.069085	-4.457049	24432.278805
HLA A*0211	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.548669	0.091322	-4.457347	35372.743899
HLA A*3201	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.600625	0.143276	-4.457349	39868.074498
HLA A*0250	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.570857	0.113362	-4.457496	37226.935442
HLA B*7301	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.536021	0.078424	-4.457598	34357.493421
HLA B*1801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.516067	0.058419	-4.457648	32814.613690
HLA B*5801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.336729	-0.121106	-4.457835	21713.446160
HLA A*1101	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.465838	0.007934	-4.457904	29230.595023
HLA A*0206	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.516377	0.058419	-4.457959	32838.055150
HLA A*3201	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.612485	0.154429	-4.458057	40971.839371
HLA B*0802	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.497770	0.039331	-4.458439	31460.781514
HLA A*2603	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.611684	0.153079	-4.458606	40896.325335
HLA B*0802	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.457901	-0.000735	-4.458636	28701.268775
HLA A*0202	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.484476	0.025675	-4.458802	30512.382538
HLA B*1502	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.600127	0.141148	-4.458979	39822.376153
HLA A*2602	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.554665	0.095477	-4.459187	35864.488021
HLA B*5101	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.507987	0.048624	-4.459364	32209.754670
HLA A*3001	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.233015	-0.226766	-4.459782	17100.761094
HLA A*0206	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.531226	0.071401	-4.459825	33980.218967
HLA B*3801	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.541200	0.081144	-4.460056	34769.603402
HLA B*0803	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.492354	0.032127	-4.460227	31070.907909
HLA A*2603	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.612986	0.152623	-4.460363	41019.078695
HLA B*0803	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.499821	0.039331	-4.460490	31609.716960
HLA B*2705	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.426387	-0.034103	-4.460491	26692.389489
HLA A*2603	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.647072	0.186500	-4.460572	44368.242928
HLA B*3801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.574306	0.113627	-4.460680	37523.758319
HLA A*2603	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.618134	0.157255	-4.460879	41508.173498
HLA B*5301	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.607058	0.146138	-4.460920	40463.006712
HLA A*2301	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.539581	0.078424	-4.461157	34640.243947
HLA B*1502	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.601072	0.139834	-4.461237	39909.075120
HLA B*1509	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.552691	0.091322	-4.461369	35701.878535
HLA A*3201	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.563536	0.101982	-4.461554	36604.652716
HLA A*2602	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.563576	0.101982	-4.461594	36608.019332
HLA A*2902	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.286382	-0.175217	-4.461598	19336.668061
HLA A*2301	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.543852	0.082233	-4.461620	34982.617822
HLA B*3801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.553426	0.091584	-4.461843	35762.383570
HLA B*5401	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.544543	0.082695	-4.461848	35038.302207
HLA A*0201	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.392856	-0.069030	-4.461885	24709.024693
HLA A*0211	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.528158	0.066046	-4.462111	33740.984139
HLA A*0101	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.381839	-0.080273	-4.462112	24090.114723
HLA A*2601	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.383307	-0.079025	-4.462332	24171.705614
HLA A*2602	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.429649	-0.032788	-4.462437	26893.575069
HLA B*5801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.349230	-0.113369	-4.462600	22347.573066
HLA A*3101	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.393532	-0.069085	-4.462617	24747.552548
HLA A*0211	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.287697	-0.175217	-4.462914	19395.338057
HLA B*2705	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.500032	0.037065	-4.462967	31625.111163
HLA B*0803	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.511624	0.048624	-4.463001	32480.628164
HLA A*0250	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.558508	0.095477	-4.463031	36183.318328
HLA B*3801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.545365	0.082233	-4.463133	35104.708722
HLA A*2301	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.545993	0.082695	-4.463298	35155.452020
HLA A*3201	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.543676	0.080331	-4.463345	34968.426795
HLA A*0219	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.462821	-0.000735	-4.463556	29028.254183
HLA A*6802	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.394545	-0.069085	-4.463630	24805.322805
HLA A*0201	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.389724	-0.073933	-4.463656	24531.479414
HLA A*2301	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.522091	0.058419	-4.463673	33272.955213
HLA B*5101	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.495803	0.032127	-4.463676	31318.646708
HLA B*5401	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.506989	0.043160	-4.463828	32135.782979
HLA A*2602	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.610000	0.146138	-4.463861	40738.000228
HLA B*1517	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.305784	-0.158117	-4.463901	20220.118164
HLA B*3501	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.350593	-0.113369	-4.463962	22417.803969

HLA B*4402	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.394900	-0.069085	-4.463985	24825.594385
HLA A*2402	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.577412	0.113362	-4.464051	37793.085439
HLA A*0250	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.577680	0.113627	-4.464054	37816.400657
HLA B*4403	1:448-456	9	VVLLADVRS	1.135797	-0.944523	-4.655328	0.191274	-4.464055	45219.767016
HLA A*0211	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.463326	-0.000735	-4.464061	29062.037348
HLA B*3901	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.512839	0.048624	-4.464215	32571.600807
HLA B*1501	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.395560	-0.069085	-4.464645	24863.362428
HLA B*1502	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.619153	0.154429	-4.464724	41605.744700
HLA A*2403	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.329868	-0.135106	-4.464974	21373.136529
HLA A*0211	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.508274	0.043160	-4.465114	32231.020333
HLA A*2602	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.464625	-0.000735	-4.465360	29149.111519
HLA B*1509	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.563196	0.097746	-4.465449	36575.950044
HLA B*5301	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.579120	0.113627	-4.465494	37942.017926
HLA B*4002	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.618228	0.152623	-4.465604	41517.156655
HLA A*3201	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.592644	0.126963	-4.465681	39142.094450
HLA A*0212	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.168597	-0.297084	-4.465681	14743.386811
HLA B*5401	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.473967	0.007934	-4.466033	29782.892514
HLA B*1517	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.491788	0.025675	-4.466113	31030.424575
HLA A*2402	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.553145	0.086816	-4.466328	35739.174641
HLA B*0801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.351392	-0.114983	-4.466375	22459.076378
HLA B*5301	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.602075	0.135619	-4.466456	40001.372552
HLA B*4403	1:406-414	9	GLGIRIVGE	1.081324	-0.881209	-4.667003	0.200115	-4.466888	46451.838922
HLA B*4403	1:469-477	9	PIVLRPVSS	1.314329	-1.105687	-4.675623	0.208642	-4.466981	47383.067400
HLA A*0301	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.345943	-0.121106	-4.467049	22179.075350
HLA A*2501	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.398067	-0.069030	-4.467097	25007.297523
HLA A*3301	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.620438	0.153079	-4.467360	41729.047158
HLA A*2402	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.579720	0.112320	-4.467400	37994.395884
HLA A*2403	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.433723	-0.034103	-4.467826	27147.043918
HLA B*0803	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.528700	0.060842	-4.467859	33783.176078
HLA A*2301	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.523830	0.055954	-4.467876	33406.424414
HLA A*0212	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.435092	-0.032788	-4.467880	27232.799919
HLA A*0203	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.398901	-0.069085	-4.467986	25055.370452
HLA B*4801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.413082	-0.055017	-4.468099	25887.035530
HLA A*0212	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.353377	-0.114983	-4.468361	22561.979844
HLA B*3901	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.494179	0.025675	-4.468505	31201.788854
HLA B*0803	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.467776	-0.000735	-4.468511	29361.347370
HLA A*2902	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.465455	-0.003120	-4.468574	29204.830497
HLA A*2501	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.511998	0.043160	-4.468838	32508.579122
HLA B*5401	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.547301	0.078424	-4.468878	35261.546001
HLA B*4002	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.623326	0.154429	-4.468897	42007.417700
HLA B*1502	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.581305	0.112320	-4.468986	38133.392708
HLA B*1509	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.540422	0.071401	-4.469021	34707.398113
HLA B*1509	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.517761	0.048624	-4.469137	32942.858025
HLA B*5101	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.495054	0.025675	-4.469379	31264.645019
HLA A*0201	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.390384	-0.079025	-4.469409	24568.800010
HLA A*0216	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.477350	0.007934	-4.469416	30015.814486
HLA B*0803	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.436925	-0.032788	-4.469713	27347.957328
HLA B*4601	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.414758	-0.055017	-4.469774	25987.081150
HLA B*4001	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.395870	-0.073933	-4.469803	24881.123830
HLA A*2602	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.556706	0.086816	-4.469890	36033.490871
HLA B*4801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.401076	-0.069030	-4.470106	25181.201683
HLA B*4501	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.615779	0.145582	-4.470197	41283.778511
HLA B*0802	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.495906	0.025675	-4.470232	31326.102533
HLA B*4403	1:202-210	9	LGAQWTPAN	0.874779	-0.688964	-4.656165	0.185815	-4.470350	45306.940612
HLA A*6801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.536515	0.066046	-4.470469	34396.548350
HLA A*2902	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.437808	-0.032788	-4.470596	27403.642926
HLA B*1502	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.616886	0.146138	-4.470748	41389.106098
HLA B*5301	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.551263	0.080331	-4.470931	35584.640383
HLA A*0202	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.503136	0.032127	-4.471009	31851.928373
HLA A*2301	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.531962	0.060842	-4.471120	34037.806255
HLA B*5401	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.402120	-0.069085	-4.471205	25241.759398
HLA B*3801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.553960	0.082695	-4.471265	35806.328358
HLA B*4403	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.612464	0.141148	-4.471316	40969.844541
HLA B*3801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.566826	0.095477	-4.471348	36882.943209
HLA A*0216	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.490801	0.019419	-4.471382	30959.998728

HLA B*4601	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.402437	-0.069085	-4.471522	25260.201073
HLA B*1517	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.479592	0.007934	-4.471658	30171.127576
HLA B*5301	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.552994	0.081144	-4.471850	35726.802705
HLA A*1101	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.497532	0.025675	-4.471858	31443.596076
HLA B*7301	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.553102	0.081144	-4.471958	35735.694601
HLA A*2902	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.393086	-0.079025	-4.472111	24722.128129
HLA A*0211	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.550649	0.078424	-4.472226	35534.431000
HLA A*3201	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.609960	0.137730	-4.472230	40734.253803
HLA B*4403	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.626686	0.154429	-4.472257	42333.653302
HLA A*2602	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.626810	0.154429	-4.472381	42345.793122
HLA B*1509	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.553546	0.081144	-4.472402	35772.251929
HLA A*3201	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.559300	0.086816	-4.472484	36249.345486
HLA A*0101	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.359183	-0.113369	-4.472552	22865.609607
HLA A*0211	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.512031	0.039331	-4.472700	32511.041365
HLA A*3001	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.212782	-0.260222	-4.473004	16322.311992
HLA A*3201	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.614205	0.141148	-4.473057	41134.411129
HLA B*4403	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.616386	0.143276	-4.473109	41341.440634
HLA A*2602	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.492540	0.019419	-4.473121	31084.189870
HLA A*0301	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.360087	-0.113369	-4.473457	22913.283897
HLA B*4501	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.586918	0.113362	-4.473557	38629.435843
HLA B*5401	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.556001	0.082233	-4.473769	35975.057145
HLA A*0212	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.399911	-0.073933	-4.473844	25113.723411
HLA B*3501	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.470856	-0.003120	-4.473976	29570.328964
HLA A*0201	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.393730	-0.080273	-4.474003	24758.801151
HLA B*1503	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.522690	0.048624	-4.474067	33318.887653
HLA B*4002	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.471234	-0.003120	-4.474354	29596.095708
HLA A*2301	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.540727	0.066046	-4.474681	34731.815911
HLA A*3301	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.629188	0.154429	-4.474759	42578.263987
HLA A*0219	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.405879	-0.069030	-4.474909	25461.195922
HLA A*0219	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.471845	-0.003120	-4.474965	29637.754014
HLA B*5801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.359986	-0.114983	-4.474970	22907.954309
HLA A*6802	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.440907	-0.034103	-4.475011	27599.884883
HLA B*3501	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.442289	-0.032788	-4.475077	27687.820314
HLA B*7301	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.524011	0.048624	-4.475387	33420.343142
HLA A*0211	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.557688	0.082233	-4.475456	36115.066818
HLA B*4501	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.483565	0.007934	-4.475631	30448.403090
HLA A*0101	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.343775	-0.132020	-4.475795	22068.603998
HLA A*3201	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.622125	0.146138	-4.475987	41891.450521
HLA B*4002	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.619386	0.143276	-4.476110	41628.033833
HLA B*4501	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.630645	0.154429	-4.476216	42721.316849
HLA A*2601	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.396016	-0.080273	-4.476289	24889.470685
HLA A*0216	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.442216	-0.034103	-4.476319	27683.177274
HLA A*2402	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.568122	0.091584	-4.476539	36993.249843
HLA A*2602	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.619917	0.143276	-4.476641	41678.960848
HLA B*4001	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.407817	-0.069030	-4.476847	25575.087244
HLA A*2603	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.590238	0.113362	-4.476877	38925.857453
HLA A*0206	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.514028	0.037065	-4.476963	32660.884581
HLA B*1509	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.528628	0.051389	-4.477239	33777.510893
HLA B*0803	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.520407	0.043160	-4.477246	33144.143048
HLA A*3101	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.398687	-0.079025	-4.477712	25043.038731
HLA B*4002	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.598518	0.120764	-4.477754	39675.076523
HLA B*1501	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.348619	-0.129234	-4.477853	22316.161710
HLA B*5701	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.408954	-0.069030	-4.477984	25642.140451
HLA B*1517	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.475139	-0.003120	-4.478259	29863.401084
HLA B*4801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.445491	-0.032788	-4.478279	27892.735973
HLA A*0203	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.409279	-0.069030	-4.478308	25661.291116
HLA A*2301	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.529706	0.051389	-4.478317	33861.489373
HLA B*3801	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.544545	0.066046	-4.478499	35038.491761
HLA B*1502	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.605559	0.126963	-4.478596	40323.589009
HLA A*6801	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.624254	0.145582	-4.478672	42097.279591
HLA B*1517	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.445905	-0.032788	-4.478693	27919.306424
HLA A*8001	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.445949	-0.032788	-4.478737	27922.176338
HLA A*3201	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.614443	0.135619	-4.478823	41156.893064
HLA A*2602	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.614452	0.135619	-4.478833	41157.783690
HLA B*5801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.351869	-0.127048	-4.478917	22483.754653

HLA A*0206	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.561379	0.082233	-4.479147	36423.314487
HLA A*0212	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.347135	-0.132020	-4.479154	22239.991927
HLA A*2602	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.592562	0.113362	-4.479200	39134.683748
HLA A*3301	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.616996	0.137730	-4.479266	41399.631228
HLA B*0801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.358339	-0.121106	-4.479445	22821.244255
HLA B*1502	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.617382	0.137730	-4.479652	41436.378183
HLA A*3301	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.577495	0.097746	-4.479748	37800.242090
HLA A*2601	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.358664	-0.121106	-4.479769	22838.288152
HLA B*4501	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.476786	-0.003120	-4.479906	29976.868040
HLA B*5301	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.523088	0.043160	-4.479927	33349.364084
HLA A*6801	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.633114	0.153079	-4.480035	42964.913297
HLA A*6801	1:266-274	9	GERAQVQRD	1.044888	-0.837722	-4.687227	0.207166	-4.480061	48666.182263
HLA B*3801	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.579769	0.099536	-4.480233	37998.712585
HLA A*0202	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.551843	0.071401	-4.480442	35632.221879
HLA A*6801	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.594216	0.113627	-4.480589	39284.014804
HLA A*3002	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.563090	0.082233	-4.480857	36567.046895
HLA B*5801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.351928	-0.129234	-4.481161	22486.795724
HLA B*3901	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.354343	-0.127048	-4.481391	22612.201416
HLA A*6802	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.354442	-0.127048	-4.481490	22617.339839
HLA A*2402	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.583549	0.101982	-4.481567	38330.916559
HLA B*5801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.352919	-0.128649	-4.481568	22538.191121
HLA B*4402	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.407869	-0.073933	-4.481801	25578.131310
HLA B*4501	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.623140	0.141148	-4.481992	41989.468354
HLA B*4402	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.448069	-0.034103	-4.482172	28058.761719
HLA A*6801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.533670	0.051389	-4.482281	34171.940187
HLA B*4002	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.627865	0.145582	-4.482283	42448.777783
HLA A*0301	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.367516	-0.114983	-4.482500	23308.611736
HLA A*2603	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.580354	0.097746	-4.482608	38049.933713
HLA A*2501	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.490613	0.007934	-4.482679	30946.602415
HLA B*5701	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.427743	-0.055017	-4.482760	26775.840122
HLA A*0202	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.569657	0.086816	-4.482840	37124.165432
HLA B*5701	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.408966	-0.073933	-4.482899	25642.834066
HLA B*5701	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.351061	-0.132020	-4.483080	22441.951254
HLA A*0301	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.351159	-0.132020	-4.483179	22447.050989
HLA A*0206	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.502898	0.019419	-4.483480	31834.529271
HLA A*0301	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.354265	-0.129234	-4.483499	22608.164903
HLA A*3201	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.597329	0.113627	-4.483702	39566.618328
HLA A*0101	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.362886	-0.121106	-4.483991	23061.394904
HLA A*2402	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.308885	-0.175217	-4.484102	20365.027901
HLA B*0802	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.492201	0.007934	-4.484268	31059.983969
HLA B*5101	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.492265	0.007934	-4.484331	31064.521139
HLA B*1501	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.405367	-0.079025	-4.484392	25431.185812
HLA A*0203	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.326454	-0.158117	-4.484571	21205.790097
HLA A*2602	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.582417	0.097746	-4.484670	38231.096343
HLA B*1509	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.567533	0.082695	-4.484838	36943.051458
HLA B*1501	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.371628	-0.113369	-4.484997	23530.329374
HLA B*5401	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.309790	-0.175217	-4.485006	20407.488534
HLA A*0219	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.450918	-0.034103	-4.485022	28243.494262
HLA A*2603	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.517437	0.032127	-4.485310	32918.273228
HLA B*5801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.350238	-0.135106	-4.485344	22399.498494
HLA B*5401	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.544245	0.058419	-4.485826	35014.237202
HLA A*0206	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.493780	0.007934	-4.485846	31173.106348
HLA A*0211	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.544484	0.058419	-4.486065	35033.563694
HLA A*0202	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.544616	0.058419	-4.486197	35044.178853
HLA A*2602	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.613284	0.126963	-4.486322	41047.270779
HLA B*1503	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.512014	0.025675	-4.486340	32509.810220
HLA A*0201	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.311216	-0.175217	-4.486432	20474.612851
HLA A*6802	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.406255	-0.080273	-4.486528	25483.244222
HLA A*3201	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.623371	0.136752	-4.486618	42011.735776
HLA B*1509	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.523694	0.037065	-4.486629	33395.944005
HLA A*0212	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.417563	-0.069085	-4.486648	26155.485611
HLA A*1101	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.485970	-0.000735	-4.486705	30617.546988
HLA A*0212	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.431916	-0.055017	-4.486933	27034.341253
HLA B*4402	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.454292	-0.032788	-4.487080	28463.761169
HLA A*8001	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.418051	-0.069030	-4.487081	26184.933818

HLA A*0216	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.373717	-0.113369	-4.487086	23643.768507
HLA B*3901	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.495227	0.007934	-4.487294	31277.163756
HLA B*2705	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.366271	-0.121106	-4.487377	23241.876043
HLA B*5701	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.418340	-0.069085	-4.487426	26202.363500
HLA A*0219	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.374231	-0.113369	-4.487601	23671.797434
HLA A*0212	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.407382	-0.080273	-4.487656	25549.503747
HLA B*4402	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.418639	-0.069030	-4.487669	26220.372175
HLA B*4402	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.407695	-0.080273	-4.487968	25567.893620
HLA A*3201	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.513899	0.025675	-4.488224	32651.167979
HLA A*0101	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.363332	-0.124898	-4.488230	23085.111412
HLA A*0216	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.414445	-0.073933	-4.488378	25968.389773
HLA B*4403	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.626310	0.137730	-4.488580	42297.025897
HLA A*2602	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.520771	0.032127	-4.488644	33171.947156
HLA B*4501	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.641452	0.152623	-4.488829	43797.796563
HLA A*3301	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.615852	0.126963	-4.488890	41290.702652
HLA A*0211	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.496851	0.007934	-4.488917	31394.303906
HLA A*3101	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.353004	-0.135927	-4.488930	22542.580997
HLA B*4601	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.408719	-0.080273	-4.488993	25628.272089
HLA B*0803	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.508481	0.019419	-4.489062	32246.368216
HLA A*6801	1:216-224	9	IEQVRTQIG	0.834121	-0.647621	-4.675590	0.186500	-4.489091	47379.478815
HLA B*3801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.586876	0.097746	-4.489130	38625.674369
HLA A*2402	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.571466	0.082233	-4.489233	37279.132943
HLA B*0802	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.420420	-0.069030	-4.489450	26328.114708
HLA B*4001	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.409213	-0.080273	-4.489486	25657.404317
HLA B*3801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.547947	0.058419	-4.489529	35314.044332
HLA B*4002	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.591580	0.101982	-4.489598	39046.287155
HLA B*7301	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.555708	0.066046	-4.489661	35950.737735
HLA A*0219	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.368745	-0.121106	-4.489851	23374.653855
HLA A*0203	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.434904	-0.055017	-4.489921	27221.016355
HLA A*3101	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.435052	-0.055017	-4.490069	27230.295485
HLA B*4501	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.629968	0.139834	-4.490134	42654.806810
HLA B*4403	1:425-433	9	HADSIVREE	0.866576	-0.713953	-4.642796	0.152623	-4.490173	43933.536856
HLA B*4601	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.411257	-0.079025	-4.490282	25778.448177
HLA A*2403	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.363372	-0.127048	-4.490420	23087.234604
HLA A*2402	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.581855	0.091322	-4.490534	38181.696874
HLA A*3201	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.489920	-0.000735	-4.490655	30897.253585
HLA A*2902	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.416881	-0.073933	-4.490814	26114.483282
HLA A*0301	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.363825	-0.127048	-4.490874	23111.352773
HLA B*3801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.510358	0.019419	-4.490939	32386.054869
HLA A*6801	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.628138	0.137191	-4.490947	42475.424753
HLA A*2501	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.458160	-0.032788	-4.490948	28718.353633
HLA A*0301	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.366154	-0.124898	-4.491051	23235.590094
HLA A*3301	1:209-217	9	ANIANALIE	0.862105	-0.714430	-4.638969	0.147675	-4.491294	43548.064386
HLA B*4002	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.436486	-0.055017	-4.491502	27320.304777
HLA B*0702	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.356471	-0.135106	-4.491578	22723.304000
HLA B*1502	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.605235	0.113627	-4.491608	40293.496075
HLA B*1509	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.490876	-0.000735	-4.491611	30965.358878
HLA B*1503	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.417706	-0.073933	-4.491639	26164.118430
HLA B*3501	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.412831	-0.079025	-4.491856	25872.054946
HLA B*5801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.367002	-0.124898	-4.491900	23281.012844
HLA B*7301	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.583500	0.091584	-4.491916	38326.562120
HLA A*2602	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.633283	0.141148	-4.492135	42981.651907
HLA B*5101	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.491431	-0.000735	-4.492165	31004.918647
HLA B*4501	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.649483	0.157255	-4.492228	44615.195640
HLA B*1502	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.558414	0.066046	-4.492368	36175.489265
HLA A*3001	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.274691	-0.217813	-4.492504	18823.076388
HLA A*3301	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.630010	0.137191	-4.492819	42658.960652
HLA B*7301	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.590649	0.097746	-4.492903	38962.727204
HLA A*6901	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.357855	-0.135106	-4.492961	22795.825579
HLA B*0801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.365921	-0.127048	-4.492970	23223.148931
HLA B*4002	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.650552	0.157255	-4.493297	44725.151197
HLA A*0206	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.419388	-0.073933	-4.493321	26265.661171
HLA B*0803	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.501345	0.007934	-4.493412	31720.894306
HLA A*3002	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.554357	0.060842	-4.493515	35839.080025
HLA B*0702	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.372422	-0.121106	-4.493528	23573.394944

