```
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.

Predictions
Allele      Position    PepLength   Sequence    Proteasome  TAP   MHC   Processing  Total
HLA B*1517  1:278-286   9   LATIGAFVY   1.578633    1.345789    -0.937134   2.924422    1.987287    8.652356
HLA A*2902  1:216-224   9   WMITVAFLY   1.184200    1.360637    -0.697806   2.544837    1.847030    4.986622
HLA B*3501  1:278-286   9   LATIGAFVY   1.578633    1.345789    -1.271264   2.924422    1.653158    18.675148
HLA A*3201  1:214-222   9   FVWMITVAF   1.324701    1.148010    -0.889280   2.472711    1.583431    7.749614
HLA B*1503  1:214-222   9   FVWMITVAF   1.324701    1.148010    -0.925180   2.472711    1.547531    8.417443
HLA B*1503  1:253-261   9   ELVSSGTIF   1.369450    1.120297    -1.023544   2.489747    1.466203    10.557078
HLA B*3501  1:214-222   9   FVWMITVAF   1.324701    1.148010    -1.048284   2.472711    1.424427    11.175934
HLA B*1517  1:208-216   9   LSVALFFVW   1.685197    0.457260    -0.794507   2.142457    1.347951    6.230265
HLA A*0250  1:292-300   9   LIGGIEVTL   2.013476    0.343151    -1.100593   2.356627    1.256035    12.606449
HLA A*8001  1:216-224   9   WMITVAFLY   1.184200    1.360637    -1.297611   2.544837    1.247225    19.843175
HLA B*5801  1:208-216   9   LSVALFFVW   1.685197    0.457260    -0.908358   2.142457    1.234099    8.097629
HLA A*2902  1:278-286   9   LATIGAFVY   1.578633    1.345789    -1.722464   2.924422    1.201958    52.779326
HLA B*5801  1:278-286   9   LATIGAFVY   1.578633    1.345789    -1.776408   2.924422    1.148014    59.759646
HLA A*0219  1:273-281   9   VLMTALATI   1.272095    0.298918    -0.463286   1.571013    1.107728    2.905933
HLA A*3002  1:278-286   9   LATIGAFVY   1.578633    1.345789    -1.830597   2.924422    1.093825    67.701227
HLA B*1503  1:206-214   9   LLLSVALFF   1.278155    1.141591    -1.401468   2.419746    1.018278    25.203903
HLA A*3002  1:216-224   9   WMITVAFLY   1.184200    1.360637    -1.535511   2.544837    1.009326    34.317103
HLA B*1517  1:204-212   9   VSLLLSVAL   1.611099    0.512458    -1.118172   2.123557    1.005386    13.127185
HLA A*0250  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.388859   1.388176    0.999317    2.448266
HLA A*0202  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.396471   1.388176    0.991705    2.491557
HLA A*0212  1:273-281   9   VLMTALATI   1.272095    0.298918    -0.627679   1.571013    0.943334    4.243058
HLA A*0250  1:273-281   9   VLMTALATI   1.272095    0.298918    -0.635329   1.571013    0.935684    4.318460
HLA A*6801  1:167-175   9   ITAESRDAR   0.938361    0.675089    -0.678348   1.613450    0.935102    4.768129
HLA A*0250  1:265-273   9   FLIGLVNIV   0.994940    0.200128    -0.299869   1.195068    0.895198    1.994663
HLA B*1503  1:216-224   9   WMITVAFLY   1.184200    1.360637    -1.660278   2.544837    0.884559    45.738053
HLA B*1517  1:258-266   9   GTIFGGAFL   1.394877    0.382481    -0.918174   1.777358    0.859184    8.282740
HLA A*0250  1:207-215   9   LLSVALFFV   1.021557    0.165031    -0.341404   1.186588    0.845184    2.194844
HLA A*0203  1:273-281   9   VLMTALATI   1.272095    0.298918    -0.734938   1.571013    0.836076    5.431724
HLA B*1517  1:276-284   9   TALATIGAF   1.215453    1.136775    -1.522767   2.352228    0.829461    33.324759
HLA A*0203  1:284-292   9   FVYNLITDL   1.173320    0.583858    -0.928075   1.757178    0.829103    8.473733
HLA A*0211  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.566343   1.388176    0.821832    3.684201
HLA A*0250  1:224-232   9   YLVLGGMGV   0.951226    0.190010    -0.320686   1.141236    0.820550    2.092598
HLA B*5301  1:278-286   9   LATIGAFVY   1.578633    1.345789    -2.104927   2.924422    0.819495    127.328936
HLA A*0211  1:265-273   9   FLIGLVNIV   0.994940    0.200128    -0.377576   1.195068    0.817492    2.385483
HLA A*0219  1:207-215   9   LLSVALFFV   1.021557    0.165031    -0.376486   1.186588    0.810102    2.379503
HLA A*0219  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.585050   1.388176    0.803126    3.846360
HLA A*0203  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.586681   1.388176    0.801495    3.860828
HLA A*0211  1:273-281   9   VLMTALATI   1.272095    0.298918    -0.779268   1.571013    0.791745    6.015445
HLA A*0250  1:284-292   9   FVYNLITDL   1.173320    0.583858    -0.983584   1.757178    0.773594    9.629056
HLA A*0203  1:265-273   9   FLIGLVNIV   0.994940    0.200128    -0.427649   1.195068    0.767419    2.677001
HLA A*0202  1:207-215   9   LLSVALFFV   1.021557    0.165031    -0.435571   1.186588    0.751017    2.726284
HLA A*6802  1:219-227   9   TVAFLYLVL   1.618736    0.478509    -1.353552   2.097245    0.743693    22.571083
HLA A*0202  1:265-273   9   FLIGLVNIV   0.994940    0.200128    -0.486292   1.195068    0.708776    3.064021
HLA A*0211  1:224-232   9   YLVLGGMGV   0.951226    0.190010    -0.432653   1.141236    0.708583    2.708027
HLA A*2902  1:214-222   9   FVWMITVAF   1.324701    1.148010    -1.781243   2.472711    0.691468    60.428701
HLA A*0212  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.700889   1.388176    0.687287    5.022142
HLA A*0212  1:265-273   9   FLIGLVNIV   0.994940    0.200128    -0.532769   1.195068    0.662299    3.410117
HLA A*0216  1:277-285   9   ALATIGAFV   1.170021    0.218155    -0.733537   1.388176    0.654638    5.414239
HLA A*2902  1:206-214   9   LLLSVALFF   1.278155    1.141591    -1.769458   2.419746    0.650288    58.810956
HLA A*0211  1:207-215   9   LLSVALFFV   1.021557    0.165031    -0.537534   1.186588    0.649054    3.447736
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HLA A*