HLA A*0206	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.525681	0.032127	-4.493555	33549.139737
HLA A*0101	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.378639	-0.114983	-4.493622	23913.264617
HLA A*0101	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.365052	-0.128649	-4.493701	23176.710599
HLA B*5101	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.361812	-0.132020	-4.493832	23004.450193
HLA A*0202	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.595893	0.101982	-4.493911	39436.049069
HLA A*2603	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.631688	0.137730	-4.493958	42824.056398
HLA A*2301	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.542654	0.048624	-4.494030	34886.232287
HLA A*0250	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.585713	0.091584	-4.494129	38522.377235
HLA B*4801	1:78-86 9		LDPALLDLG	0.630546	-0.699631	-4.425253	-0.069085	-4.494338	26622.733948
HLA A*0219	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.414194	-0.080273	-4.494467	25953.362110
HLA B*4801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.276826	-0.217813	-4.494639	18915.868516
HLA B*4501	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.630492	0.135619	-4.494873	42706.296846
HLA A*0301	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.366248	-0.128649	-4.494897	23240.618717
HLA A*6901	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.381562	-0.113369	-4.494931	24074.741299
HLA A*3301	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.641229	0.146138	-4.495091	43775.292930
HLA B*3901	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.494548	-0.000735	-4.495283	31228.301432
HLA B*4501	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.607638	0.112320	-4.495319	40517.111247
HLA B*5101	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.461261	-0.034103	-4.495364	28924.166925
HLA A*6802	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.440400	-0.055017	-4.495417	27567.652259
HLA B*4801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.421491	-0.073933	-4.495424	26393.143960
HLA A*1101	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.461345	-0.034103	-4.495449	28929.800629
HLA A*0250	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.597442	0.101982	-4.495459	39576.894111
HLA A*2403	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.363621	-0.132020	-4.495641	23100.477735
HLA A*2301	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.538824	0.043160	-4.495664	34579.953713
HLA B*5401	1:76-84 9		PKLDPALLD	0.940422	-0.901091	-4.535138	0.039331	-4.495807	34287.677246
HLA A*0250	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.578559	0.082695	-4.495864	37892.991983
HLA A*2403	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.440985	-0.055017	-4.496002	27604.812630
HLA A*0219	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.416985	-0.079025	-4.496010	26120.700187
HLA A*3002	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.587339	0.091322	-4.496017	38666.861554
HLA B*4002	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.649264	0.153079	-4.496186	44592.754503
HLA B*1801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.539532	0.043160	-4.496371	34636.308773
HLA A*3001	1:41-49 9		SEVIPHTAS	0.820502	-1.024433	-4.292561	-0.203931	-4.496492	19613.756875
HLA B*4002	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.417593	-0.079025	-4.496618	26157.325153
HLA B*5101	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.381872	-0.114983	-4.496855	24091.939340
HLA B*5301	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.588516	0.091584	-4.496932	38771.804607
HLA B*5701	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.416719	-0.080273	-4.496993	26104.737026
HLA B*4501	1:61-69 9		LVLSGGPAS	0.960251	-0.839487	-4.617939	0.120764	-4.497175	41489.539649
HLA A*6801	1:87-95 9		VPVLGICYG	0.826712	-0.689960	-4.634065	0.136752	-4.497313	43059.152843
HLA B*3801	1:44-52 9		IPHTASIEE	0.804394	-0.767329	-4.534483	0.037065	-4.497418	34235.963866
HLA A*0101	1:58-66 9		PVALVLSGG	0.638622	-0.767856	-4.368200	-0.129234	-4.497434	23345.334863
HLA A*0250	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.597016	0.099536	-4.497480	39538.159782
HLA A*3101	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.384191	-0.113369	-4.497560	24220.923764
HLA A*3201	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.597296	0.099536	-4.497760	39563.621727
HLA B*5101	1:78-86 9		LDPALLDLG	0.630546	-0.699631	-4.428793	-0.069085	-4.497879	26840.668359
HLA A*0216	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.494844	-0.003120	-4.497964	31249.595336
HLA B*1517	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.322921	-0.175217	-4.498137	21033.949787
HLA A*0250	1:83-91 9		LDLGVPVLG	0.788514	-0.708183	-4.578857	0.080331	-4.498526	37919.035533
HLA B*5701	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.377448	-0.121106	-4.498554	23847.764853
HLA B*3801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.590088	0.091322	-4.498766	38912.382373
HLA B*4801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.419785	-0.079025	-4.498811	26289.686091
HLA B*1501	1:41-49 9		SEVIPHTAS	0.820502	-1.024433	-4.294920	-0.203931	-4.498851	19720.579400
HLA A*2602	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.581087	0.082233	-4.498854	38114.211873
HLA B*0802	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.464844	-0.034103	-4.498947	29163.780701
HLA B*4002	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.634613	0.135619	-4.498994	43113.463307
HLA B*4501	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.652248	0.153079	-4.499169	44900.186569
HLA B*5401	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.547797	0.048624	-4.499173	35301.819565
HLA A*2603	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.642730	0.143276	-4.499454	43926.882444
HLA B*4002	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.639305	0.139834	-4.499470	43581.766819
HLA A*0211	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.525207	0.025675	-4.499532	33512.497342
HLA A*0250	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.586549	0.086816	-4.499733	38596.639761
HLA B*0702	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.444730	-0.055017	-4.499747	27843.888294
HLA B*5301	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.595264	0.095477	-4.499786	39378.914130
HLA A*2402	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.582541	0.082695	-4.499846	38242.059693
HLA B*3801	1:83-91 9		LDLGVPVLG	0.788514	-0.708183	-4.580255	0.080331	-4.499924	38041.289166
HLA A*0206	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.525611	0.025675	-4.499936	33543.695265

HLA A*3301	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.595492	0.095477	-4.500014	39399.584003
HLA B*1502	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.345180	-0.154863	-4.500043	22140.114051
HLA A*0202	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.543246	0.043160	-4.500086	34933.824844
HLA A*3301	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.641238	0.141148	-4.500090	43776.240218
HLA A*2603	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.654539	0.154429	-4.500110	45137.644677
HLA A*0206	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.466021	-0.034103	-4.500124	29242.932100
HLA A*2403	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.270499	-0.229683	-4.500182	18642.284157
HLA B*5701	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.421197	-0.079025	-4.500223	26375.301996
HLA A*2301	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.537297	0.037065	-4.500232	34458.569343
HLA A*2301	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.539978	0.039331	-4.500647	34671.929009
HLA A*2902	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.368719	-0.132020	-4.500739	23373.262899
HLA A*0202	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.566849	0.066046	-4.500803	36884.938589
HLA B*4601	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.368910	-0.132020	-4.500929	23383.507331
HLA B*4002	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.637742	0.136752	-4.500990	43425.259780
HLA A*3002	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.567039	0.066046	-4.500993	36901.105149
HLA A*0211	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.538089	0.037065	-4.501024	34521.449187
HLA B*0801	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.431942	-0.069085	-4.501027	27035.950081
HLA A*0301	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.365202	-0.135927	-4.501129	23184.736528
HLA A*0206	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.540584	0.039331	-4.501254	34720.356191
HLA A*0101	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.366553	-0.135106	-4.501659	23256.969258
HLA B*7301	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.601260	0.099536	-4.501723	39926.351152
HLA B*1502	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.562594	0.060842	-4.501752	36525.329915
HLA A*0206	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.550546	0.048624	-4.501922	35525.973564
HLA B*5801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.347231	-0.154863	-4.502094	22244.925426
HLA A*0202	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.593617	0.091322	-4.502295	39229.859015
HLA B*0802	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.469547	-0.032788	-4.502336	29481.358563
HLA A*2602	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.568409	0.066046	-4.502363	37017.673686
HLA A*2602	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.594169	0.091584	-4.502585	39279.764590
HLA B*3801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.581049	0.078424	-4.502626	38110.912917
HLA B*3801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.574093	0.071401	-4.502691	37505.289923
HLA A*3002	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.585441	0.082695	-4.502746	38498.210211
HLA A*2403	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.422741	-0.080273	-4.503014	26469.214455
HLA B*5301	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.585760	0.082695	-4.503065	38526.545496
HLA A*0201	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.389745	-0.113369	-4.503114	24532.673857
HLA A*3002	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.535453	0.032127	-4.503326	34312.542257
HLA A*2601	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.388488	-0.114983	-4.503471	24461.771822
HLA B*5801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.367577	-0.135927	-4.503504	23311.890489
HLA A*0301	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.368409	-0.135106	-4.503515	23356.577885
HLA A*2602	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.640879	0.137191	-4.503688	43740.021045
HLA A*2403	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.434951	-0.069030	-4.503981	27223.961768
HLA A*2301	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.523452	0.019419	-4.504033	33377.340348
HLA A*3301	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.639784	0.135619	-4.504165	43629.890965
HLA B*4403	1:253-261	9	LTCVFVDHG	0.691438	-0.551604	-4.644041	0.139834	-4.504207	44059.685668
HLA A*2602	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.595534	0.091322	-4.504212	39403.420842
HLA A*6901	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.375563	-0.128649	-4.504213	23744.519952
HLA A*8001	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.449520	-0.055017	-4.504537	28152.727891
HLA B*4501	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.596142	0.091584	-4.504559	39458.670088
HLA A*0219	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.471822	-0.032788	-4.504610	29636.150688
HLA B*1502	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.470718	-0.034103	-4.504821	29560.892110
HLA A*2602	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.618510	0.113627	-4.504883	41544.117791
HLA A*2902	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.449995	-0.055017	-4.505012	28183.509941
HLA A*2501	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.470943	-0.034103	-4.505047	29576.248528
HLA B*1509	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.544658	0.039331	-4.505328	35047.591551
HLA A*6901	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.350483	-0.154863	-4.505345	22412.104635
HLA B*4601	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.384271	-0.121106	-4.505376	24225.379279
HLA B*1502	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.504656	-0.000735	-4.505391	31963.611781
HLA A*2301	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.537671	0.032127	-4.505544	34488.222404
HLA A*2402	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.571816	0.066046	-4.505770	37309.194778
HLA B*3901	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.502710	-0.003120	-4.505830	31820.754550
HLA A*0202	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.513854	0.007934	-4.505920	32647.812007
HLA B*4601	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.392642	-0.113369	-4.506011	24696.863436
HLA B*0803	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.531830	0.025675	-4.506155	34027.495934
HLA A*0250	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.385173	-0.121106	-4.506279	24275.757329
HLA B*2705	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.503328	-0.003120	-4.506448	31866.061370
HLA A*0201	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.391472	-0.114983	-4.506455	24630.416552

HLA B*4403	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.642190	0.135619	-4.506571	43872.259335
HLA A*2402	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.578023	0.071401	-4.506622	37846.281507
HLA B*0803	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.472590	-0.034103	-4.506693	29688.624439
HLA B*5301	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.598027	0.091322	-4.506705	39630.242581
HLA A*0211	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.555334	0.048624	-4.506710	35919.827200
HLA B*4403	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.620072	0.113362	-4.506710	41693.845090
HLA A*1101	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.503707	-0.003120	-4.506826	31893.828551
HLA B*3801	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.558217	0.051389	-4.506828	36159.053748
HLA B*4501	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.644046	0.137191	-4.506855	44060.162387
HLA A*6801	1:116-124	9	GRTELKVLG	0.786426	-0.631997	-4.661303	0.154429	-4.506874	45846.170034
HLA A*2403	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.432997	-0.073933	-4.506929	27101.701315
HLA A*6801	1:459-467	9	VQGDGRTYG	0.772938	-0.629662	-4.650216	0.143276	-4.506940	44690.564568
HLA B*1502	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.598607	0.091584	-4.507023	39683.233596
HLA B*4001	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.392099	-0.114983	-4.507083	24666.019428
HLA B*5801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.349078	-0.158117	-4.507195	22339.716084
HLA B*5101	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.504111	-0.003120	-4.507230	31923.519599
HLA B*5301	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.606962	0.099536	-4.507426	40454.032792
HLA B*4601	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.372368	-0.135106	-4.507474	23570.461949
HLA B*1517	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.375751	-0.132020	-4.507771	23754.798594
HLA B*1502	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.599223	0.091322	-4.507901	39739.520133
HLA A*0101	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.381049	-0.127048	-4.508098	24046.365348
HLA B*1502	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.594965	0.086816	-4.508149	39351.867906
HLA B*4501	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.621914	0.113627	-4.508287	41871.058956
HLA B*4403	1:121-129	9	KVLGGKLHS	0.986765	-0.841183	-4.653888	0.145582	-4.508306	45070.054799
HLA B*4001	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.395071	-0.113369	-4.508441	24835.400492
HLA B*4403	1:162-170	9	PVAAFEAFD	1.020247	-0.862992	-4.665718	0.157255	-4.508463	46314.581393
HLA A*0202	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.590840	0.082233	-4.508607	38979.804452
HLA A*2902	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.395308	-0.113369	-4.508678	24848.974233
HLA B*1509	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.540810	0.032127	-4.508683	34738.392869
HLA A*3301	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.622118	0.113362	-4.508757	41890.770642
HLA B*0801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.395515	-0.113369	-4.508885	24860.806907
HLA B*4002	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.528482	0.019419	-4.509063	33766.183372
HLA A*2603	1:286-294	9	VDAAETFLE	0.900383	-0.773420	-4.636030	0.126963	-4.509067	43254.336109
HLA A*6901	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.384198	-0.124898	-4.509095	24221.316865
HLA A*2402	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.560541	0.051389	-4.509152	36353.036918
HLA B*5301	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.607028	0.097746	-4.509281	40460.161107
HLA B*0702	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.334168	-0.175217	-4.509384	21585.783532
HLA A*0250	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.600900	0.091322	-4.509579	39893.317264
HLA A*2603	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.611600	0.101982	-4.509617	40888.361306
HLA A*2603	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.601777	0.091322	-4.510455	39973.898811
HLA B*4002	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.647770	0.137191	-4.510579	44439.588331
HLA A*0250	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.576642	0.066046	-4.510595	37726.083202
HLA A*3301	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.624273	0.113627	-4.510646	42099.101564
HLA B*4403	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.657055	0.146138	-4.510917	45399.930905
HLA A*6802	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.431972	-0.079025	-4.510997	27037.851548
HLA B*4002	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.648994	0.137730	-4.511264	44565.020317
HLA A*0219	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.456252	-0.055017	-4.511269	28592.475472
HLA A*3101	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.384482	-0.127048	-4.511530	24237.177246
HLA A*0202	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.590048	0.078424	-4.511624	38908.803839
HLA A*0212	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.382567	-0.129234	-4.511801	24130.549323
HLA B*4501	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.648609	0.136752	-4.511857	44525.498794
HLA A*2601	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.383279	-0.128649	-4.511928	24170.136470
HLA A*3101	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.396955	-0.114983	-4.511939	24943.388713
HLA A*0101	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.376076	-0.135927	-4.512002	23772.539710
HLA B*4501	1:143-151	9	DAVTAAPDG	0.837028	-0.699298	-4.649798	0.137730	-4.512068	44647.550044
HLA A*3301	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.563837	0.051389	-4.512448	36630.008965
HLA B*5301	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.583982	0.071401	-4.512580	38369.090902
HLA A*3002	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.584066	0.071401	-4.512665	38376.564240
HLA A*2402	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.571189	0.058419	-4.512770	37255.342772
HLA B*5301	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.568740	0.055954	-4.512787	37045.921332
HLA B*4002	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.625255	0.112320	-4.512935	42194.409400
HLA B*4601	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.385943	-0.127048	-4.512992	24318.871533
HLA A*2603	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.648719	0.135619	-4.513100	44536.821500
HLA B*0801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.378251	-0.135106	-4.513357	23891.928403
HLA A*0250	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.584762	0.071401	-4.513360	38438.066906

HLA A*0212	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.434350	-0.079025	-4.513375	27186.284539
HLA A*3201	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.584780	0.071401	-4.513379	38439.730507
HLA A*3001	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.283783	-0.229683	-4.513466	19221.315693
HLA A*2403	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.392397	-0.121106	-4.513503	24682.972186
HLA B*1501	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.386653	-0.127048	-4.513701	24358.635852
HLA B*1509	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.386926	-0.127048	-4.513974	24373.926841
HLA B*4402	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.389150	-0.124898	-4.514048	24499.118907
HLA B*1501	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.433875	-0.080273	-4.514149	27156.591659
HLA A*2301	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.539992	0.025675	-4.514318	34673.054455
HLA B*1517	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.440461	-0.073933	-4.514393	27571.530118
HLA A*0216	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.481612	-0.032788	-4.514400	30311.825934
HLA A*6801	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.606024	0.091584	-4.514441	40366.805087
HLA B*1502	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.551648	0.037065	-4.514583	35616.225862
HLA A*3201	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.565975	0.051389	-4.514586	36810.783077
HLA A*0301	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.359761	-0.154863	-4.514624	22896.060167
HLA B*1801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.356643	-0.158117	-4.514760	22732.279703
HLA A*3301	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.580934	0.066046	-4.514888	38100.811641
HLA B*1501	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.386261	-0.128649	-4.514910	24336.638944
HLA B*4801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.310983	-0.203931	-4.514914	20463.650014
HLA A*3201	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.610423	0.095477	-4.514945	40777.689401
HLA B*4002	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.628688	0.113627	-4.515061	42529.229039
HLA B*4403	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.652542	0.137191	-4.515351	44930.559966
HLA A*2402	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.594108	0.078424	-4.515684	39274.240000
HLA A*2603	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.661855	0.146138	-4.515717	45904.492434
HLA B*2705	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.482958	-0.032788	-4.515747	30405.934333
HLA B*1501	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.380060	-0.135927	-4.515987	23991.660549
HLA B*7301	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.617990	0.101982	-4.516008	41494.477926
HLA B*1503	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.523973	0.007934	-4.516040	33417.450461
HLA A*2603	1:103-111	9	LGGIVAHTG	0.860185	-0.722994	-4.653475	0.137191	-4.516284	45027.162198
HLA B*4601	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.401490	-0.114983	-4.516473	25205.189143
HLA A*2601	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.403205	-0.113369	-4.516574	25304.926770
HLA A*0250	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.559935	0.043160	-4.516774	36302.332509
HLA A*0206	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.387670	-0.129234	-4.516904	24415.762401
HLA B*3801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.565705	0.048624	-4.517081	36787.888840
HLA B*4501	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.597435	0.080331	-4.517103	39576.251796
HLA A*0219	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.402129	-0.114983	-4.517113	25242.305624
HLA B*0702	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.438104	-0.079025	-4.517129	27422.328878
HLA A*0216	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.341928	-0.175217	-4.517145	21974.963708
HLA B*1502	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.359061	-0.158117	-4.517178	22859.178090
HLA A*2601	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.385363	-0.132020	-4.517383	24286.397322
HLA B*5401	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.543361	0.025675	-4.517687	34943.086489
HLA A*6802	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.404474	-0.113369	-4.517843	25378.959152
HLA A*3002	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.485369	-0.032788	-4.518157	30575.173128
HLA B*0801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.389047	-0.129234	-4.518281	24493.287950
HLA A*6801	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.537774	0.019419	-4.518355	34496.432789
HLA A*2501	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.439350	-0.079025	-4.518375	27501.068139
HLA A*0203	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.382450	-0.135927	-4.518376	24124.023026
HLA B*3901	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.484293	-0.034103	-4.518396	30499.509903
HLA B*3801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.517710	-0.000735	-4.518444	32938.937480
HLA A*0250	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.600729	0.082233	-4.518496	39877.565629
HLA B*7301	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.605442	0.086816	-4.518625	40312.683176
HLA A*0212	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.405378	-0.113369	-4.518748	25431.873721
HLA A*0201	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.393896	-0.124898	-4.518794	24768.312886
HLA B*0801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.390266	-0.128649	-4.518916	24562.155185
HLA B*4002	1:97-105	9	QAMAQALGG	0.707847	-0.594485	-4.632917	0.113362	-4.519555	42945.393158
HLA A*0301	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.361551	-0.158117	-4.519668	22990.640220
HLA A*2603	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.485632	-0.034103	-4.519735	30593.704471
HLA B*4403	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.656794	0.136752	-4.520042	45372.676535
HLA A*0216	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.388121	-0.132020	-4.520141	24441.136197
HLA A*8001	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.439982	-0.080273	-4.520255	27541.118483
HLA A*0101	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.365407	-0.154863	-4.520269	23195.651233
HLA B*4403	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.634345	0.113627	-4.520719	43086.882252
HLA B*3801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.581693	0.060842	-4.520851	38167.446980
HLA B*4403	1:342-350	9	VVESGGGSG	0.794299	-0.641220	-4.674002	0.153079	-4.520923	47206.524478
HLA A*2601	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.393936	-0.127048	-4.520985	24770.590885

HLA B*1501	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.362930	-0.158117	-4.521047	23063.765458
HLA B*4001	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.442150	-0.079025	-4.521175	27678.984230
HLA A*8001	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.389247	-0.132020	-4.521267	24504.553548
HLA A*3101	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.392637	-0.128649	-4.521286	24696.596223
HLA A*0201	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.389334	-0.132020	-4.521353	24509.459015
HLA A*0216	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.406389	-0.114983	-4.521372	25491.103541
HLA B*0702	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.447878	-0.073933	-4.521811	28046.469034
HLA A*0201	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.394897	-0.127048	-4.521946	24825.460082
HLA A*2603	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.663169	0.141148	-4.522020	46043.523614
HLA A*3001	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.309902	-0.212130	-4.522033	20412.788530
HLA B*5101	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.489370	-0.032788	-4.522158	30858.165064
HLA A*0250	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.600696	0.078424	-4.522272	39874.545479
HLA A*2402	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.559352	0.037065	-4.522287	36253.660052
HLA B*3501	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.367523	-0.154863	-4.522386	23308.990030
HLA B*4002	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.617927	0.095477	-4.522449	41488.417395
HLA A*3301	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.542001	0.019419	-4.522582	34833.804600
HLA B*7301	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.519556	-0.003120	-4.522676	33079.297742
HLA B*2705	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.386756	-0.135927	-4.522683	24364.434753
HLA B*4501	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.588779	0.066046	-4.522733	38795.303856
HLA A*6901	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.386808	-0.135927	-4.522735	24367.334721
HLA B*3501	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.467851	-0.055017	-4.522868	29366.430743
HLA A*6801	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.614562	0.091322	-4.523241	41168.249996
HLA B*1509	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.531179	0.007934	-4.523246	33976.542582
HLA A*0203	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.388143	-0.135106	-4.523249	24442.326241
HLA A*0206	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.454252	-0.069030	-4.523282	28461.143531
HLA A*0201	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.394162	-0.129234	-4.523396	24783.458817
HLA B*3801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.579362	0.055954	-4.523409	37963.165815
HLA A*2902	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.443229	-0.080273	-4.523502	27747.800403
HLA B*5401	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.555694	0.032127	-4.523567	35949.570817
HLA A*3301	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.522886	-0.000735	-4.523620	33333.851886
HLA B*4501	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.625685	0.101982	-4.523703	42236.202960
HLA B*1502	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.606403	0.082695	-4.523708	40401.979574
HLA A*3002	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.560813	0.037065	-4.523748	36375.857322
HLA A*3201	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.606457	0.082695	-4.523762	40407.007002
HLA A*2902	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.454703	-0.069085	-4.523789	28490.721443
HLA B*4801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.443616	-0.080273	-4.523890	27772.580028
HLA B*1503	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.454938	-0.069030	-4.523968	28506.138778
HLA B*7301	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.606823	0.082695	-4.524128	40441.122594
HLA A*0211	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.543735	0.019419	-4.524316	34973.156498
HLA B*0801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.369457	-0.154863	-4.524320	23413.000924
HLA B*5701	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.410998	-0.113369	-4.524368	25763.112300
HLA A*3001	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.314970	-0.209501	-4.524471	20652.383243
HLA A*2402	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.585314	0.060842	-4.524472	38486.965217
HLA B*1503	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.491729	-0.032788	-4.524517	31026.228080
HLA B*4002	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.573169	0.048624	-4.524545	37425.635141
HLA A*2601	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.399681	-0.124898	-4.524579	25100.412419
HLA A*2403	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.445707	-0.079025	-4.524732	27906.621917
HLA B*5301	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.607169	0.082233	-4.524936	40473.296338
HLA B*1517	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.404027	-0.121106	-4.525133	25352.886057
HLA A*8001	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.349947	-0.175217	-4.525164	22384.477361
HLA B*3801	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.557338	0.032127	-4.525211	36085.967150
HLA B*1509	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.586209	0.060842	-4.525367	38566.375119
HLA A*3301	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.605764	0.080331	-4.525432	40342.572190
HLA B*4601	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.370634	-0.154863	-4.525497	23476.544529
HLA A*3002	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.491395	-0.034103	-4.525499	31002.402752
HLA B*7301	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.533599	0.007934	-4.525666	34166.394645
HLA B*4001	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.393706	-0.132020	-4.525726	24757.461763
HLA A*2601	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.389853	-0.135927	-4.525780	24538.779693
HLA A*2603	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.446826	-0.079025	-4.525851	27978.577067
HLA A*0201	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.229115	-0.297084	-4.526199	16947.876657
HLA A*0101	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.351044	-0.175217	-4.526261	22441.101411
HLA A*0250	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.587231	0.060842	-4.526389	38657.240313
HLA B*1501	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.401605	-0.124898	-4.526503	25211.871535
HLA B*1501	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.411698	-0.114983	-4.526682	25804.679721
HLA B*1503	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.471725	-0.055017	-4.526742	29629.577957

HLA A*0201	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.391025	-0.135927	-4.526952	24605.112473
HLA A*2501	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.471993	-0.055017	-4.527010	29647.856964
HLA A*0201	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.398367	-0.128649	-4.527017	25024.620219
HLA A*0216	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.458037	-0.069085	-4.527123	28710.275888
HLA A*3002	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.607643	0.080331	-4.527312	40517.549635
HLA B*5701	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.412455	-0.114983	-4.527438	25849.670243
HLA B*5301	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.606074	0.078424	-4.527650	40371.391326
HLA A*8001	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.412782	-0.114983	-4.527765	25869.115849
HLA A*2402	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.567209	0.039331	-4.527878	36915.481372
HLA A*3201	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.619395	0.091322	-4.528074	41628.934655
HLA A*2501	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.447845	-0.080273	-4.528119	28044.344919
HLA A*0216	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.473177	-0.055017	-4.528194	29728.804646
HLA A*2602	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.398990	-0.129234	-4.528224	25060.521759
HLA A*2603	1:87-95	9	VPVLGICYG	0.826712	-0.689960	-4.665001	0.136752	-4.528249	46238.224596
HLA A*8001	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.459546	-0.069085	-4.528631	28810.164312
HLA A*0212	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.393901	-0.135106	-4.529007	24768.580875
HLA A*6801	1:387-395	9	GRELGLPEE	0.855151	-0.709013	-4.675240	0.146138	-4.529102	47341.302862
HLA B*0803	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.525996	-0.003120	-4.529116	33573.469169
HLA A*2501	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.408019	-0.121106	-4.529125	25586.988834
HLA B*4403	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.620723	0.091584	-4.529139	41756.371792
HLA A*0206	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.528407	-0.000735	-4.529142	33760.338396
HLA A*3002	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.607584	0.078424	-4.529161	40512.070119
HLA A*3201	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.561295	0.032127	-4.529168	36416.221518
HLA A*0203	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.450500	-0.079025	-4.529525	28216.309990
HLA B*1517	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.460582	-0.069030	-4.529612	28878.980539
HLA A*0201	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.394535	-0.135106	-4.529642	24804.786035
HLA B*3801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.572840	0.043160	-4.529680	37397.300277
HLA B*7301	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.590525	0.060842	-4.529683	38951.557251
HLA A*6802	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.414755	-0.114983	-4.529739	25986.940563
HLA B*4001	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.460824	-0.069085	-4.529909	28895.076928
HLA A*2501	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.400907	-0.129234	-4.530141	25171.395213
HLA A*2603	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.622060	0.091584	-4.530476	41885.105414
HLA A*6801	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.612723	0.082233	-4.530490	40994.232452
HLA B*1502	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.611151	0.080331	-4.530820	40846.133639
HLA B*4001	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.321450	-0.209501	-4.530951	20962.836894
HLA B*4601	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.406156	-0.124898	-4.531054	25477.454696
HLA A*2402	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.579842	0.048624	-4.531218	38005.085752
HLA A*0216	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.410157	-0.121106	-4.531263	25713.264129
HLA B*7301	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.476608	-0.055017	-4.531624	29964.545537
HLA A*0203	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.418282	-0.113369	-4.531651	26198.819942
HLA B*3901	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.457833	-0.073933	-4.531765	28696.766279
HLA B*3901	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.499113	-0.032788	-4.531902	31558.286321
HLA A*2402	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.587875	0.055954	-4.531921	38714.584803
HLA B*4403	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.587903	0.055954	-4.531949	38717.098184
HLA A*0250	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.590379	0.058419	-4.531960	38938.494578
HLA B*4403	1:61-69	9	LVLSGGPAS	0.960251	-0.839487	-4.652777	0.120764	-4.532013	44954.873477
HLA A*0250	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.588316	0.055954	-4.532363	38753.979856
HLA A*0203	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.405341	-0.127048	-4.532389	25429.672478
HLA A*3101	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.397310	-0.135106	-4.532416	24963.773124
HLA B*5401	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.498580	-0.034103	-4.532683	31519.555118
HLA B*5301	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.591107	0.058419	-4.532689	39003.851778
HLA A*0203	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.417826	-0.114983	-4.532809	26171.338220
HLA B*1502	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.611313	0.078424	-4.532889	40861.383626
HLA B*4002	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.632435	0.099536	-4.532899	42897.791946
HLA B*5301	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.584332	0.051389	-4.532943	38400.031677
HLA B*4801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.419593	-0.113369	-4.532962	26278.026286
HLA B*4002	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.624837	0.091584	-4.533253	42153.797417
HLA A*0203	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.453024	-0.080273	-4.533297	28380.730181
HLA B*1503	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.530519	-0.003120	-4.533639	33924.931400
HLA A*2403	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.378836	-0.154863	-4.533699	23924.134008
HLA A*2601	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.398621	-0.135106	-4.533727	25039.245577
HLA B*5401	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.533042	-0.000735	-4.533777	34122.616487
HLA A*6801	1:226-234	9	GHAICGLSG	0.874566	-0.733418	-4.674998	0.141148	-4.533850	47314.930757
HLA A*3301	1:432-440	9	EELTAAGLD	0.962462	-0.871140	-4.625199	0.091322	-4.533877	42188.931346
HLA A*0101	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.376085	-0.158117	-4.534202	23773.054143

HLA B*3801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.573876	0.039331	-4.534546	37486.627817
HLA A*2602	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.577946	0.043160	-4.534785	37839.525551
HLA A*0219	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.465725	-0.069085	-4.534810	29223.005563
HLA A*3101	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.409929	-0.124898	-4.534827	25699.774396
HLA B*3501	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.465903	-0.069085	-4.534989	29235.023119
HLA A*2402	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.578293	0.043160	-4.535133	37869.834414
HLA B*4402	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.421811	-0.113369	-4.535180	26412.569727
HLA B*0801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.410301	-0.124898	-4.535198	25721.750990
HLA A*3002	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.238499	-0.297084	-4.535583	17318.055923
HLA A*3301	1:348-356	9	GSGTANIKS	1.212474	-1.120890	-4.627226	0.091584	-4.535642	42386.360772
HLA B*0802	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.455394	-0.080273	-4.535668	28536.072202
HLA A*1101	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.461825	-0.073933	-4.535757	28961.745684
HLA B*0802	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.462158	-0.073933	-4.536091	28984.002769
HLA B*4801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.415042	-0.121106	-4.536148	26004.097773
HLA A*6802	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.400224	-0.135927	-4.536150	25131.799621
HLA B*7301	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.573310	0.037065	-4.536245	37437.785225
HLA B*1509	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.579513	0.043160	-4.536352	37976.312188
HLA B*1502	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.594890	0.058419	-4.536471	39345.056040
HLA A*6802	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.404507	-0.132020	-4.536526	25380.881388
HLA B*4403	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.636102	0.099536	-4.536566	43261.590753
HLA B*2705	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.456787	-0.080273	-4.537061	28627.764755
HLA A*6801	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.574241	0.037065	-4.537176	37518.074767
HLA B*4001	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.410183	-0.127048	-4.537232	25714.794340
HLA B*4801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.401478	-0.135927	-4.537405	25204.507366
HLA B*1503	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.362207	-0.175217	-4.537423	23025.367553
HLA A*8001	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.463794	-0.073933	-4.537726	29093.341453
HLA A*2402	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.563426	0.025675	-4.537751	36595.346625
HLA B*2705	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.468739	-0.069030	-4.537769	29426.544719
HLA A*2501	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.410808	-0.127048	-4.537856	25751.825351
HLA B*4001	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.408675	-0.129234	-4.537908	25625.637948
HLA A*2301	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.545849	0.007934	-4.537916	35143.852521
HLA B*4001	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.417008	-0.121106	-4.538114	26122.113326
HLA A*1101	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.469212	-0.069085	-4.538297	29458.560186
HLA A*0216	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.409194	-0.129234	-4.538428	25656.293912
HLA A*1101	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.505650	-0.032788	-4.538438	32036.840526
HLA B*5701	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.409436	-0.129234	-4.538670	25670.594059
HLA A*6802	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.413797	-0.124898	-4.538694	25929.644540
HLA B*5701	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.411706	-0.127048	-4.538754	25805.098526
HLA A*3002	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.594728	0.055954	-4.538774	39330.371966
HLA A*0203	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.414001	-0.124898	-4.538899	25941.851468
HLA A*2602	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.621921	0.082695	-4.539226	41871.738515
HLA B*4001	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.410667	-0.128649	-4.539316	25743.467837
HLA A*3201	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.605601	0.066046	-4.539555	40327.515830
HLA A*0212	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.412601	-0.127048	-4.539649	25858.342016
HLA B*5301	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.600529	0.060842	-4.539687	39859.232522
HLA A*1101	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.470755	-0.069030	-4.539785	29563.450959
HLA B*4601	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.410651	-0.129234	-4.539884	25742.492970
HLA A*2301	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.539238	-0.000735	-4.539973	34612.894367
HLA B*7301	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.583307	0.043160	-4.540147	38309.563810
HLA B*1509	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.471187	-0.069030	-4.540217	29592.893649
HLA A*8001	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.419278	-0.121106	-4.540384	26258.983587
HLA B*1517	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.485444	-0.055017	-4.540461	30580.466651
HLA B*4501	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.635990	0.095477	-4.540512	43250.358272
HLA B*1517	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.460460	-0.080273	-4.540733	28870.857613
HLA B*0702	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.412283	-0.128649	-4.540933	25839.463657
HLA B*0802	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.485996	-0.055017	-4.541013	30619.369055
HLA A*2603	1:296-304	9	LSGVSAPEG	0.703401	-0.589774	-4.654661	0.113627	-4.541034	45150.344326
HLA A*2301	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.538042	-0.003120	-4.541162	34517.714245
HLA A*0216	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.462281	-0.079025	-4.541306	28992.157528
HLA B*2705	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.472228	-0.069085	-4.541313	29663.900466
HLA B*1502	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.623547	0.082233	-4.541314	42028.785147
HLA A*3201	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.623749	0.082233	-4.541516	42048.343609
HLA B*5701	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.416804	-0.124898	-4.541702	26109.821575
HLA A*6801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.366706	-0.175217	-4.541922	23265.148842
HLA A*6801	1:454-462	9	VRSVGVQGD	0.870068	-0.734449	-4.677850	0.135619	-4.542231	47626.699218

HLA B*5701	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.406438	-0.135927	-4.542365	25493.999691
HLA B*5701	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.407267	-0.135106	-4.542373	25542.731866
HLA A*0206	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.473422	-0.069085	-4.542507	29745.535624
HLA A*2602	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.421865	-0.121106	-4.542971	26415.856381
HLA A*2402	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.575150	0.032127	-4.543023	37596.705909
HLA A*0201	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.384912	-0.158117	-4.543029	24261.184169
HLA B*4501	1:274-282	9	DFVAATGAN	0.641972	-0.542436	-4.642615	0.099536	-4.543079	43915.239649
HLA B*4601	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.367906	-0.175217	-4.543123	23329.553241
HLA B*5101	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.469273	-0.073933	-4.543205	29462.704034
HLA B*4601	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.407458	-0.135927	-4.543384	25553.927170
HLA A*3201	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.586552	0.043160	-4.543391	38596.848565
HLA A*2603	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.630257	0.086816	-4.543441	42683.199461
HLA A*0219	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.414252	-0.129234	-4.543486	25956.872467
HLA A*2403	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.407610	-0.135927	-4.543537	25562.914604
HLA B*0802	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.428887	-0.114983	-4.543871	26846.477189
HLA A*0212	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.418998	-0.124898	-4.543896	26242.084103
HLA B*4001	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.389310	-0.154863	-4.544173	24508.133116
HLA A*0250	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.583514	0.039331	-4.544183	38327.806195
HLA B*7301	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.470356	-0.073933	-4.544288	29536.274509
HLA B*4801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.409257	-0.135106	-4.544363	25660.041723
HLA B*1801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.511937	-0.032788	-4.544725	32504.006881
HLA B*4001	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.386676	-0.158117	-4.544793	24359.953663
HLA A*0216	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.475788	-0.069030	-4.544818	29908.024312
HLA A*3101	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.390360	-0.154863	-4.545223	24567.470901
HLA B*1503	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.285291	-0.260222	-4.545514	19288.190248
HLA B*0702	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.465300	-0.080273	-4.545573	29194.404696
HLA B*4403	1:414-422	9	EVTAKRLDT	0.476628	-0.364308	-4.657922	0.112320	-4.545603	45490.650996
HLA B*4801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.417356	-0.128649	-4.546005	26143.036726
HLA B*0702	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.477021	-0.069085	-4.546106	29993.089581
HLA A*2902	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.410183	-0.135927	-4.546110	25714.794340
HLA B*1502	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.617549	0.071401	-4.546147	41452.297041
HLA B*4601	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.417664	-0.128649	-4.546313	26161.570745
HLA A*3001	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.298519	-0.247969	-4.546488	19884.701759
HLA A*8001	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.433203	-0.113369	-4.546573	27114.606701
HLA A*0211	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.512705	-0.034103	-4.546809	32561.558456
HLA A*0202	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.583885	0.037065	-4.546820	38360.581372
HLA B*4501	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.602784	0.055954	-4.546831	40066.779671
HLA B*5301	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.586164	0.039331	-4.546834	38562.411167
HLA A*8001	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.411191	-0.135927	-4.547118	25774.543633
HLA A*0212	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.411236	-0.135927	-4.547162	25777.193080
HLA A*0206	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.544101	-0.003120	-4.547221	35002.684296
HLA A*3201	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.625664	0.078424	-4.547240	42234.146571
HLA B*1503	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.415535	-0.132020	-4.547555	26033.657211
HLA B*4002	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.645665	0.097746	-4.547919	44224.699294
HLA B*1502	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.421014	-0.127048	-4.548063	26364.174722
HLA A*3002	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.591537	0.043160	-4.548377	39042.485091
HLA B*2705	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.474496	-0.073933	-4.548428	29819.167069
HLA A*0219	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.373771	-0.175217	-4.548987	23646.710624
HLA A*3002	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.574692	0.025675	-4.549017	37557.064989
HLA B*4002	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.480397	-0.069085	-4.549483	30227.164853
HLA B*1801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.413801	-0.135927	-4.549728	25929.925095
HLA A*1101	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.494786	-0.055017	-4.549802	31245.369201
HLA A*6901	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.345955	-0.203931	-4.549886	22179.675290
HLA A*0216	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.469618	-0.080273	-4.549891	29486.143677
HLA B*0802	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.471098	-0.079025	-4.550123	29586.810692
HLA A*0250	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.598844	0.048624	-4.550220	39704.922393
HLA B*1517	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.481417	-0.069085	-4.550502	30298.218349
HLA B*4501	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.648386	0.097746	-4.550639	44502.621262
HLA A*2602	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.587708	0.037065	-4.550643	38699.717304
HLA A*2602	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.606633	0.055954	-4.550679	40423.405135
HLA B*0702	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.421482	-0.129234	-4.550715	26392.572831
HLA A*2602	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.609290	0.058419	-4.550871	40671.497373
HLA B*5701	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.422299	-0.128649	-4.550949	26442.307383
HLA A*2602	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.629435	0.078424	-4.551011	42602.456945
HLA B*4001	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.416186	-0.135106	-4.551292	26072.698915

HLA B*4801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.424252	-0.127048	-4.551300	26561.449501
HLA A*3301	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.638250	0.086816	-4.551434	43476.033422
HLA B*4002	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.632884	0.081144	-4.551740	42942.140663
HLA B*4801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.436986	-0.114983	-4.551969	27351.804284
HLA A*0202	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.591880	0.039331	-4.552550	39073.334738
HLA A*0202	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.601199	0.048624	-4.552575	39920.735621
HLA B*0702	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.437940	-0.114983	-4.552923	27411.946221
HLA A*0201	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.398116	-0.154863	-4.552979	25010.138706
HLA A*3101	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.423935	-0.129234	-4.553168	26542.057826
HLA B*4601	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.395099	-0.158117	-4.553216	24837.012826
HLA B*3801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.579031	0.025675	-4.553357	37934.218768
HLA A*3301	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.636232	0.082695	-4.553537	43274.464891
HLA A*2501	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.484549	-0.069085	-4.553634	30517.500094
HLA B*2705	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.440362	-0.113369	-4.553732	27565.266155
HLA B*4403	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.561835	0.007934	-4.553902	36461.561496
HLA B*5301	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.602803	0.048624	-4.554179	40068.513763
HLA A*2602	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.605613	0.051389	-4.554224	40328.606682
HLA B*2705	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.336468	-0.217813	-4.554281	21700.411200
HLA A*0211	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.551258	-0.003120	-4.554378	35584.255367
HLA A*0250	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.591582	0.037065	-4.554517	39046.498392
HLA B*4403	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.650040	0.095477	-4.554562	44672.435421
HLA B*4002	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.641788	0.086816	-4.554972	43831.692268
HLA A*3301	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.626425	0.071401	-4.555024	42308.239672
HLA B*1503	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.476084	-0.079025	-4.555109	29928.417948
HLA B*0702	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.428147	-0.127048	-4.555196	26800.766662
HLA A*2603	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.650735	0.095477	-4.555258	44744.027912
HLA B*4002	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.637940	0.082233	-4.555707	43444.998035
HLA B*1509	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.481854	-0.073933	-4.555787	30328.720953
HLA B*0801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.420032	-0.135927	-4.555959	26304.623884
HLA A*6801	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.642820	0.086816	-4.556003	43935.913676
HLA A*2601	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.401257	-0.154863	-4.556120	25191.693387
HLA B*4801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.424383	-0.132020	-4.556403	26569.497612
HLA B*5101	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.501493	-0.055017	-4.556510	31731.707359
HLA B*4403	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.595959	0.039331	-4.556629	39442.023172
HLA B*4402	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.425161	-0.132020	-4.557181	26617.117525
HLA A*2602	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.637564	0.080331	-4.557233	43407.409086
HLA B*4403	1:179-187	9	HPEVMHTPH	0.590316	-0.488334	-4.659503	0.101982	-4.557521	45656.577752
HLA A*2402	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.577236	0.019419	-4.557817	37777.754319
HLA B*1501	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.340065	-0.217813	-4.557878	21880.892118
HLA B*4402	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.442935	-0.114983	-4.557918	27729.042681
HLA B*3901	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.477733	-0.080273	-4.558006	30042.294463
HLA B*7301	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.590198	0.032127	-4.558071	38922.277680
HLA A*1101	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.477907	-0.080273	-4.558180	30054.323756
HLA B*4402	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.429562	-0.128649	-4.558211	26888.192431
HLA B*5801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.354521	-0.203931	-4.558453	22621.500370
HLA A*2602	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.619325	0.060842	-4.558483	41622.178965
HLA A*2601	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.383305	-0.175217	-4.558522	24171.574848
HLA B*1509	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.555506	-0.003120	-4.558625	35934.015528
HLA B*4402	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.437550	-0.121106	-4.558656	27387.340203
HLA A*6801	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.656442	0.097746	-4.558696	45335.872298
HLA A*3101	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.354928	-0.203931	-4.558859	22642.681988
HLA A*6802	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.355565	-0.203931	-4.559496	22675.902316
HLA B*7301	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.585175	0.025675	-4.559501	38474.682775
HLA B*4002	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.625701	0.066046	-4.559655	42237.802442
HLA B*5301	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.591918	0.032127	-4.559791	39076.717003
HLA B*1517	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.480809	-0.079025	-4.559834	30255.795386
HLA B*4501	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.642660	0.082695	-4.559965	43919.753836
HLA A*6801	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.640306	0.080331	-4.559974	43682.321741
HLA A*2602	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.631568	0.071401	-4.560167	42812.242685
HLA A*6802	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.425476	-0.135106	-4.560582	26636.419938
HLA B*0702	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.424661	-0.135927	-4.560587	26586.464115
HLA A*0206	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.527932	-0.032788	-4.560720	33723.465330
HLA B*4501	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.643245	0.082233	-4.561012	43978.956351
HLA A*0206	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.403113	-0.158117	-4.561230	25299.588356
HLA B*3901	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.482533	-0.079025	-4.561558	30376.175720

HLA B*4002	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.644297	0.082695	-4.561602	44085.674354
HLA B*7301	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.613028	0.051389	-4.561639	41023.073245
HLA A*2902	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.343829	-0.217813	-4.561642	22071.350109
HLA B*4801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.436779	-0.124898	-4.561677	27338.786003
HLA B*2705	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.506707	-0.055017	-4.561724	32114.927627
HLA B*4001	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.436859	-0.124898	-4.561757	27343.815058
HLA A*0206	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.446795	-0.114983	-4.561779	27976.609443
HLA B*5801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.352334	-0.209501	-4.561835	22507.851211
HLA B*4002	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.613261	0.051389	-4.561872	41045.050228
HLA B*1502	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.581303	0.019419	-4.561884	38133.186411
HLA A*2902	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.446990	-0.114983	-4.561974	27989.174343
HLA B*0803	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.493054	-0.069030	-4.562084	31121.039177
HLA A*3201	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.620612	0.058419	-4.562194	41745.755967
HLA B*3801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.570456	0.007934	-4.562522	37192.513062
HLA A*6801	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.618510	0.055954	-4.562556	41544.117791
HLA A*2603	1:83-91	9	LDLGVPVLG	0.788514	-0.708183	-4.642916	0.080331	-4.562585	43945.659982
HLA B*0702	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.430797	-0.132020	-4.562817	26964.814483
HLA B*1509	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.588650	0.025675	-4.562975	38783.762267
HLA B*4501	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.650169	0.086816	-4.563352	44685.729409
HLA A*0216	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.405360	-0.158117	-4.563476	25430.773075
HLA A*3301	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.596034	0.032127	-4.563907	39448.851826
HLA B*5801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.346108	-0.217813	-4.563921	22187.475984
HLA A*2603	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.629968	0.066046	-4.563922	42654.806810
HLA A*2403	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.434766	-0.129234	-4.563999	27212.329243
HLA A*2403	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.439211	-0.124898	-4.564109	27492.291653
HLA B*4002	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.624964	0.060842	-4.564122	42166.113774
HLA B*5801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.352125	-0.212130	-4.564255	22497.016736
HLA B*7301	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.563663	-0.000735	-4.564398	36615.347742
HLA A*3301	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.642963	0.078424	-4.564539	43950.415062
HLA B*0803	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.509585	-0.055017	-4.564602	32328.463702
HLA A*0301	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.360684	-0.203931	-4.564615	22944.790954
HLA B*5401	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.561572	-0.003120	-4.564692	36439.475851
HLA A*6901	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.355421	-0.209501	-4.564923	22668.420429
HLA B*4402	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.429919	-0.135106	-4.565025	26910.311769
HLA A*3201	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.621618	0.055954	-4.565664	41842.527440
HLA A*1101	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.410925	-0.154863	-4.565788	25758.792019
HLA A*3002	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.491971	-0.073933	-4.565904	31043.521288
HLA A*3301	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.624616	0.058419	-4.566197	42132.366414
HLA B*4001	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.391082	-0.175217	-4.566298	24608.307343
HLA B*2705	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.451426	-0.114983	-4.566409	28276.517094
HLA A*1101	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.487399	-0.079025	-4.566424	30718.420415
HLA A*0219	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.408381	-0.158117	-4.566498	25608.314823
HLA B*2705	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.487474	-0.079025	-4.566499	30723.738739
HLA B*1517	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.439535	-0.127048	-4.566584	27512.824091
HLA A*2402	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.565879	-0.000735	-4.566613	36802.619150
HLA B*3901	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.511655	-0.055017	-4.566672	32482.912560
HLA A*0250	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.592400	0.025675	-4.566725	39120.078188
HLA B*1801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.434787	-0.132020	-4.566807	27213.654217
HLA B*1509	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.511862	-0.055017	-4.566878	32498.380389
HLA A*0202	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.586305	0.019419	-4.566886	38574.930301
HLA B*1517	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.451915	-0.114983	-4.566898	28308.353350
HLA B*4403	1:122-130	9	VLGGKLHSD	0.877825	-0.780079	-4.664663	0.097746	-4.566916	46202.217934
HLA A*0203	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.435062	-0.132020	-4.567082	27230.884743
HLA A*0206	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.512390	-0.055017	-4.567407	32537.962317
HLA A*1101	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.454086	-0.113369	-4.567455	28450.213645
HLA A*8001	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.438281	-0.129234	-4.567514	27433.457517
HLA B*3501	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.443036	-0.124898	-4.567934	27735.493906
HLA A*0211	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.535314	-0.032788	-4.568102	34301.592009
HLA A*2602	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.593819	0.025675	-4.568144	39248.114971
HLA B*1509	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.453294	-0.114983	-4.568277	28398.392384
HLA A*2403	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.439714	-0.128649	-4.568363	27524.138358
HLA A*2301	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.534344	-0.034103	-4.568447	34225.038056
HLA B*0801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.364645	-0.203931	-4.568576	23155.029412
HLA A*0250	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.567857	-0.000735	-4.568592	36970.642134
HLA A*0219	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.443837	-0.124898	-4.568735	27786.706798

HLA B*0801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.410871	-0.158117	-4.568988	25755.587118
HLA B*4801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.414227	-0.154863	-4.569089	25955.327851
HLA B*0702	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.455953	-0.113369	-4.569323	28572.837589
HLA B*0802	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.500307	-0.069085	-4.569392	31645.134836
HLA A*2902	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.444497	-0.124898	-4.569395	27828.979685
HLA A*8001	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.411651	-0.158117	-4.569768	25801.887863
HLA A*3002	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.609109	0.039331	-4.569779	40654.558723
HLA A*2902	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.440740	-0.129234	-4.569974	27589.285745
HLA B*5701	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.415131	-0.154863	-4.569994	26009.444135
HLA A*2603	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.641417	0.071401	-4.570016	43794.242589
HLA B*1502	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.609351	0.039331	-4.570021	40677.218511
HLA A*0250	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.589557	0.019419	-4.570138	38864.835807
HLA A*8001	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.443386	-0.127048	-4.570434	27757.859765
HLA A*2902	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.412746	-0.158117	-4.570863	25867.016698
HLA B*4002	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.642324	0.071401	-4.570923	43885.790032
HLA B*5301	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.444110	-0.127048	-4.571158	27804.149739
HLA B*4501	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.642641	0.071401	-4.571240	43917.853069
HLA B*4501	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.590790	0.019419	-4.571371	38975.376298
HLA A*3201	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.608512	0.037065	-4.571448	40598.733176
HLA B*5101	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.492453	-0.079025	-4.571478	31077.968498
HLA B*4403	1:259-267	9	DHGLLRAGE	0.945168	-0.862935	-4.653721	0.082233	-4.571489	45052.746619
HLA B*4801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.442286	-0.129234	-4.571520	27687.670526
HLA B*1502	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.614762	0.043160	-4.571602	41187.185181
HLA A*0202	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.570883	-0.000735	-4.571618	37229.150837
HLA A*1101	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.439700	-0.132020	-4.571719	27523.244957
HLA A*3301	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.608917	0.037065	-4.571852	40636.527917
HLA A*0212	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.443872	-0.128649	-4.572521	27788.961734
HLA A*3301	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.628528	0.055954	-4.572574	42513.586584
HLA B*4501	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.653752	0.081144	-4.572608	45055.915225
HLA B*4402	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.443600	-0.129234	-4.572833	27771.528321
HLA A*2603	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.569739	-0.003120	-4.572859	37131.195414
HLA A*2603	1:152-160	9	FDVVASSAG	0.815306	-0.759352	-4.629002	0.055954	-4.573049	42560.070724
HLA A*3201	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.612514	0.039331	-4.573183	40974.499294
HLA B*5101	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.460067	-0.113369	-4.573437	28844.785973
HLA B*5701	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.415782	-0.158117	-4.573899	26048.449528
HLA A*0219	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.442054	-0.132020	-4.574074	27672.845561
HLA A*3301	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.453190	-0.121106	-4.574296	28391.633374
HLA A*0203	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.445677	-0.128649	-4.574326	27904.659353
HLA A*8001	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.419633	-0.154863	-4.574495	26280.443138
HLA B*1502	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.623241	0.048624	-4.574618	41999.237300
HLA B*0802	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.447782	-0.127048	-4.574830	28040.248864
HLA B*4402	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.447942	-0.127048	-4.574990	28050.565997
HLA A*3002	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.623909	0.048624	-4.575285	42063.814882
HLA B*4403	1:517-525	9	KPPATIEWE	0.833815	-0.746999	-4.662236	0.086816	-4.575419	45944.740859
HLA A*3201	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.624090	0.048624	-4.575466	42081.340696
HLA B*3801	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.506740	-0.069030	-4.575770	32117.360054
HLA B*4403	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.658495	0.082695	-4.575800	45550.738894
HLA A*0211	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.461157	-0.114983	-4.576141	28917.282777
HLA B*3501	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.446990	-0.129234	-4.576224	27989.174343
HLA A*6801	1:134-142	9	VQPVWMSHG	0.720369	-0.624892	-4.671765	0.095477	-4.576288	46964.025750
HLA B*3901	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.507273	-0.069085	-4.576358	32156.825840
HLA A*2603	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.659097	0.082695	-4.576402	45613.867257
HLA B*0802	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.444908	-0.132020	-4.576928	27855.338707
HLA B*3901	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.456104	-0.121106	-4.577210	28582.732158
HLA A*6801	1:223-231	9	IGDGHAICG	0.891696	-0.809001	-4.660305	0.082695	-4.577610	45740.881474
HLA A*0301	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.368212	-0.209501	-4.577713	23345.966350
HLA A*8001	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.443010	-0.135106	-4.578116	27733.843450
HLA B*0801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.330157	-0.247969	-4.578126	21387.363296
HLA A*2602	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.497957	-0.080273	-4.578231	31474.400408
HLA A*2501	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.463354	-0.114983	-4.578338	29063.924078
HLA A*2603	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.656832	0.078424	-4.578408	45376.604084
HLA A*0212	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.360665	-0.217813	-4.578478	22943.797945
HLA A*0301	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.352468	-0.226766	-4.579234	22514.792885
HLA B*2705	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.404408	-0.175217	-4.579625	25375.115118
HLA A*3201	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.587569	0.007934	-4.579636	38687.366966

HLA B*1509	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.545549	-0.034103	-4.579652	35119.525029
HLA A*3301	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.640729	0.060842	-4.579887	43724.879432
HLA A*6802	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.425394	-0.154863	-4.580256	26631.376913
HLA B*0702	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.422285	-0.158117	-4.580402	26441.449097
HLA B*1517	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.444636	-0.135927	-4.580563	27837.863652
HLA A*3002	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.588509	0.007934	-4.580575	38771.175358
HLA A*2603	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.641422	0.060842	-4.580580	43794.716435
HLA B*5301	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.606332	0.025675	-4.580658	40395.422999
HLA B*4801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.422562	-0.158117	-4.580679	26458.333832
HLA A*2301	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.548206	-0.032788	-4.580994	35335.065544
HLA A*0301	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.369022	-0.212130	-4.581153	23389.580224
HLA A*2902	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.446062	-0.135106	-4.581168	27929.427962
HLA A*2902	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.452723	-0.128649	-4.581372	28361.084299
HLA A*8001	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.456491	-0.124898	-4.581389	28608.257402
HLA A*1101	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.446375	-0.135106	-4.581481	27949.530842
HLA A*0202	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.512599	-0.069030	-4.581629	32553.632472
HLA B*1502	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.607526	0.025675	-4.581851	40506.591345
HLA A*0203	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.426991	-0.154863	-4.581854	26729.526837
HLA A*0250	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.589881	0.007934	-4.581947	38893.861755
HLA A*6801	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.640449	0.058419	-4.582030	43696.739427
HLA A*2501	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.450157	-0.132020	-4.582177	28194.032311
HLA B*1502	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.549801	-0.032788	-4.582589	35465.101045
HLA B*7301	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.502602	-0.080273	-4.582876	31812.836785
HLA A*2301	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.527881	-0.055017	-4.582897	33719.451884
HLA A*3101	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.285851	-0.297084	-4.582935	19313.040822
HLA B*3801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.579896	-0.003120	-4.583015	38009.814923
HLA B*5801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.356272	-0.226766	-4.583038	22712.857305
HLA A*0219	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.448017	-0.135106	-4.583123	28055.422432
HLA A*0219	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.454537	-0.128649	-4.583186	28479.780198
HLA B*3501	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.448108	-0.135106	-4.583215	28061.342349
HLA B*3501	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.447547	-0.135927	-4.583474	28025.083503
HLA A*8001	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.454957	-0.128649	-4.583606	28507.372525
HLA A*0212	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.428857	-0.154863	-4.583720	26844.589182
HLA B*4501	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.642174	0.058419	-4.583755	43870.597958
HLA A*2603	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.635271	0.051389	-4.583882	43178.819730
HLA B*4002	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.642336	0.058419	-4.583917	43886.977134
HLA B*4403	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.627673	0.043160	-4.584512	42429.951218
HLA B*4403	1:470-478	9	IVLRPVSSE	0.744457	-0.663313	-4.665845	0.081144	-4.584701	46328.113434
HLA B*4403	1:185-193	9	TPHGQQVLS	1.181185	-1.115139	-4.650777	0.066046	-4.584731	44748.385208
HLA A*6801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.456134	-0.128649	-4.584783	28584.742411
HLA A*0301	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.367211	-0.217813	-4.585024	23292.224888
HLA B*4501	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.636539	0.051389	-4.585151	43305.144178
HLA B*0803	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.511535	-0.073933	-4.585468	32473.951619
HLA A*0206	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.472134	-0.113369	-4.585504	29657.482023
HLA A*0216	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.449605	-0.135927	-4.585532	28158.211338
HLA B*5801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.355943	-0.229683	-4.585626	22695.661452
HLA A*3002	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.464588	-0.121106	-4.585694	29146.588533
HLA B*0803	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.516655	-0.069085	-4.585740	32859.024571
HLA A*3002	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.582734	-0.003120	-4.585854	38259.028051
HLA A*2602	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.634641	0.048624	-4.586017	43116.262267
HLA A*3002	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.454518	-0.132020	-4.586538	28478.547645
HLA A*2402	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.594928	0.007934	-4.586994	39348.461826
HLA A*6801	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.583883	-0.003120	-4.587002	38360.373846
HLA B*1503	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.460232	-0.127048	-4.587280	28855.711338
HLA B*1801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.327061	-0.260222	-4.587283	21235.408773
HLA A*2603	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.624348	0.037065	-4.587283	42106.390242
HLA A*6802	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.290479	-0.297084	-4.587563	19519.969912
HLA B*0802	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.412469	-0.175217	-4.587686	25850.509320
HLA B*4501	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.648567	0.060842	-4.587725	44521.163201
HLA B*5401	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.554954	-0.032788	-4.587742	35888.360780
HLA A*2902	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.290702	-0.297084	-4.587786	19530.004574
HLA B*1801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.475435	-0.113369	-4.588805	29883.764292
HLA A*6901	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.376846	-0.212130	-4.588977	23814.760189
HLA B*0802	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.475644	-0.113369	-4.589014	29898.156196
HLA A*2402	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.585899	-0.003120	-4.589018	38538.844495

HLA B*3801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.555041	-0.034103	-4.589144	35895.545125
HLA A*2902	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.434340	-0.154863	-4.589203	27185.696246
HLA B*7301	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.462384	-0.127048	-4.589432	28999.059501
HLA A*1101	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.474514	-0.114983	-4.589498	29820.457644
HLA A*0219	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.462492	-0.127048	-4.589540	29006.276958
HLA B*2705	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.462553	-0.127048	-4.589602	29010.357184
HLA A*0219	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.292573	-0.297084	-4.589657	19614.287423
HLA B*1502	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.520827	-0.069030	-4.589857	33176.254393
HLA A*0101	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.380389	-0.209501	-4.589891	24009.838343
HLA A*0216	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.454835	-0.135106	-4.589941	28499.354123
HLA B*5301	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.597907	0.007934	-4.589973	39619.309933
HLA B*0803	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.475019	-0.114983	-4.590003	29855.162778
HLA A*3002	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.476711	-0.113369	-4.590080	29971.679000
HLA A*2602	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.598036	0.007934	-4.590102	39631.100171
HLA A*0212	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.432026	-0.158117	-4.590143	27041.216008
HLA B*4501	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.622703	0.032127	-4.590577	41947.238148
HLA A*0101	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.386721	-0.203931	-4.590652	24362.457700
HLA A*0216	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.435938	-0.154863	-4.590801	27285.889114
HLA B*3901	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.477623	-0.113369	-4.590992	30034.656736
HLA A*6901	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.343352	-0.247969	-4.591321	22047.124492
HLA A*2601	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.379407	-0.212130	-4.591538	23955.605430
HLA A*3301	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.640186	0.048624	-4.591562	43670.271261
HLA A*3001	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.271086	-0.320678	-4.591764	18667.514387
HLA A*3201	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.611445	0.019419	-4.592026	40873.764613
HLA B*4402	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.437193	-0.154863	-4.592056	27364.828764
HLA A*0211	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.523151	-0.069085	-4.592236	33354.235682
HLA A*1101	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.456705	-0.135927	-4.592632	28622.344712
HLA B*5401	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.537809	-0.055017	-4.592826	34499.232231
HLA B*4601	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.389167	-0.203931	-4.593098	24500.046687
HLA A*0101	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.381040	-0.212130	-4.593170	24045.845001
HLA B*4002	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.630271	0.037065	-4.593206	42684.584952
HLA B*0702	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.438609	-0.154863	-4.593472	27454.243063
HLA B*3501	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.296452	-0.297084	-4.593536	19790.261590
HLA B*1502	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.601525	0.007934	-4.593591	39950.766290
HLA B*4501	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.636800	0.043160	-4.593640	43331.156627
HLA B*4002	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.636880	0.043160	-4.593720	43339.127529
HLA A*3301	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.619703	0.025675	-4.594029	41658.447349
HLA B*7301	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.560181	-0.034103	-4.594285	36322.959485
HLA A*0219	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.458557	-0.135927	-4.594483	28744.622005
HLA B*1517	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.481260	-0.113369	-4.594629	30287.238369
HLA A*0202	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.561927	-0.032788	-4.594715	36469.255175
HLA B*5101	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.473654	-0.121106	-4.594760	29761.470976
HLA B*4403	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.666622	0.071401	-4.595221	46411.146270
HLA A*2603	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.603402	0.007934	-4.595469	40123.827293
HLA B*0802	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.460561	-0.135106	-4.595667	28877.574484
HLA B*4402	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.378019	-0.217813	-4.595832	23879.135814
HLA A*3301	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.635167	0.039331	-4.595837	43168.542878
HLA A*0206	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.460009	-0.135927	-4.595935	28840.885059
HLA A*0211	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.541414	-0.055017	-4.596430	34786.724689
HLA B*4002	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.595785	-0.000735	-4.596520	39426.236436
HLA B*7301	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.563924	-0.032788	-4.596712	36637.341777
HLA B*1517	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.442019	-0.154863	-4.596881	27670.600047
HLA A*6801	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.596241	-0.000735	-4.596976	39467.636722
HLA A*3301	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.640292	0.043160	-4.597131	43680.903865
HLA A*2403	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.421959	-0.175217	-4.597175	26421.573273
HLA A*3301	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.517031	-0.080273	-4.597304	32887.479073
HLA B*0802	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.461418	-0.135927	-4.597345	28934.652754
HLA B*4403	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.518328	-0.079025	-4.597353	32985.836384
HLA B*0702	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.472560	-0.124898	-4.597457	29686.536554
HLA A*0201	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.388067	-0.209501	-4.597569	24438.095238
HLA A*6801	1:413-421	9	GEVTAKRLD	0.950238	-0.871814	-4.676194	0.078424	-4.597770	47445.398286
HLA B*3801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.565012	-0.032788	-4.597800	36729.225235
HLA B*5401	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.484460	-0.113369	-4.597829	30511.227080
HLA B*1509	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.462736	-0.135106	-4.597842	29022.601307
HLA B*0803	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.517656	-0.080273	-4.597929	32934.839227

HLA A*2602	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.637270	0.039331	-4.597940	43378.065350
HLA A*0202	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.564229	-0.034103	-4.598333	36663.117354
HLA B*4501	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.635428	0.037065	-4.598363	43194.473273
HLA A*2603	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.647371	0.048624	-4.598747	44398.736867
HLA A*0301	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.369069	-0.229683	-4.598752	23392.111062
HLA A*6801	1:405-413	9	PGLGIRIVG	1.006365	-0.934964	-4.670158	0.071401	-4.598757	46790.562887
HLA B*0803	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.519747	-0.079025	-4.598772	33093.796301
HLA A*0216	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.474491	-0.124898	-4.599389	29818.844434
HLA A*2601	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.395600	-0.203931	-4.599531	24865.649170
HLA A*0201	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.395938	-0.203931	-4.599869	24885.027656
HLA B*4002	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.632083	0.032127	-4.599956	42862.995221
HLA A*0211	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.442014	-0.158117	-4.600131	27670.300659
HLA B*1509	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.567526	-0.032788	-4.600314	36942.451889
HLA A*1101	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.473537	-0.127048	-4.600585	29753.421751
HLA A*0201	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.388749	-0.212130	-4.600879	24476.465471
HLA B*4001	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.383223	-0.217813	-4.601036	24166.998487
HLA B*4403	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.661935	0.060842	-4.601093	45912.936710
HLA B*3501	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.397670	-0.203931	-4.601601	24984.444518
HLA A*2603	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.568818	-0.032788	-4.601606	37052.535595
HLA A*0203	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.397738	-0.203931	-4.601669	24988.364555
HLA A*0202	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.598950	-0.003120	-4.602070	39714.589534
HLA A*0216	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.475160	-0.127048	-4.602209	29864.855139
HLA A*2603	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.660666	0.058419	-4.602248	45779.005130
HLA B*2705	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.473664	-0.128649	-4.602313	29762.115008
HLA B*7301	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.384748	-0.217813	-4.602560	24251.998386
HLA A*0250	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.599620	-0.003120	-4.602739	39775.869449
HLA B*5401	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.473565	-0.129234	-4.602799	29755.353367
HLA B*4403	1:433-441	9	ELTAAGLDN	0.769760	-0.737633	-4.635071	0.032127	-4.602944	43158.968922
HLA B*5801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.355386	-0.247969	-4.603355	22666.580999
HLA A*2301	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.529765	-0.073933	-4.603697	33866.069356
HLA B*4002	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.643167	0.039331	-4.603837	43971.105649
HLA B*1517	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.475238	-0.128649	-4.603887	29870.187278
HLA A*0219	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.449431	-0.154863	-4.604294	28146.940966
HLA A*2403	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.446219	-0.158117	-4.604336	27939.553169
HLA B*0802	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.483247	-0.121106	-4.604353	30426.173673
HLA B*5101	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.429181	-0.175217	-4.604398	26864.637887
HLA B*2705	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.475186	-0.129234	-4.604420	29866.632413
HLA B*1502	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.601574	-0.003120	-4.604694	39955.305261
HLA B*4402	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.446609	-0.158117	-4.604726	27964.655320
HLA B*1801	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.535843	-0.069085	-4.604928	34343.370187
HLA A*2301	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.536057	-0.069030	-4.605087	34360.281588
HLA A*0250	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.572305	-0.032788	-4.605093	37351.200837
HLA A*6801	1:65-73	9	GGPASVYAD	1.026523	-0.965681	-4.665997	0.060842	-4.605156	46344.407246
HLA B*0702	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.387424	-0.217813	-4.605237	24401.897249
HLA A*1101	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.480390	-0.124898	-4.605288	30226.674280
HLA B*5301	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.604601	-0.000735	-4.605335	40234.683535
HLA A*3101	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.447321	-0.158117	-4.605438	28010.532473
HLA A*2301	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.536466	-0.069085	-4.605551	34392.640860
HLA A*2603	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.625097	0.019419	-4.605679	42179.118277
HLA B*0803	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.484695	-0.121106	-4.605800	30527.737781
HLA A*6801	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.649168	0.043160	-4.606008	44582.864684
HLA A*0201	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.388248	-0.217813	-4.606061	24448.277327
HLA A*0211	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.537086	-0.069030	-4.606116	34441.795893
HLA A*0206	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.474228	-0.132020	-4.606247	29800.782443
HLA B*4403	1:383-391	9	VRAVGRELG	0.612712	-0.554293	-4.664729	0.058419	-4.606310	46209.217033
HLA B*1501	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.396887	-0.209501	-4.606389	24939.475732
HLA A*8001	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.402561	-0.203931	-4.606492	25267.444820
HLA B*1501	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.379905	-0.226766	-4.606672	23983.095791
HLA B*1517	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.471587	-0.135106	-4.606693	29620.122195
HLA A*2601	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.388930	-0.217813	-4.606743	24486.663547
HLA A*1101	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.310076	-0.297084	-4.607160	20420.962054
HLA A*3201	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.538206	-0.069030	-4.607236	34530.788311
HLA B*2705	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.452380	-0.154863	-4.607243	28338.692316
HLA A*3101	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.397818	-0.209501	-4.607319	24992.961243
HLA A*2301	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.527345	-0.080273	-4.607618	33677.886107

HLA A*2501	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.471899	-0.135927	-4.607826	29641.441994
HLA A*2501	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.479500	-0.128649	-4.608149	30164.762572
HLA B*5801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.347999	-0.260222	-4.608222	22284.312277
HLA A*2601	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.398800	-0.209501	-4.608301	25049.542618
HLA B*1801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.493529	-0.114983	-4.608512	31155.066764
HLA B*2705	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.476516	-0.132020	-4.608536	29958.224114
HLA B*0802	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.484065	-0.124898	-4.608963	30483.509202
HLA A*2301	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.487864	-0.121106	-4.608970	30751.342327
HLA A*0219	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.400052	-0.209501	-4.609553	25121.876482
HLA A*0206	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.529734	-0.080273	-4.610008	33863.687688
HLA A*2902	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.400776	-0.209501	-4.610277	25163.770598
HLA B*4501	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.649762	0.039331	-4.610432	44643.927116
HLA A*3002	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.435327	-0.175217	-4.610544	27247.536548
HLA B*5301	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.607577	-0.003120	-4.610697	40511.412627
HLA A*6901	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.393011	-0.217813	-4.610824	24717.848692
HLA A*1101	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.482369	-0.128649	-4.611018	30364.674676
HLA B*5401	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.537145	-0.073933	-4.611077	34446.454365
HLA B*1517	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.481863	-0.129234	-4.611097	30329.377260
HLA B*1501	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.399049	-0.212130	-4.611179	25063.911354
HLA B*1503	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.542257	-0.069085	-4.611342	34854.351383
HLA B*0801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.393941	-0.217813	-4.611754	24770.858899
HLA B*4801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.436915	-0.175217	-4.612132	27347.365537
HLA A*2402	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.578141	-0.034103	-4.612244	37856.520101
HLA B*1801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.487568	-0.124898	-4.612466	30730.387939
HLA A*2301	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.533529	-0.079025	-4.612554	34160.850003
HLA B*1801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.485625	-0.127048	-4.612673	30593.207949
HLA A*2603	1:319-327	9	GAVRDVLDG	0.742748	-0.699588	-4.655862	0.043160	-4.612701	45275.333030
HLA A*3301	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.610479	-0.003120	-4.613599	40782.984211
HLA A*2603	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.652948	0.039331	-4.613618	44972.630648
HLA A*0211	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.484528	-0.129234	-4.613761	30516.014264
HLA A*0301	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.365900	-0.247969	-4.613869	23222.018247
HLA A*0216	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.485327	-0.128649	-4.613976	30572.195923
HLA B*4601	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.404521	-0.209501	-4.614022	25381.705248
HLA A*0202	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.478283	-0.135927	-4.614210	30080.349508
HLA A*3201	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.581461	-0.032788	-4.614249	38147.010769
HLA A*3101	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.387978	-0.226766	-4.614744	24433.071874
HLA B*4402	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.402813	-0.212130	-4.614943	25282.075320
HLA A*2603	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.640705	0.025675	-4.615031	43722.514028
HLA A*0250	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.581115	-0.034103	-4.615219	38116.686277
HLA A*8001	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.397872	-0.217813	-4.615685	24996.071247
HLA B*1503	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.494621	-0.121106	-4.615727	31233.539062
HLA B*1801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.460937	-0.154863	-4.615799	28902.581222
HLA A*0211	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.535577	-0.080273	-4.615851	34322.381901
HLA B*1503	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.535779	-0.080273	-4.616053	34338.354120
HLA A*2602	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.547290	-0.069030	-4.616319	35260.592208
HLA A*2501	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.412399	-0.203931	-4.616330	25846.314208
HLA A*0101	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.356260	-0.260222	-4.616482	22712.242943
HLA A*0101	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.389900	-0.226766	-4.616666	24541.434878
HLA A*0206	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.412772	-0.203931	-4.616703	25868.556058
HLA B*4403	1:44-52	9	IPHTASIEE	0.804394	-0.767329	-4.653893	0.037065	-4.616828	45070.542450
HLA A*0216	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.399065	-0.217813	-4.616878	25064.860523
HLA B*4001	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.387572	-0.229683	-4.617255	24410.215395
HLA B*1801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.488611	-0.128649	-4.617260	30804.290769
HLA A*2601	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.390659	-0.226766	-4.617425	24584.355928
HLA A*3002	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.548460	-0.069030	-4.617490	35355.716725
HLA A*0206	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.490449	-0.127048	-4.617497	30934.885395
HLA B*4601	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.399831	-0.217813	-4.617644	25109.104513
HLA B*7301	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.357432	-0.260222	-4.617655	22773.638263
HLA B*0802	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.489135	-0.129234	-4.618369	30841.475654
HLA B*1501	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.370759	-0.247969	-4.618728	23483.276786
HLA B*0702	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.414882	-0.203931	-4.618813	25994.533341
HLA A*2501	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.464334	-0.154863	-4.619197	29129.564087
HLA B*4403	1:292-300	9	FLEALSGVS	1.118601	-1.067212	-4.671129	0.051389	-4.619740	46895.223180
HLA A*2501	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.484662	-0.135106	-4.619768	30525.425745
HLA B*0802	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.491165	-0.128649	-4.619814	30985.970591

HLA B*5701	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.415956	-0.203931	-4.619887	26058.879638
HLA B*1503	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.495293	-0.124898	-4.620191	31281.901882
HLA A*2501	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.445266	-0.175217	-4.620482	27878.253660
HLA A*3201	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.547290	-0.073933	-4.621222	35260.592208
HLA B*5301	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.489372	-0.132020	-4.621392	30858.332004
HLA A*2501	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.508208	-0.113369	-4.621578	32226.138448
HLA A*0301	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.361572	-0.260222	-4.621795	22991.759639
HLA B*3901	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.485977	-0.135927	-4.621904	30618.043904
HLA B*4002	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.647631	0.025675	-4.621957	44425.406213
HLA B*1503	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.486297	-0.135927	-4.622224	30640.579264
HLA B*1509	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.493630	-0.128649	-4.622279	31162.315061
HLA A*2403	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.418432	-0.203931	-4.622363	26207.892406
HLA B*3801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.567347	-0.055017	-4.622364	36927.266064
HLA B*3501	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.362190	-0.260222	-4.622412	23024.495617
HLA B*4501	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.621930	-0.000735	-4.622665	41872.644610
HLA B*1503	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.468053	-0.154863	-4.622916	29380.096667
HLA B*3901	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.491041	-0.132020	-4.623060	30977.087439
HLA A*0212	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.419473	-0.203931	-4.623404	26270.777065
HLA A*6801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.491398	-0.132020	-4.623417	31002.570472
HLA B*0803	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.510069	-0.113369	-4.623438	32364.511826
HLA A*0206	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.544451	-0.079025	-4.623477	35030.910407
HLA B*3501	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.405773	-0.217813	-4.623586	25454.998275
HLA B*3901	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.495100	-0.128649	-4.623750	31268.027967
HLA B*5101	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.494931	-0.129234	-4.624165	31255.851066
HLA A*6901	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.363957	-0.260222	-4.624179	23118.355506
HLA A*3301	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.632148	0.007934	-4.624215	42869.488466
HLA B*2705	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.499388	-0.124898	-4.624286	31578.267684
HLA B*5301	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.591671	-0.032788	-4.624460	39054.526232
HLA A*0250	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.550647	-0.073933	-4.624580	35534.238763
HLA B*5101	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.495972	-0.128649	-4.624621	31330.848073
HLA A*6802	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.218557	-0.406216	-4.624772	16540.807562
HLA B*4403	1:468-476	9	HPIVLRPVS	1.150677	-1.131258	-4.644319	0.019419	-4.624900	44087.820893
HLA A*0101	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.407143	-0.217813	-4.624956	25535.409198
HLA A*2603	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.551072	-0.073933	-4.625005	35569.050573
HLA B*1517	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.421190	-0.203931	-4.625122	26374.873937
HLA A*0211	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.546340	-0.079025	-4.625366	35183.610982
HLA A*2301	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.512200	-0.113369	-4.625569	32523.707273
HLA A*2402	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.592851	-0.032788	-4.625639	39160.733273
HLA B*4801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.416383	-0.209501	-4.625885	26084.549842
HLA B*1801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.496670	-0.129234	-4.625904	31381.228972
HLA B*5701	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.408221	-0.217813	-4.626034	25598.895962
HLA A*3101	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.408231	-0.217813	-4.626044	25599.449917
HLA B*0802	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.468511	-0.158117	-4.626628	29411.106919
HLA B*4402	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.451480	-0.175217	-4.626697	28280.035688
HLA B*7301	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.558006	-0.069030	-4.627035	36141.452550
HLA B*1502	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.330021	-0.297084	-4.627105	21380.653560
HLA A*3201	1:381-389	9	DEVRAVGRE	0.793874	-0.796994	-4.624198	-0.003120	-4.627317	42091.814147
HLA B*2705	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.469204	-0.158117	-4.627321	29458.082087
HLA A*0206	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.492460	-0.135106	-4.627566	31078.472887
HLA B*7301	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.548643	-0.079025	-4.627668	35370.638973
HLA A*0211	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.514486	-0.113369	-4.627855	32695.357655
HLA B*3901	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.503340	-0.124898	-4.628238	31866.923341
HLA A*2601	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.331351	-0.297084	-4.628435	21446.221395
HLA B*1509	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.515299	-0.113369	-4.628668	32756.614847
HLA A*0211	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.493604	-0.135106	-4.628710	31160.460685
HLA A*2902	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.424849	-0.203931	-4.628780	26597.972991
HLA B*3901	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.453963	-0.175217	-4.629180	28442.211320
HLA A*6802	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.419736	-0.209501	-4.629237	26286.699551
HLA A*0201	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.399916	-0.229683	-4.629599	25113.995138
HLA B*3901	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.474742	-0.154863	-4.629605	29836.110312
HLA B*1502	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.516486	-0.113369	-4.629855	32846.228078
HLA A*2601	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.400266	-0.229683	-4.629949	25134.247024
HLA A*2501	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.505523	-0.124898	-4.630421	32027.482842
HLA B*4403	1:111-119	9	GTREYGRTE	0.739639	-0.740374	-4.629785	-0.000735	-4.630519	42636.811500
HLA A*0211	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.421343	-0.209501	-4.630844	26384.150102

HLA B*1509	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.551958	-0.079025	-4.630983	35641.668683
HLA A*3201	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.552073	-0.079025	-4.631098	35651.117992
HLA A*0216	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.421641	-0.209501	-4.631143	26402.283717
HLA B*4501	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.656895	0.025675	-4.631221	45383.232592
HLA A*6901	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.404678	-0.226766	-4.631445	25390.906834
HLA B*0803	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.495559	-0.135927	-4.631485	31301.030902
HLA B*5301	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.597489	-0.034103	-4.631592	39581.176475
HLA B*1509	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.551399	-0.080273	-4.631672	35595.807654
HLA B*5701	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.422180	-0.209501	-4.631681	26435.012842
HLA A*2402	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.510849	-0.121106	-4.631955	32422.693416
HLA A*0101	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.384104	-0.247969	-4.632073	24216.076046
HLA A*0212	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.422584	-0.209501	-4.632085	26459.622094
HLA B*4002	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.598182	-0.034103	-4.632285	39644.395192
HLA A*2403	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.372126	-0.260222	-4.632348	23557.331708
HLA B*3901	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.503246	-0.129234	-4.632480	31860.028227
HLA A*3201	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.598494	-0.034103	-4.632598	39672.930203
HLA B*5101	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.508100	-0.124898	-4.632998	32218.119813
HLA B*0803	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.504383	-0.129234	-4.633617	31943.559400
HLA A*2402	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.553643	-0.080273	-4.633916	35780.187289
HLA B*1502	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.560266	-0.073933	-4.634198	36330.034288
HLA B*0803	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.502191	-0.132020	-4.634211	31782.732851
HLA A*3301	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.601441	-0.032788	-4.634229	39942.986396
HLA A*2402	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.565209	-0.069085	-4.634294	36745.919915
HLA A*0203	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.424980	-0.209501	-4.634481	26606.032169
HLA B*1509	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.430555	-0.203931	-4.634487	26949.793373
HLA A*6801	1:76-84	9	PKLDPALLD	0.940422	-0.901091	-4.673847	0.039331	-4.634516	47189.672271
HLA A*3101	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.404944	-0.229683	-4.634627	25406.433484
HLA B*4601	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.423091	-0.212130	-4.635222	26490.559188
HLA A*0203	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.409109	-0.226766	-4.635876	25651.297681
HLA B*1503	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.520961	-0.114983	-4.635945	33186.486322
HLA A*0202	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.503953	-0.132020	-4.635973	31911.950615
HLA B*5401	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.557068	-0.079025	-4.636093	36063.523708
HLA A*3101	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.388168	-0.247969	-4.636137	24443.780817
HLA B*3801	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.562221	-0.073933	-4.636153	36493.925344
HLA A*3101	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.376386	-0.260222	-4.636608	23789.521871
HLA A*6901	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.406974	-0.229683	-4.636657	25525.464786
HLA A*2602	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.581975	-0.055017	-4.636992	38192.232823
HLA A*1101	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.507767	-0.129234	-4.637000	32193.379221
HLA A*2402	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.582038	-0.055017	-4.637055	38197.811856
HLA A*2601	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.389176	-0.247969	-4.637145	24500.576863
HLA B*4001	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.410679	-0.226766	-4.637445	25744.164192
HLA B*5801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.340500	-0.297084	-4.637584	21902.802123
HLA A*3301	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.568677	-0.069030	-4.637707	37040.510540
HLA B*1501	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.377619	-0.260222	-4.637842	23857.184718
HLA B*0803	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.503187	-0.135106	-4.638294	31855.719537
HLA A*3002	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.502436	-0.135927	-4.638362	31800.619753
HLA A*2403	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.426289	-0.212130	-4.638419	26686.325258
HLA B*2705	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.378493	-0.260222	-4.638716	23905.245140
HLA B*0803	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.511963	-0.127048	-4.639011	32505.941212
HLA B*1517	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.514343	-0.124898	-4.639240	32684.569861
HLA A*0211	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.512308	-0.127048	-4.639357	32531.801964
HLA A*3301	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.507351	-0.132020	-4.639370	32162.567193
HLA A*8001	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.412683	-0.226766	-4.639449	25863.238656
HLA A*2403	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.391530	-0.247969	-4.639499	24633.747973
HLA A*6801	1:302-310	9	PEGKRKIIG	0.925250	-0.876626	-4.688313	0.048624	-4.639689	48787.969132
HLA A*0202	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.584757	-0.055017	-4.639774	38437.651017
HLA B*5401	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.511333	-0.128649	-4.639982	32458.846612
HLA B*0702	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.343169	-0.297084	-4.640253	22037.823200
HLA B*5701	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.428138	-0.212130	-4.640268	26800.186711
HLA B*0702	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.430802	-0.209501	-4.640303	26965.106238
HLA A*3301	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.606276	-0.034103	-4.640379	40390.178505
HLA A*2402	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.508366	-0.132020	-4.640385	32237.821334
HLA A*0201	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.393269	-0.247969	-4.641238	24732.562360
HLA B*4601	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.415037	-0.226766	-4.641803	26003.816416
HLA A*0211	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.509804	-0.132020	-4.641823	32344.732881

HLA B*1509	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.509804	-0.132020	-4.641823	32344.732881
HLA B*5101	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.506284	-0.135927	-4.642211	32083.669973
HLA A*0212	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.430393	-0.212130	-4.642524	26939.735368
HLA B*0802	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.487819	-0.154863	-4.642682	30748.181624
HLA A*2902	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.416019	-0.226766	-4.642786	26062.686259
HLA A*0211	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.488087	-0.154863	-4.642950	30767.150718
HLA B*5701	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.416804	-0.226766	-4.643570	26109.821575
HLA A*2602	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.468380	-0.175217	-4.643596	29402.198062
HLA A*0203	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.426035	-0.217813	-4.643848	26670.737845
HLA A*0201	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.417152	-0.226766	-4.643918	26130.735130
HLA A*0203	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.431897	-0.212130	-4.644027	27033.171256
HLA B*4402	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.383834	-0.260222	-4.644056	24201.015009
HLA A*8001	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.435034	-0.209501	-4.644535	27229.117008
HLA B*0702	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.396803	-0.247969	-4.644772	24934.619092
HLA B*3801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.564565	-0.080273	-4.644839	36691.491434
HLA B*5101	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.509754	-0.135106	-4.644860	32341.058480
HLA B*1509	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.576038	-0.069085	-4.645123	37673.667509
HLA A*6802	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.433474	-0.212130	-4.645604	27131.480956
HLA B*1517	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.428067	-0.217813	-4.645880	26795.837483
HLA A*0212	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.397956	-0.247969	-4.645925	25000.939856
HLA A*0203	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.398565	-0.247969	-4.646534	25035.994759
HLA A*2602	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.612565	-0.034103	-4.646669	40979.376270
HLA B*4403	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.672531	0.025675	-4.646857	47046.925707
HLA A*2402	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.568421	-0.079025	-4.647446	37018.675007
HLA A*2601	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.387226	-0.260222	-4.647449	24390.810798
HLA B*4001	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.399949	-0.247969	-4.647918	25115.897305
HLA B*4001	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.387886	-0.260222	-4.648109	24427.917389
HLA A*6801	1:445-453	9	QCPVVLLAD	0.831051	-0.805376	-4.673786	0.025675	-4.648111	47183.035174
HLA B*4601	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.418437	-0.229683	-4.648120	26208.175972
HLA A*2403	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.438800	-0.209501	-4.648301	27466.276176
HLA B*4801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.436410	-0.212130	-4.648541	27315.575592
HLA B*3901	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.444728	-0.203931	-4.648659	27843.737662
HLA B*1509	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.473875	-0.175217	-4.649092	29776.609413
HLA B*0702	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.436981	-0.212130	-4.649112	27351.508345
HLA B*5101	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.491642	-0.158117	-4.649759	31020.018308
HLA B*1509	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.494981	-0.154863	-4.649843	31259.402172
HLA A*0250	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.595388	-0.055017	-4.650405	39390.206634
HLA A*0201	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.390584	-0.260222	-4.650806	24580.100339
HLA A*2403	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.433607	-0.217813	-4.651420	27139.848610
HLA A*8001	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.439319	-0.212130	-4.651449	27499.134096
HLA B*1517	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.354456	-0.297084	-4.651540	22618.073995
HLA B*5101	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.403710	-0.247969	-4.651679	25334.376716
HLA B*5701	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.422398	-0.229683	-4.652081	26448.316164
HLA A*2402	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.583053	-0.069030	-4.652083	38287.187294
HLA A*2301	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.520282	-0.132020	-4.652302	33134.641185
HLA B*3801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.537403	-0.114983	-4.652386	34466.959131
HLA B*1503	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.443081	-0.209501	-4.652582	27738.344926
HLA A*6901	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.355630	-0.297084	-4.652714	22679.337451
HLA B*4601	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.393175	-0.260222	-4.653397	24727.210922
HLA B*4501	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.518548	-0.135106	-4.653654	33002.614923
HLA B*0803	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.427062	-0.226766	-4.653828	26733.865303
HLA B*0803	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.525423	-0.128649	-4.654072	33529.180992
HLA B*5301	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.599462	-0.055017	-4.654479	39761.454797
HLA B*1502	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.450554	-0.203931	-4.654485	28219.821092
HLA A*0101	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.424903	-0.229683	-4.654586	26601.282715
HLA B*4801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.394592	-0.260222	-4.654814	24808.006831
HLA A*2402	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.425380	-0.229683	-4.655063	26630.512490
HLA A*0211	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.530178	-0.124898	-4.655076	33898.329967
HLA B*1801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.520282	-0.135106	-4.655388	33134.641185
HLA A*0219	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.437761	-0.217813	-4.655574	27400.678073
HLA B*1503	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.527053	-0.128649	-4.655703	33655.301673
HLA B*3801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.576865	-0.079025	-4.655890	37745.477108
HLA B*7301	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.587132	-0.069085	-4.656217	38648.457793
HLA B*0702	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.429501	-0.226766	-4.656267	26884.410681
HLA A*2902	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.396049	-0.260222	-4.656271	24891.355846

HLA B*3901	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.498524	-0.158117	-4.656641	31515.462968
HLA A*0250	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.587745	-0.069030	-4.656775	38703.067228
HLA B*4601	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.408874	-0.247969	-4.656843	25637.424366
HLA B*4403	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.576903	-0.080273	-4.657176	37748.744431
HLA B*3801	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.588290	-0.069085	-4.657376	38751.673723
HLA B*5301	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.409424	-0.247969	-4.657393	25669.899693
HLA B*0801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.448576	-0.209501	-4.658077	28091.568558
HLA A*0250	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.483010	-0.175217	-4.658227	30409.553389
HLA B*0802	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.454504	-0.203931	-4.658435	28477.623265
HLA A*2301	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.543580	-0.114983	-4.658563	34960.671468
HLA B*0801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.361546	-0.297084	-4.658630	22990.391468
HLA A*3002	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.531886	-0.127048	-4.658935	34031.914261
HLA B*4402	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.432332	-0.226766	-4.659098	27060.240394
HLA B*1503	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.411379	-0.247969	-4.659348	25785.701041
HLA B*1509	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.523616	-0.135927	-4.659543	33389.982482
HLA A*1101	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.456106	-0.203931	-4.660037	28582.886788
HLA A*2402	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.586352	-0.073933	-4.660285	38579.104248
HLA B*4402	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.412396	-0.247969	-4.660365	25846.174383
HLA A*0216	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.433755	-0.226766	-4.660522	27149.100071
HLA A*0250	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.591613	-0.069085	-4.660698	39049.244573
HLA B*1502	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.545734	-0.114983	-4.660718	35134.537663
HLA A*8001	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.400534	-0.260222	-4.660756	25149.752783
HLA B*5701	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.400562	-0.260222	-4.660784	25151.385525
HLA B*4801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.431432	-0.229683	-4.661115	27004.229960
HLA A*3002	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.606520	-0.055017	-4.661537	40412.909563
HLA A*0216	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.457762	-0.203931	-4.661694	28692.109267
HLA A*0206	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.536879	-0.124898	-4.661777	34425.403081
HLA B*3901	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.364718	-0.297084	-4.661802	23158.912988
HLA B*4801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.435083	-0.226766	-4.661849	27232.210620
HLA B*5301	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.592825	-0.069085	-4.661910	39158.402935
HLA B*0801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.432313	-0.229683	-4.661996	27059.069277
HLA B*3801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.548760	-0.113369	-4.662130	35380.207829
HLA A*6802	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.414285	-0.247969	-4.662254	25958.838475
HLA B*3901	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.444460	-0.217813	-4.662273	27826.570962
HLA B*5701	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.414353	-0.247969	-4.662322	25962.911393
HLA B*1503	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.504235	-0.158117	-4.662352	31932.674155
HLA A*0211	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.526466	-0.135927	-4.662393	33609.814577
HLA B*1509	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.533204	-0.129234	-4.662438	34135.356235
HLA B*1801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.487249	-0.175217	-4.662465	30707.786528
HLA A*0219	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.414612	-0.247969	-4.662581	25978.366203
HLA A*3002	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.527812	-0.135106	-4.662918	33714.162163
HLA A*2902	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.433243	-0.229683	-4.662926	27117.100495
HLA B*1503	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.533752	-0.129234	-4.662985	34178.411124
HLA B*5401	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.538129	-0.124898	-4.663027	34524.624206
HLA B*1501	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.433387	-0.229683	-4.663070	27126.050702
HLA B*0803	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.488430	-0.175217	-4.663647	30791.461561
HLA A*2301	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.536670	-0.127048	-4.663718	34408.831923
HLA A*2301	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.539010	-0.124898	-4.663908	34594.735696
HLA A*6802	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.446323	-0.217813	-4.664136	27946.204555
HLA A*0202	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.550873	-0.113369	-4.664242	35552.698240
HLA A*3002	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.585323	-0.079025	-4.664348	38487.798067
HLA B*1509	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.543253	-0.121106	-4.664359	34934.391813
HLA A*3301	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.585375	-0.079025	-4.664400	38492.379063
HLA A*6801	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.585617	-0.079025	-4.664642	38513.833709
HLA B*1502	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.543549	-0.121106	-4.664655	34958.212820
HLA A*3002	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.585130	-0.080273	-4.665404	38470.728246
HLA B*3901	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.417544	-0.247969	-4.665513	26154.353649
HLA A*3002	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.596859	-0.069085	-4.665944	39523.831276
HLA A*3002	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.508138	-0.158117	-4.666255	32220.908677
HLA A*0202	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.587428	-0.079025	-4.666453	38674.811342
HLA B*0702	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.437019	-0.229683	-4.666702	27353.875945
HLA B*4001	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.369701	-0.297084	-4.666785	23426.177451
HLA B*2705	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.457340	-0.209501	-4.666841	28664.183063
HLA A*6801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.545781	-0.121106	-4.666887	35138.339348
HLA B*0803	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.541999	-0.124898	-4.666896	34833.616154

HLA B*7301	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.545812	-0.121106	-4.666918	35140.810663
HLA A*0212	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.406863	-0.260222	-4.667086	25518.975384
HLA B*4501	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.587273	-0.080273	-4.667546	38661.004861
HLA A*2501	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.458087	-0.209501	-4.667588	28713.537781
HLA B*5101	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.512811	-0.154863	-4.667674	32569.486370
HLA A*6901	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.347106	-0.320678	-4.667784	22238.548183
HLA A*2301	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.539247	-0.128649	-4.667896	34613.643383
HLA B*5301	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.594300	-0.073933	-4.668233	39291.666347
HLA A*0202	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.588006	-0.080273	-4.668279	38726.315310
HLA A*0202	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.543798	-0.124898	-4.668696	34978.265295
HLA B*4601	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.371861	-0.297084	-4.668945	23542.935100
HLA B*4001	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.457424	-0.212130	-4.669555	28669.766128
HLA B*3501	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.460074	-0.209501	-4.669576	28845.254118
HLA A*1101	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.511505	-0.158117	-4.669622	32471.667853
HLA A*2602	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.595795	-0.073933	-4.669727	39427.089611
HLA A*0101	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.372793	-0.297084	-4.669877	23593.553211
HLA A*0203	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.409718	-0.260222	-4.669940	25687.264478
HLA A*2301	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.541378	-0.129234	-4.670612	34783.901919
HLA B*1502	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.591627	-0.079025	-4.670652	39050.512106
HLA B*1503	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.373900	-0.297084	-4.670984	23653.747605
HLA B*5301	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.592233	-0.079025	-4.671258	39105.054968
HLA B*0801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.459323	-0.212130	-4.671453	28795.361436
HLA A*0206	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.516709	-0.154863	-4.671572	32863.113390
HLA B*4402	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.442239	-0.229683	-4.671922	27684.674944
HLA A*6801	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.591660	-0.080273	-4.671933	39053.469843
HLA A*2301	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.537154	-0.135106	-4.672260	34447.199779
HLA B*5801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.351587	-0.320678	-4.672265	22469.163235
HLA B*3801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.545462	-0.127048	-4.672510	35112.496001
HLA A*6801	1:258-266	9	VDHGLLRAG	0.752616	-0.744682	-4.680839	0.007934	-4.672905	47955.566819
HLA A*3101	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.460840	-0.212130	-4.672971	28896.171183
HLA A*3201	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.592811	-0.080273	-4.673084	39157.131900
HLA B*7301	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.559843	-0.113369	-4.673212	36294.674045
HLA B*4501	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.639481	-0.034103	-4.673584	43599.453346
HLA A*0212	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.444105	-0.229683	-4.673788	27803.848905
HLA B*3501	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.461782	-0.212130	-4.673913	28958.925585
HLA A*3301	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.498846	-0.175217	-4.674062	31538.829463
HLA A*0202	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.559476	-0.114983	-4.674460	36264.056341
HLA B*7301	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.539285	-0.135927	-4.675212	34616.639608
HLA B*4501	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.596222	-0.079025	-4.675247	39465.928634
HLA A*6802	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.445740	-0.229683	-4.675423	27908.735601
HLA B*2705	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.471657	-0.203931	-4.675588	29624.929832
HLA A*0206	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.457965	-0.217813	-4.675777	28705.461390
HLA A*2301	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.539875	-0.135927	-4.675801	34663.676854
HLA A*3201	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.621068	-0.055017	-4.676085	41789.591909
HLA A*3002	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.546900	-0.129234	-4.676133	35228.940944
HLA B*0801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.415930	-0.260222	-4.676152	26057.328952
HLA A*0250	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.595990	-0.080273	-4.676263	39444.797170
HLA B*4801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.428753	-0.247969	-4.676722	26838.199987
HLA A*0206	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.548145	-0.128649	-4.676794	35330.095765
HLA B*1502	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.622410	-0.055017	-4.677426	41918.881498
HLA A*0219	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.465358	-0.212130	-4.677489	29198.353425
HLA B*0802	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.468514	-0.209501	-4.678015	29411.266030
HLA A*0250	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.599495	-0.079025	-4.678520	39764.466382
HLA A*0219	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.475160	-0.203931	-4.679092	29864.855139
HLA A*6801	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.646835	-0.032788	-4.679623	44344.006796
HLA B*1509	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.555607	-0.124898	-4.680504	35942.375659
HLA A*1101	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.471023	-0.209501	-4.680524	29581.689172
HLA A*6802	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.454088	-0.226766	-4.680854	28450.367558
HLA B*0803	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.526118	-0.154863	-4.680981	33582.915192
HLA A*0250	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.549254	-0.132020	-4.681274	35420.425300
HLA A*3001	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.275156	-0.406216	-4.681371	18843.249680
HLA B*4002	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.648665	-0.032788	-4.681453	44531.280241
HLA A*3002	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.567110	-0.114983	-4.682093	36907.094561
HLA A*0219	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.422137	-0.260222	-4.682360	26432.438778
HLA B*4501	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.649762	-0.032788	-4.682551	44643.927116

HLA A*2602	1:365-373	9	DDLKFTLVE	0.925160	-1.004185	-4.603821	-0.079025	-4.682846	40162.483554
HLA B*5401	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.547818	-0.135106	-4.682924	35303.538417
HLA A*2902	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.435045	-0.247969	-4.683014	27229.853550
HLA A*2402	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.553873	-0.129234	-4.683106	35799.161870
HLA B*5301	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.562625	-0.121106	-4.683731	36527.898779
HLA A*3301	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.525700	-0.158117	-4.683817	33550.591745
HLA A*0203	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.454187	-0.229683	-4.683870	28456.832652
HLA A*0211	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.480940	-0.203931	-4.684871	30264.962882
HLA B*4002	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.467104	-0.217813	-4.684917	29315.953789
HLA A*2403	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.458251	-0.226766	-4.685018	28724.413434
HLA B*5401	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.549120	-0.135927	-4.685046	35409.504611
HLA B*3801	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.564413	-0.121106	-4.685519	36678.591404
HLA A*3002	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.530773	-0.154863	-4.685636	33944.758444
HLA A*0211	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.557101	-0.128649	-4.685750	36066.255206
HLA B*1502	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.550793	-0.135106	-4.685899	35546.159412
HLA B*0803	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.528848	-0.158117	-4.686965	33794.692124
HLA A*0301	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.366692	-0.320678	-4.687370	23264.393683
HLA B*7301	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.558823	-0.128649	-4.687472	36209.558035
HLA B*0802	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.469705	-0.217813	-4.687518	29492.046388
HLA A*2403	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.390950	-0.297084	-4.688034	24600.853292
HLA A*8001	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.391392	-0.297084	-4.688476	24625.886543
HLA B*4002	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.563769	-0.124898	-4.688667	36624.262651
HLA A*3301	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.633760	-0.055017	-4.688777	43028.880608
HLA A*0219	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.462123	-0.226766	-4.688890	28981.650860
HLA B*4403	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.654854	-0.034103	-4.688957	45170.377954
HLA B*3801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.554056	-0.135106	-4.689162	35814.271278
HLA B*1517	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.480186	-0.209501	-4.689687	30212.451131
HLA A*6802	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.429616	-0.260222	-4.689838	26891.538268
HLA A*2902	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.477806	-0.212130	-4.689936	30047.333176
HLA B*1502	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.621132	-0.069085	-4.690217	41795.696436
HLA B*4501	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.621327	-0.069030	-4.690356	41814.467787
HLA A*2501	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.472632	-0.217813	-4.690445	29691.515599
HLA B*5101	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.481100	-0.209501	-4.690601	30276.098577
HLA A*3201	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.622189	-0.069085	-4.691274	41897.569926
HLA B*7301	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.370672	-0.320678	-4.691350	23478.576705
HLA A*1101	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.473607	-0.217813	-4.691420	29758.251025
HLA B*5301	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.578101	-0.113369	-4.691470	37853.038668
HLA A*0250	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.578110	-0.113369	-4.691480	37853.857800
HLA A*8001	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.461992	-0.229683	-4.691675	28972.872089
HLA B*1503	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.464999	-0.226766	-4.691765	29174.195566
HLA A*0206	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.483393	-0.209501	-4.692894	30436.380722
HLA B*5701	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.396030	-0.297084	-4.693114	24890.278594
HLA A*2402	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.579783	-0.113369	-4.693152	37999.946017
HLA B*7301	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.578787	-0.114983	-4.693770	37912.881899
HLA A*0202	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.558931	-0.135106	-4.694037	36218.570082
HLA A*2301	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.519888	-0.175217	-4.695104	33104.540071
HLA A*2602	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.626439	-0.069085	-4.695524	42309.612992
HLA A*2601	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.374992	-0.320678	-4.695670	23713.325842
HLA A*6801	1:386-394	9	VGRELGLPE	0.644930	-0.679033	-4.662045	-0.034103	-4.696149	45924.612237
HLA B*2705	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.399740	-0.297084	-4.696824	25103.807410
HLA A*0216	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.448867	-0.247969	-4.696836	28110.419441
HLA A*0250	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.568085	-0.129234	-4.697319	36990.047911
HLA B*3801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.572619	-0.124898	-4.697517	37378.287479
HLA B*0803	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.493895	-0.203931	-4.697826	31181.370953
HLA B*3801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.561932	-0.135927	-4.697858	36469.649766
HLA B*3501	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.468389	-0.229683	-4.698072	29402.834319
HLA B*4801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.401069	-0.297084	-4.698153	25180.793004
HLA B*7301	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.568973	-0.129234	-4.698207	37065.767664
HLA B*1502	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.618199	-0.080273	-4.698473	41514.461503
HLA B*0702	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.438645	-0.260222	-4.698867	27456.471019
HLA B*0803	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.490362	-0.209501	-4.699863	30928.693906
HLA A*0250	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.584952	-0.114983	-4.699935	38454.914197
HLA B*5401	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.541966	-0.158117	-4.700083	34830.978010
HLA B*5401	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.545683	-0.154863	-4.700545	35130.356285
HLA A*2402	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.571936	-0.128649	-4.700585	37319.489967

HLA A*0216	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.488491	-0.212130	-4.700622	30795.792904
HLA A*8001	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.452742	-0.247969	-4.700710	28362.311768
HLA B*7301	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.525517	-0.175217	-4.700734	33536.437343
HLA A*2301	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.545873	-0.154863	-4.700736	35145.753816
HLA A*0202	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.573928	-0.127048	-4.700977	37491.089649
HLA B*4403	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.627139	-0.073933	-4.701072	42377.877317
HLA A*3001	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.295164	-0.406160	-4.701324	19731.677881
HLA A*0202	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.544052	-0.158117	-4.702169	34998.707949
HLA B*4002	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.633589	-0.069030	-4.702618	43011.890915
HLA B*2705	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.472959	-0.229683	-4.702642	29713.851261
HLA B*4403	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.633626	-0.069085	-4.702711	43015.614109
HLA B*3801	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.574194	-0.128649	-4.702843	37514.015614
HLA A*3301	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.574264	-0.128649	-4.702913	37520.104508
HLA B*4403	1:218-226	9	QVRTQIGDG	0.558518	-0.591306	-4.670447	-0.032788	-4.703235	46821.708455
HLA B*0802	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.476481	-0.226766	-4.703247	29955.793153
HLA B*5401	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.443233	-0.260222	-4.703456	27748.100630
HLA B*4002	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.623493	-0.080273	-4.703766	42023.555938
HLA A*2301	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.545896	-0.158117	-4.704013	35147.655214
HLA A*2402	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.577020	-0.127048	-4.704068	37758.956639
HLA A*0202	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.549717	-0.154863	-4.704579	35458.194676
HLA B*5101	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.500878	-0.203931	-4.704809	31686.762984
HLA A*0202	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.576242	-0.128649	-4.704891	37691.403184
HLA B*3901	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.495422	-0.209501	-4.704924	31291.211006
HLA B*3501	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.478647	-0.226766	-4.705413	30105.583447
HLA B*4801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.385201	-0.320678	-4.705879	24277.333330
HLA B*1509	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.547853	-0.158117	-4.705970	35306.403357
HLA B*4501	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.581078	-0.124898	-4.705975	38113.387107
HLA B*1517	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.446459	-0.260222	-4.706681	27954.974712
HLA A*2402	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.591721	-0.114983	-4.706704	39058.963378
HLA A*0216	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.446527	-0.260222	-4.706750	27959.360822
HLA A*0212	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.480139	-0.226766	-4.706905	30209.182387
HLA A*1101	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.459085	-0.247969	-4.707054	28779.631983
HLA A*2603	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.652093	-0.055017	-4.707110	44884.157698
HLA B*2705	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.480661	-0.226766	-4.707427	30245.485271
HLA A*6801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.578357	-0.129234	-4.707590	37875.366351
HLA A*3201	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.572636	-0.135106	-4.707742	37379.702992
HLA A*2603	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.639082	-0.069030	-4.708112	43559.374184
HLA B*3801	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.579271	-0.129234	-4.708504	37955.156976
HLA A*3301	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.639490	-0.069085	-4.708576	43600.396829
HLA A*0201	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.387924	-0.320678	-4.708602	24430.031918
HLA B*0802	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.496975	-0.212130	-4.709106	31403.306701
HLA B*4002	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.635301	-0.073933	-4.709234	43181.856541
HLA B*7301	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.577683	-0.132020	-4.709702	37816.605240
HLA B*5301	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.581409	-0.128649	-4.710058	38142.470875
HLA B*3801	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.578145	-0.132020	-4.710165	37856.929702
HLA A*2603	1:373-381	9	EPLRLLFKD	0.901196	-0.981469	-4.630024	-0.080273	-4.710298	42660.345356
HLA B*1501	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.389914	-0.320678	-4.710592	24542.231489
HLA B*5301	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.535465	-0.175217	-4.710681	34313.470405
HLA A*0250	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.552801	-0.158117	-4.710918	35710.957420
HLA B*0802	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.481361	-0.229683	-4.711044	30294.284764
HLA A*2402	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.576294	-0.135106	-4.711400	37695.889390
HLA A*2501	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.414591	-0.297084	-4.711675	25977.101373
HLA A*0101	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.391989	-0.320678	-4.712667	24659.748525
HLA B*4403	1:3-11	9	QPADIDVPE	0.708138	-0.777168	-4.644070	-0.069030	-4.713099	44062.546057
HLA B*1502	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.581759	-0.132020	-4.713779	38173.228904
HLA A*1101	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.501987	-0.212130	-4.714117	31767.777499
HLA B*5101	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.496548	-0.217813	-4.714361	31372.402227
HLA B*5401	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.511671	-0.203931	-4.715603	32484.142686
HLA B*5101	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.504266	-0.212130	-4.716396	31934.920013
HLA A*2402	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.591655	-0.124898	-4.716553	39053.047295
HLA A*0250	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.580770	-0.135927	-4.716696	38086.385891
HLA B*4001	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.396274	-0.320678	-4.716952	24904.286514
HLA A*2501	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.456745	-0.260222	-4.716967	28624.977176
HLA A*0250	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.590135	-0.127048	-4.717183	38916.592835
HLA A*2501	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.505154	-0.212130	-4.717284	32000.291765

HLA B*7301	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.593074	-0.124898	-4.717972	39180.864692
HLA A*3201	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.593448	-0.124898	-4.718345	39214.581489
HLA A*2603	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.597592	-0.121106	-4.718698	39590.599307
HLA A*0219	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.489262	-0.229683	-4.718945	30850.486814
HLA A*0250	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.584031	-0.135106	-4.719137	38373.450172
HLA A*2301	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.489509	-0.229683	-4.719192	30868.016052
HLA A*0250	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.594343	-0.124898	-4.719240	39295.492677
HLA A*2603	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.650512	-0.069085	-4.719597	44721.038098
HLA A*2402	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.584003	-0.135927	-4.719929	38370.959100
HLA B*4501	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.650956	-0.069085	-4.720041	44766.787360
HLA A*3201	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.606764	-0.113369	-4.720134	40435.653414
HLA A*3002	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.591765	-0.128649	-4.720415	39062.978373
HLA B*5301	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.595529	-0.124898	-4.720427	39402.994508
HLA A*3201	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.591953	-0.129234	-4.721187	39079.888142
HLA B*1801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.424743	-0.297084	-4.721827	26591.498635
HLA A*2501	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.495119	-0.226766	-4.721886	31269.381249
HLA B*1509	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.512557	-0.209501	-4.722058	32550.462619
HLA B*1502	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.462144	-0.260222	-4.722367	28983.061983
HLA A*3101	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.401983	-0.320678	-4.722661	25233.840443
HLA B*4501	1:150-158	9	DGFDVVASS	1.170019	-1.243952	-4.648738	-0.073933	-4.722671	44538.749055
HLA A*2602	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.586827	-0.135927	-4.722753	38621.286445
HLA B*1517	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.474839	-0.247969	-4.722807	29842.728858
HLA B*1502	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.548302	-0.175217	-4.723519	35342.903923
HLA A*2602	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.608670	-0.114983	-4.723653	40613.451365
HLA B*4601	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.403243	-0.320678	-4.723921	25307.117214
HLA B*1517	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.494365	-0.229683	-4.724048	31215.126763
HLA A*2403	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.403445	-0.320678	-4.724123	25318.894102
HLA B*4402	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.404326	-0.320678	-4.725004	25370.310893
HLA B*1517	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.513088	-0.212130	-4.725219	32590.284290
HLA B*5101	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.498538	-0.226766	-4.725304	31516.485956
HLA B*3801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.570578	-0.154863	-4.725440	37202.977317
HLA B*3801	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.567702	-0.158117	-4.725819	36957.444023
HLA B*7301	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.522138	-0.203931	-4.726069	33276.555468
HLA A*3301	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.596986	-0.129234	-4.726220	39535.379218
HLA B*1517	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.499553	-0.226766	-4.726319	31590.228393
HLA A*3002	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.601715	-0.124898	-4.726613	39968.276593
HLA B*0802	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.478793	-0.247969	-4.726762	30115.682948
HLA B*4402	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.429747	-0.297084	-4.726831	26899.686396
HLA B*1502	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.598212	-0.128649	-4.726862	39647.183423
HLA A*3301	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.600301	-0.127048	-4.727349	39838.321508
HLA A*0216	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.498315	-0.229683	-4.727998	31500.292551
HLA A*0250	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.599368	-0.128649	-4.728017	39752.851526
HLA A*2301	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.518983	-0.209501	-4.728484	33035.661448
HLA A*0250	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.573757	-0.154863	-4.728619	37476.286520
HLA A*1101	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.468481	-0.260222	-4.728703	29409.038551
HLA B*1509	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.499104	-0.229683	-4.728787	31557.603421
HLA B*0803	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.511216	-0.217813	-4.729029	32450.067861
HLA B*3801	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.553814	-0.175217	-4.729031	35794.320460
HLA B*2705	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.517038	-0.212130	-4.729168	32888.012830
HLA B*0802	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.469679	-0.260222	-4.729901	29490.291405
HLA B*1801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.503848	-0.226766	-4.730614	31904.182755
HLA B*5301	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.601483	-0.129234	-4.730716	39946.876154
HLA A*6802	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.410773	-0.320678	-4.731451	25749.735718
HLA A*2602	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.606577	-0.124898	-4.731474	40418.157009
HLA A*2501	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.502429	-0.229683	-4.732112	31800.103644
HLA A*6801	1:78-86	9	LDPALLDLG	0.630546	-0.699631	-4.663293	-0.069085	-4.732378	46056.727296
HLA A*3201	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.605381	-0.127048	-4.732429	40307.013309
HLA A*3201	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.597240	-0.135927	-4.733166	39558.485225
HLA A*6801	1:180-188	9	PEVMHTPHG	0.794262	-0.849279	-4.678452	-0.055017	-4.733469	47692.704636
HLA B*5301	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.597587	-0.135927	-4.733514	39590.170947
HLA B*2705	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.485576	-0.247969	-4.733545	30589.732523
HLA B*3901	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.521570	-0.212130	-4.733700	33233.018534
HLA B*0802	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.437186	-0.297084	-4.734270	27364.384645
HLA A*2902	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.414377	-0.320678	-4.735055	25964.315996
HLA A*2603	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.621738	-0.113369	-4.735107	41854.073568

HLA A*6801	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.608097	-0.127048	-4.735145	40559.876450
HLA B*1502	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.606050	-0.129234	-4.735284	40369.207338
HLA B*1801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.517543	-0.217813	-4.735356	32926.287993
HLA B*4402	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.329328	-0.406160	-4.735488	21346.559018
HLA A*3201	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.620523	-0.114983	-4.735507	41737.174932
HLA B*0803	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.488421	-0.247969	-4.736390	30790.795255
HLA B*5101	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.507381	-0.229683	-4.737064	32164.829219
HLA A*3301	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.622259	-0.114983	-4.737243	41904.370314
HLA A*3201	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.605322	-0.132020	-4.737342	40301.562266
HLA B*0803	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.507853	-0.229683	-4.737537	32199.823882
HLA A*2602	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.625673	-0.113369	-4.739042	42235.060509
HLA A*2602	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.607552	-0.132020	-4.739571	40509.001914
HLA A*0206	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.528205	-0.212130	-4.740335	33744.635036
HLA B*4501	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.627099	-0.113369	-4.740469	42373.980083
HLA B*3901	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.510821	-0.229683	-4.740504	32420.588646
HLA B*3901	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.514091	-0.226766	-4.740858	32665.655607
HLA B*5701	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.420293	-0.320678	-4.740971	26320.424493
HLA A*3301	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.628579	-0.113369	-4.741949	42518.646748
HLA B*7301	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.533313	-0.209501	-4.742814	34143.852043
HLA B*7301	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.588302	-0.154863	-4.743165	38752.721948
HLA A*1101	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.516403	-0.226766	-4.743170	32840.009361
HLA A*2603	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.614194	-0.129234	-4.743427	41133.298481
HLA A*0203	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.422851	-0.320678	-4.743529	26475.945500
HLA B*1509	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.495836	-0.247969	-4.743805	31321.018824
HLA B*5301	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.609119	-0.135106	-4.744225	40655.438479
HLA A*2602	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.616618	-0.128649	-4.745267	41363.588173
HLA B*4501	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.590823	-0.154863	-4.745686	38978.328345
HLA B*4002	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.632552	-0.113369	-4.745922	42909.397130
HLA A*2602	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.619181	-0.127048	-4.746230	41608.445778
HLA B*1801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.498770	-0.247969	-4.746739	31533.370045
HLA B*5101	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.487096	-0.260222	-4.747318	30696.990254
HLA B*4501	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.626404	-0.121106	-4.747510	42306.179776
HLA B*5401	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.538056	-0.209501	-4.747557	34518.834685
HLA B*0803	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.536043	-0.212130	-4.748173	34359.166294
HLA A*6801	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.612474	-0.135927	-4.748400	40970.731120
HLA B*0801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.427870	-0.320678	-4.748548	26783.663399
HLA A*2301	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.545208	-0.203931	-4.749139	35091.986884
HLA B*1502	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.531489	-0.217813	-4.749302	34000.814079
HLA A*0211	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.531515	-0.217813	-4.749328	34002.837486
HLA B*4002	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.628375	-0.121106	-4.749481	42498.639616
HLA B*7301	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.591389	-0.158117	-4.749506	39029.180781
HLA A*0212	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.428847	-0.320678	-4.749525	26844.008283
HLA A*3301	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.613601	-0.135927	-4.749528	41077.259989
HLA A*3201	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.594874	-0.154863	-4.749737	39343.566102
HLA A*2402	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.540274	-0.209501	-4.749775	34695.571049
HLA A*2402	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.591927	-0.158117	-4.750044	39077.562615
HLA B*3801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.546305	-0.203931	-4.750236	35180.756007
HLA A*2301	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.523522	-0.226766	-4.750289	33382.757819
HLA B*1502	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.625419	-0.124898	-4.750317	42210.391121
HLA A*2501	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.429653	-0.320678	-4.750331	26893.866053
HLA A*1101	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.521429	-0.229683	-4.751112	33222.233068
HLA A*3201	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.622678	-0.128649	-4.751327	41944.741993
HLA A*2501	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.503664	-0.247969	-4.751633	31890.722944
HLA A*6801	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.636791	-0.114983	-4.751774	43330.218970
HLA A*2301	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.539872	-0.212130	-4.752003	34663.489328
HLA A*2402	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.597550	-0.154863	-4.752413	39586.744241
HLA B*1509	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.534736	-0.217813	-4.752549	34255.972690
HLA B*1502	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.616630	-0.135927	-4.752557	41364.707050
HLA B*4002	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.620718	-0.132020	-4.752738	41755.920000
HLA B*4002	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.617922	-0.135106	-4.753028	41487.968502
HLA A*2301	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.535220	-0.217813	-4.753033	34294.170099
HLA A*2602	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.543702	-0.209501	-4.753203	34970.507786
HLA B*0803	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.493679	-0.260222	-4.753901	31165.855541
HLA A*0219	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.433375	-0.320678	-4.754053	27125.316968
HLA A*2603	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.622840	-0.132020	-4.754859	41960.402148

HLA B*4501	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.624080	-0.132020	-4.756100	42080.430085
HLA B*3801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.526802	-0.229683	-4.756485	33635.825665
HLA A*0202	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.529995	-0.226766	-4.756761	33884.028861
HLA B*1503	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.527375	-0.229683	-4.757058	33680.254708
HLA B*5801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.351253	-0.406216	-4.757469	22451.908957
HLA B*5301	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.602824	-0.154863	-4.757687	40070.464707
HLA B*1801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.528172	-0.229683	-4.757855	33742.079367
HLA B*1503	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.545871	-0.212130	-4.758001	35145.563682
HLA B*1801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.545892	-0.212130	-4.758022	35147.274926
HLA A*2602	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.623129	-0.135106	-4.758235	41988.332578
HLA A*6801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.461362	-0.297084	-4.758446	28930.896199
HLA B*4002	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.643910	-0.114983	-4.758893	44046.339641
HLA A*6801	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.645742	-0.113369	-4.759112	44232.595273
HLA B*5401	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.547250	-0.212130	-4.759380	35257.349507
HLA B*5801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.354030	-0.406160	-4.760190	22595.937444
HLA A*0206	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.512421	-0.247969	-4.760390	32540.250746
HLA B*5301	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.602340	-0.158117	-4.760457	40025.833566
HLA A*2603	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.606452	-0.154863	-4.761315	40406.569809
HLA B*4403	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.636645	-0.124898	-4.761543	43315.687883
HLA B*5401	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.535199	-0.226766	-4.761966	34292.500391
HLA B*5401	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.544280	-0.217813	-4.762093	35017.078664
HLA A*2603	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.552750	-0.209501	-4.762251	35706.707442
HLA A*0216	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.442148	-0.320678	-4.762826	27678.834490
HLA A*3301	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.638179	-0.124898	-4.763077	43468.977978
HLA B*4501	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.634925	-0.128649	-4.763575	43144.495264
HLA B*1801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.443057	-0.320678	-4.763735	27736.844352
HLA A*0202	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.559916	-0.203931	-4.763847	36300.761411
HLA A*2301	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.516316	-0.247969	-4.764285	32833.436569
HLA B*3801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.554846	-0.209501	-4.764347	35879.430897
HLA A*0211	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.552327	-0.212130	-4.764457	35671.953887
HLA A*0211	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.537957	-0.226766	-4.764724	34510.992367
HLA B*4002	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.504625	-0.260222	-4.764848	31961.363905
HLA B*4403	1:230-238	9	CGLSGGVDS	0.985054	-1.098423	-4.651579	-0.113369	-4.764948	44831.011976
HLA A*3201	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.561572	-0.203931	-4.765503	36439.475851
HLA A*2603	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.638795	-0.127048	-4.765843	43530.634200
HLA A*8001	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.446180	-0.320678	-4.766857	27936.983739
HLA A*2602	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.563158	-0.203931	-4.767089	36572.784231
HLA A*2603	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.652192	-0.114983	-4.767175	44894.357226
HLA B*0803	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.470255	-0.297084	-4.767339	29529.404426
HLA A*0101	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.361481	-0.406216	-4.767696	22986.909219
HLA A*2603	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.639396	-0.128649	-4.768046	43590.962918
HLA B*1509	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.542013	-0.226766	-4.768779	34834.746848
HLA A*2601	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.363280	-0.406216	-4.769496	23082.364042
HLA B*2705	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.449267	-0.320678	-4.769945	28136.283956
HLA A*0301	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.364128	-0.406216	-4.770344	23127.487254
HLA A*3201	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.612288	-0.158117	-4.770405	40953.224739
HLA A*0250	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.543819	-0.226766	-4.770586	34979.968394
HLA A*3301	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.635764	-0.135106	-4.770870	43227.902058
HLA A*6901	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.364718	-0.406160	-4.770878	23158.912988
HLA B*3501	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.450622	-0.320678	-4.771300	28224.248756
HLA B*4501	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.656639	-0.114983	-4.771623	45356.478991
HLA A*0211	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.524772	-0.247969	-4.772741	33478.973825
HLA B*4002	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.645815	-0.127048	-4.772864	44240.013991
HLA A*0202	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.563579	-0.209501	-4.773080	36608.217378
HLA B*1509	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.476046	-0.297084	-4.773130	29925.827509
HLA A*0301	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.367018	-0.406160	-4.773178	23281.894495
HLA B*4403	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.555369	-0.217813	-4.773182	35922.742152
HLA B*4403	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.644986	-0.128649	-4.773635	44155.609859
HLA A*3002	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.564979	-0.209501	-4.774480	36726.443526
HLA B*4002	1:318-326	9	EGAVRDVLD	0.902949	-1.031598	-4.646003	-0.128649	-4.774652	44259.164821
HLA A*2602	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.620145	-0.154863	-4.775008	41700.838008
HLA B*4501	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.648108	-0.127048	-4.775157	44474.221326
HLA B*4403	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.640158	-0.135106	-4.775264	43667.436337
HLA B*0702	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.454708	-0.320678	-4.775386	28491.029708
HLA B*1517	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.454821	-0.320678	-4.775499	28498.429068

HLA A*0250	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.566116	-0.209501	-4.775617	36822.733552
HLA A*6901	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.369758	-0.406216	-4.775974	23429.219241
HLA A*3002	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.572164	-0.203931	-4.776095	37339.078853
HLA B*3801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.516685	-0.260222	-4.776908	32861.335580
HLA B*1509	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.565914	-0.212130	-4.778044	36805.605742
HLA A*3002	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.548434	-0.229683	-4.778117	35353.612812
HLA B*1509	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.457706	-0.320678	-4.778384	28688.384202
HLA A*3002	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.518548	-0.260222	-4.778771	33002.614923
HLA B*4403	1:400-408	9	QPFPGPGLG	0.498724	-0.625772	-4.652363	-0.127048	-4.779412	44912.090493
HLA B*4002	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.650568	-0.129234	-4.779802	44726.844936
HLA A*0206	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.553053	-0.226766	-4.779819	35731.634982
HLA A*2603	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.655331	-0.124898	-4.780228	45220.011651
HLA B*1501	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.374605	-0.406160	-4.780765	23692.168020
HLA A*2402	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.555729	-0.226766	-4.782495	35952.488183
HLA B*4403	1:333-341	9	LVQGTLYPD	0.665171	-0.786277	-4.661796	-0.121106	-4.782902	45898.284398
HLA B*4501	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.654196	-0.129234	-4.783429	45102.007064
HLA A*2601	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.378247	-0.406160	-4.784406	23891.669899
HLA A*0250	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.580958	-0.203931	-4.784889	38102.872908
HLA B*7301	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.573458	-0.212130	-4.785589	37450.547059
HLA B*4002	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.631068	-0.154863	-4.785930	42762.938276
HLA B*4403	1:339-347	9	YPDVVESGG	0.686537	-0.801520	-4.671335	-0.114983	-4.786319	46917.553915
HLA A*0211	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.556847	-0.229683	-4.786530	36045.189001
HLA B*0801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.273264	-0.513500	-4.786764	18761.366496
HLA A*2902	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.380634	-0.406216	-4.786849	24023.350762
HLA A*3002	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.560999	-0.226766	-4.787765	36391.407004
HLA B*3901	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.467386	-0.320678	-4.788064	29334.991495
HLA B*3801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.570270	-0.217813	-4.788083	37176.621075
HLA A*0212	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.382137	-0.406160	-4.788297	24106.671667
HLA B*5401	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.558687	-0.229683	-4.788370	36198.198215
HLA B*7301	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.562094	-0.226766	-4.788860	36483.265784
HLA A*6801	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.635024	-0.154863	-4.789887	43154.299469
HLA A*2603	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.655009	-0.135106	-4.790115	45186.509039
HLA A*2603	1:289-297	9	AETFLEALS	0.785461	-0.921388	-4.654682	-0.135927	-4.790609	45152.542704
HLA A*3301	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.635919	-0.154863	-4.790782	43243.339452
HLA B*4403	1:173-181	9	LAGVQYHPE	0.534674	-0.666694	-4.659031	-0.132020	-4.791051	45606.958333
HLA B*3801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.564356	-0.226766	-4.791123	36673.829463
HLA A*0206	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.561556	-0.229683	-4.791239	36438.095942
HLA B*5301	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.581775	-0.209501	-4.791277	38174.674522
HLA A*3002	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.573804	-0.217813	-4.791617	37480.341590
HLA A*3301	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.565416	-0.226766	-4.792182	36763.417719
HLA B*1502	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.583178	-0.209501	-4.792679	38298.166728
HLA A*0206	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.532810	-0.260222	-4.793032	34104.346023
HLA A*0101	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.388791	-0.406160	-4.794951	24478.849057
HLA A*0202	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.583495	-0.212130	-4.795626	38326.147438
HLA A*0201	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.389646	-0.406216	-4.795862	24527.100290
HLA A*0201	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.389820	-0.406160	-4.795980	24536.921234
HLA A*0202	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.548060	-0.247969	-4.796029	35323.215686
HLA A*2603	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.621482	-0.175217	-4.796698	41829.400420
HLA A*3001	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.283506	-0.513500	-4.797006	19209.049356
HLA A*2402	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.594011	-0.203931	-4.797943	39265.529726
HLA B*3801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.550212	-0.247969	-4.798181	35498.692840
HLA B*5101	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.502767	-0.297084	-4.799851	31824.886341
HLA A*0202	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.582154	-0.217813	-4.799967	38207.938848
HLA B*7301	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.552209	-0.247969	-4.800178	35662.306126
HLA B*3501	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.394190	-0.406216	-4.800406	24785.067778
HLA A*6801	1:149-157	9	PDGFDVVAS	1.197454	-1.322352	-4.675604	-0.124898	-4.800502	47381.016747
HLA B*4001	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.394345	-0.406216	-4.800561	24793.918933
HLA B*5301	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.582847	-0.217813	-4.800660	38268.964242
HLA A*1101	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.480066	-0.320678	-4.800744	30204.116534
HLA A*0211	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.540594	-0.260222	-4.800816	34721.107532
HLA B*3801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.589479	-0.212130	-4.801610	38857.898029
HLA A*3101	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.395471	-0.406216	-4.801686	24858.251648
HLA A*2603	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.575697	-0.226766	-4.802464	37644.126594
HLA A*2301	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.542647	-0.260222	-4.802869	34885.666099
HLA B*0801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.397644	-0.406216	-4.803860	24982.957769

HLA B*4403	1:58-66	9	PVALVLSGG	0.638622	-0.767856	-4.675240	-0.129234	-4.804474	47341.302862
HLA B*4403	1:345-353	9	SGGGSGTAN	0.650816	-0.805679	-4.649758	-0.154863	-4.804620	44643.444081
HLA A*3201	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.587088	-0.217813	-4.804900	38644.485403
HLA B*4002	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.646950	-0.158117	-4.805067	44355.763266
HLA A*0203	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.399263	-0.406160	-4.805422	25076.253353
HLA B*4601	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.399834	-0.406160	-4.805993	25109.240350
HLA A*2603	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.602726	-0.203931	-4.806657	40061.361116
HLA A*2402	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.589801	-0.217813	-4.807614	38886.708422
HLA B*4501	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.649962	-0.158117	-4.808079	44664.460926
HLA A*0202	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.548063	-0.260222	-4.808285	35323.406781
HLA A*2402	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.596683	-0.212130	-4.808813	39507.798063
HLA B*4501	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.591481	-0.217813	-4.809294	39037.416248
HLA B*4403	1:341-349	9	DVVESGGGS	0.924896	-1.083013	-4.651922	-0.158117	-4.810039	44866.435461
HLA B*5301	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.597999	-0.212130	-4.810129	39627.669922
HLA A*0250	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.592957	-0.217813	-4.810770	39170.267919
HLA B*5701	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.404953	-0.406160	-4.811113	25406.983274
HLA B*5301	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.607443	-0.203931	-4.811375	40498.922305
HLA A*2402	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.563980	-0.247969	-4.811949	36642.098981
HLA B*1501	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.406436	-0.406216	-4.812651	25493.861771
HLA B*1502	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.586495	-0.226766	-4.813262	38591.837578
HLA A*0203	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.407288	-0.406216	-4.813504	25543.975546
HLA A*0250	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.602004	-0.212130	-4.814135	39994.880989
HLA A*6801	1:398-406	9	ARQPFPGPG	0.311811	-0.446917	-4.679786	-0.135106	-4.814893	47839.480984
HLA B*4601	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.410503	-0.406216	-4.816718	25733.720831
HLA A*3002	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.569067	-0.247969	-4.817036	37073.789400
HLA B*4801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.410975	-0.406216	-4.817191	25761.718582
HLA A*3301	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.613999	-0.203931	-4.817930	41114.832921
HLA A*3201	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.591169	-0.226766	-4.817935	39009.338334
HLA B*4002	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.642939	-0.175217	-4.818156	43948.037458
HLA B*5101	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.497685	-0.320678	-4.818363	31454.654935
HLA B*0802	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.497972	-0.320678	-4.818649	31475.422063
HLA B*4501	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.643844	-0.175217	-4.819061	44039.668144
HLA A*6801	1:41-49	9	SEVIPHTAS	0.820502	-1.024433	-4.615307	-0.203931	-4.819238	41238.911436
HLA B*4801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.413597	-0.406160	-4.819757	25917.723778
HLA B*5401	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.499165	-0.320678	-4.819843	31562.042535
HLA B*4001	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.414050	-0.406160	-4.820210	25944.798829
HLA A*3201	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.611461	-0.209501	-4.820962	40875.312500
HLA A*0202	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.592120	-0.229683	-4.821803	39094.901693
HLA B*4002	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.609943	-0.212130	-4.822074	40732.711258
HLA A*3002	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.611555	-0.212130	-4.823685	40884.158693
HLA A*0250	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.596001	-0.229683	-4.825684	39445.864144
HLA B*3901	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.419649	-0.406160	-4.825809	26281.438377
HLA B*0702	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.421357	-0.406160	-4.827517	26385.006528
HLA A*3301	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.530434	-0.297084	-4.827518	33918.324959
HLA A*3101	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.421658	-0.406160	-4.827818	26403.283570
HLA A*0206	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.507673	-0.320678	-4.828351	32186.413470
HLA A*6802	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.422436	-0.406160	-4.828595	26450.605582
HLA A*2602	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.508871	-0.320678	-4.829549	32275.339803
HLA B*5701	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.423709	-0.406216	-4.829925	26528.276804
HLA B*1502	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.618827	-0.212130	-4.830957	41574.469998
HLA A*2402	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.572610	-0.260222	-4.832832	37377.478638
HLA A*3301	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.624458	-0.209501	-4.833960	42117.097775
HLA B*5301	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.604356	-0.229683	-4.834039	40212.052723
HLA A*2403	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.428970	-0.406160	-4.835129	26851.560947
HLA B*5301	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.608910	-0.226766	-4.835676	40635.868405
HLA A*2301	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.538857	-0.297084	-4.835941	34582.572845
HLA A*0250	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.591387	-0.247969	-4.839356	39028.969638
HLA A*3002	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.518732	-0.320678	-4.839410	33016.544020
HLA A*3301	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.610538	-0.229683	-4.840221	40788.500370
HLA B*1503	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.519636	-0.320678	-4.840314	33085.382783
HLA A*3201	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.581146	-0.260222	-4.841368	38119.367063
HLA B*4403	1:396-404	9	IVARQPFPG	0.425569	-0.600786	-4.666399	-0.175217	-4.841616	46387.299878
HLA B*5301	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.581672	-0.260222	-4.841894	38165.588690
HLA A*2602	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.615420	-0.226766	-4.842186	41249.621527
HLA A*3201	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.630903	-0.212130	-4.843033	42746.747349

HLA B*0803	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.524455	-0.320678	-4.845133	33454.531884
HLA A*2602	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.548302	-0.297084	-4.845386	35342.903923
HLA B*3501	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.439406	-0.406160	-4.845566	27504.639036
HLA B*7301	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.615911	-0.229683	-4.845594	41296.287483
HLA B*1502	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.598252	-0.247969	-4.846221	39650.829867
HLA A*3201	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.616832	-0.229683	-4.846515	41383.956477
HLA A*2403	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.440421	-0.406216	-4.846637	27568.994533
HLA A*8001	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.440651	-0.406216	-4.846867	27583.614638
HLA B*5401	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.549818	-0.297084	-4.846902	35466.444106
HLA A*2602	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.635097	-0.212130	-4.847227	43161.537336
HLA A*2602	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.629968	-0.217813	-4.847781	42654.806810
HLA B*0801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.441725	-0.406160	-4.847885	27651.894512
HLA A*3002	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.441734	-0.406216	-4.847950	27652.492894
HLA A*0219	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.442040	-0.406160	-4.848200	27671.947334
HLA B*3801	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.551164	-0.297084	-4.848248	35576.555925
HLA A*3301	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.631328	-0.217813	-4.849141	42788.625034
HLA B*4501	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.588988	-0.260222	-4.849211	38813.987521
HLA A*2402	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.552256	-0.297084	-4.849340	35666.164917
HLA B*1502	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.620053	-0.229683	-4.849736	41692.040656
HLA A*8001	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.445710	-0.406160	-4.851869	27906.772889
HLA B*4402	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.446922	-0.406216	-4.853138	27984.783556
HLA A*2301	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.532991	-0.320678	-4.853669	34118.555538
HLA B*1801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.448193	-0.406216	-4.854409	28066.807996
HLA B*4403	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.642549	-0.212130	-4.854680	43908.588009
HLA B*7301	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.557609	-0.297084	-4.854693	36108.424559
HLA A*2603	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.637571	-0.217813	-4.855384	43408.113580
HLA B*4402	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.342067	-0.513500	-4.855567	21981.978872
HLA A*0250	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.595809	-0.260222	-4.856031	39428.369409
HLA A*0211	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.535641	-0.320678	-4.856319	34327.395635
HLA A*2902	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.451125	-0.406160	-4.857285	28256.943350
HLA A*3301	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.645496	-0.212130	-4.857626	44207.476597
HLA A*2602	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.628051	-0.229683	-4.857734	42466.923472
HLA A*0212	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.452493	-0.406216	-4.858708	28346.052113
HLA B*1517	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.452615	-0.406160	-4.858775	28354.027382
HLA B*0702	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.455364	-0.406216	-4.861579	28534.065372
HLA B*4501	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.649551	-0.212130	-4.861681	44622.195724
HLA B*4501	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.567098	-0.297084	-4.864182	36906.096258
HLA A*2603	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.652988	-0.212130	-4.865119	44976.766886
HLA B*4002	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.638652	-0.226766	-4.865418	43516.271320
HLA A*0216	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.460831	-0.406160	-4.866991	28895.545889
HLA A*2602	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.607455	-0.260222	-4.867678	40500.017793
HLA A*0202	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.547402	-0.320678	-4.868080	35269.749680
HLA A*2602	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.620530	-0.247969	-4.868499	41737.852318
HLA A*6801	1:132-140	9	PEVQPVWMS	0.979901	-1.189402	-4.660135	-0.209501	-4.869637	45723.068320
HLA A*0219	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.463690	-0.406216	-4.869906	29086.417040
HLA A*3201	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.622226	-0.247969	-4.870195	41901.196663
HLA A*6801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.465901	-0.406216	-4.872117	29234.864961
HLA A*3301	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.625520	-0.247969	-4.873489	42220.211465
HLA B*4403	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.613902	-0.260222	-4.874125	41105.714438
HLA B*4002	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.646295	-0.229683	-4.875978	44288.864991
HLA B*4501	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.628330	-0.247969	-4.876299	42494.271494
HLA A*3301	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.616083	-0.260222	-4.876305	41312.599512
HLA B*5801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.363271	-0.513500	-4.876771	23081.864556
HLA B*3801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.557493	-0.320678	-4.878171	36098.854042
HLA A*6801	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.630800	-0.247969	-4.878769	42736.573333
HLA A*1101	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.472675	-0.406160	-4.878834	29694.407040
HLA A*0301	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.365385	-0.513500	-4.878885	23194.521887
HLA B*2705	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.473422	-0.406216	-4.879637	29745.535624
HLA B*4501	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.653876	-0.226766	-4.880643	45068.835696
HLA B*4501	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.651294	-0.229683	-4.880977	44801.675351
HLA A*6801	1:125-133	9	GKLHSDLPE	0.522162	-0.739975	-4.663326	-0.217813	-4.881139	46060.215693
HLA B*2705	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.475856	-0.406160	-4.882016	29912.716854
HLA A*2603	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.623996	-0.260222	-4.884218	42072.235466
HLA B*1801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.481083	-0.406160	-4.887243	30274.952066
HLA B*0802	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.482622	-0.406216	-4.888838	30382.420969

HLA A*1101	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.485390	-0.406216	-4.891606	30576.661839
HLA A*0101	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.379055	-0.513500	-4.892555	23936.173740
HLA A*0216	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.486985	-0.406216	-4.893201	30689.186083
HLA A*2501	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.487084	-0.406216	-4.893300	30696.159929
HLA B*1502	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.572998	-0.320678	-4.893676	37410.857856
HLA A*2603	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.664935	-0.229683	-4.894618	46231.221104
HLA B*4002	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.647321	-0.247969	-4.895290	44393.693116
HLA A*6801	1:340-348	9	PDVVESGGG	0.724207	-0.936337	-4.683879	-0.212130	-4.896010	48292.452595
HLA B*4403	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.669362	-0.226766	-4.896128	46704.829860
HLA B*4002	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.492173	-0.406160	-4.898333	31057.967661
HLA B*4403	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.650401	-0.247969	-4.898370	44709.668559
HLA B*4403	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.668941	-0.229683	-4.898624	46659.624188
HLA A*3101	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.386420	-0.513500	-4.899920	24345.593370
HLA A*6901	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.386481	-0.513500	-4.899981	24349.017992
HLA B*5301	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.602921	-0.297084	-4.900005	40079.353540
HLA B*5101	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.494844	-0.406216	-4.901060	31249.595336
HLA A*0250	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.580751	-0.320678	-4.901429	38084.737581
HLA A*6801	1:374-382	9	PLRLLFKDE	0.702874	-0.929640	-4.675163	-0.226766	-4.901929	47332.851947
HLA B*0802	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.496010	-0.406160	-4.902170	31333.560133
HLA A*6801	1:489-497	9	PYEVLERIS	0.882838	-1.112521	-4.676906	-0.229683	-4.906589	47523.234390
HLA A*2402	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.586209	-0.320678	-4.906887	38566.375119
HLA B*5401	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.500852	-0.406160	-4.907012	31684.877399
HLA A*2501	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.501092	-0.406160	-4.907251	31702.366215
HLA A*0201	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.394911	-0.513500	-4.908411	24826.265913
HLA B*5101	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.502927	-0.406160	-4.909086	31836.595994
HLA B*1503	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.505044	-0.406160	-4.911203	31992.156252
HLA B*3901	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.505368	-0.406216	-4.911583	32016.049384
HLA B*1517	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.509282	-0.406216	-4.915498	32305.910324
HLA B*4601	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.402117	-0.513500	-4.915617	25241.622843
HLA B*4403	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.594942	-0.320678	-4.915620	39349.739072
HLA A*2601	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.402392	-0.513500	-4.915892	25257.604763
HLA A*2603	1:66-74	9	GPASVYADG	0.573341	-0.821310	-4.669056	-0.247969	-4.917025	46671.994574
HLA A*6802	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.403849	-0.513500	-4.917349	25342.464321
HLA A*2603	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.596995	-0.320678	-4.917673	39536.234755
HLA B*4002	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.597033	-0.320678	-4.917711	39539.657090
HLA B*1501	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.404892	-0.513500	-4.918392	25403.409852
HLA A*2603	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.621942	-0.297084	-4.919026	41873.777258
HLA B*5301	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.598414	-0.320678	-4.919092	39665.633585
HLA B*0702	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.408426	-0.513500	-4.921926	25610.947183
HLA A*0203	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.408689	-0.513500	-4.922189	25626.469753
HLA A*3201	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.602030	-0.320678	-4.922708	39997.261106
HLA B*5701	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.410138	-0.513500	-4.923638	25712.151306
HLA A*6801	1:357-365	9	HHNVGGLPD	0.582691	-0.842913	-4.663516	-0.260222	-4.923739	46080.403749
HLA B*0803	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.521029	-0.406216	-4.927245	33191.693252
HLA B*4501	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.607474	-0.320678	-4.928152	40501.770636
HLA B*1509	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.524424	-0.406160	-4.930584	33452.179158
HLA B*4002	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.634836	-0.297084	-4.931920	43135.626712
HLA B*0803	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.526377	-0.406160	-4.932537	33602.905923
HLA A*0206	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.527728	-0.406160	-4.933888	33707.596767
HLA A*0202	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.527704	-0.406216	-4.933920	33705.773272
HLA A*0202	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.530716	-0.406160	-4.936876	33940.351433
HLA A*8001	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.424999	-0.513500	-4.938499	26607.183679
HLA A*2301	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.535897	-0.406216	-4.942113	34347.643711
HLA A*2902	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.431103	-0.513500	-4.944603	26983.785119
HLA B*4801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.432543	-0.513500	-4.946043	27073.418963
HLA A*0212	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.433899	-0.513500	-4.947399	27158.060840
HLA B*4403	1:295-303	9	ALSGVSAPE	0.384162	-0.681246	-4.651254	-0.297084	-4.948338	44797.555215
HLA A*0211	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.543025	-0.406160	-4.949185	34916.064477
HLA B*4001	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.436840	-0.513500	-4.950340	27342.631668
HLA A*2301	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.544548	-0.406160	-4.950708	35038.681315
HLA A*0206	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.545180	-0.406216	-4.951395	35089.708833
HLA B*1509	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.545199	-0.406216	-4.951414	35091.227518
HLA B*1503	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.546110	-0.406216	-4.952326	35164.962661
HLA B*5401	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.546491	-0.406216	-4.952706	35195.794815
HLA A*0211	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.546538	-0.406216	-4.952753	35199.603128

HLA A*3301	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.632576	-0.320678	-4.953254	42911.718544
HLA A*2403	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.444300	-0.513500	-4.957800	27816.336215
HLA B*4501	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.554131	-0.406160	-4.960291	35820.471854
HLA A*6801	1:358-366	9	HNVGGLPDD	0.550176	-0.870854	-4.640371	-0.320678	-4.961049	43688.939105
HLA B*7301	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.556258	-0.406160	-4.962417	35996.277098
HLA B*3501	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.452246	-0.513500	-4.965746	28329.955040
HLA A*3301	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.561394	-0.406216	-4.967609	36424.496782
HLA A*0216	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.457723	-0.513500	-4.971222	28689.470629
HLA B*1517	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.458155	-0.513500	-4.971655	28718.042909
HLA B*4403	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.566163	-0.406160	-4.972323	36826.717905
HLA A*0219	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.467757	-0.513500	-4.981257	29360.076665
HLA B*7301	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.575758	-0.406216	-4.981974	37649.421881
HLA B*3801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.577149	-0.406160	-4.983309	37770.193258
HLA A*1101	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.469876	-0.513500	-4.983376	29503.695744
HLA A*2402	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.579710	-0.406216	-4.985926	37993.573711
HLA B*1502	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.581940	-0.406216	-4.988156	38189.133713
HLA B*3801	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.584477	-0.406216	-4.990693	38412.913712
HLA B*2705	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.478076	-0.513500	-4.991576	30066.032557
HLA A*3002	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.588154	-0.406160	-4.994314	38739.516379
HLA B*0802	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.481293	-0.513500	-4.994792	30289.532364
HLA A*2402	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.591584	-0.406160	-4.997744	39046.709630
HLA B*1502	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.594951	-0.406160	-5.001111	39350.590592
HLA A*2603	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.595212	-0.406216	-5.001428	39374.227627
HLA A*0250	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.595752	-0.406216	-5.001968	39423.250467
HLA A*0250	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.597634	-0.406160	-5.003794	39594.454748
HLA B*1801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.491377	-0.513500	-5.004876	31001.061024
HLA A*0206	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.492345	-0.513500	-5.005844	31070.235555
HLA B*5101	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.492488	-0.513500	-5.005988	31080.490526
HLA A*2501	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.493066	-0.513500	-5.006566	31121.880995
HLA B*0803	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.495178	-0.513500	-5.008678	31273.610632
HLA B*5301	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.603647	-0.406160	-5.009807	40146.408452
HLA B*5301	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.608028	-0.406216	-5.014244	40553.513641
HLA B*4002	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.502673	-0.513500	-5.016173	31818.000321
HLA B*5401	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.504672	-0.513500	-5.018172	31964.822241
HLA B*1503	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.506230	-0.513500	-5.019730	32079.678132
HLA A*3201	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.616726	-0.406160	-5.022886	41373.882986
HLA B*3901	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.510027	-0.513500	-5.023527	32361.360388
HLA B*1509	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.511890	-0.513500	-5.025390	32500.490209
HLA A*3201	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.625690	-0.406216	-5.031905	42236.659949
HLA A*2602	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.628359	-0.406216	-5.034574	42497.030256
HLA A*2602	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.631688	-0.406160	-5.037848	42824.056398
HLA B*4501	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.638769	-0.406216	-5.044985	43528.043822
HLA A*3301	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.640186	-0.406160	-5.046346	43670.271261
HLA B*4002	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.642253	-0.406216	-5.048469	43878.668092
HLA A*2301	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.539186	-0.513500	-5.052686	34608.775070
HLA A*0211	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.546822	-0.513500	-5.060322	35222.652211
HLA A*6801	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.656722	-0.406160	-5.062881	45365.067877
HLA B*4403	1:225-233	9	DGHAICGLS	0.823661	-1.229877	-4.659172	-0.406216	-5.065388	45621.764451
HLA A*0202	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.559375	-0.513500	-5.072875	36255.621388
HLA A*2603	1:142-150	9	GDAVTAAPD	0.597008	-1.003168	-4.668004	-0.406160	-5.074164	46559.015877
HLA B*3801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.566156	-0.513500	-5.079656	36826.120225
HLA A*2402	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.574725	-0.513500	-5.088224	37559.909611
HLA A*0250	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.591873	-0.513500	-5.105373	39072.700596
HLA B*7301	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.596027	-0.513500	-5.109527	39448.211589
HLA A*3002	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.597110	-0.513500	-5.110610	39546.716590
HLA B*5301	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.602768	-0.513500	-5.116268	40065.262402
HLA B*4501	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.602850	-0.513500	-5.116350	40072.849322
HLA A*3301	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.603466	-0.513500	-5.116966	40129.688488
HLA B*1502	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.610629	-0.513500	-5.124129	40797.107067
HLA A*2602	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.616999	-0.513500	-5.130499	41399.855196
HLA A*3201	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.623058	-0.513500	-5.136558	41981.518564
HLA B*4403	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.633123	-0.513500	-5.146623	42965.843049
HLA A*6801	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.644641	-0.513500	-5.158140	44120.508906
HLA A*2603	1:420-428	9	LDTLRHADS	0.552849	-1.066349	-4.647096	-0.513500	-5.160596	44370.643266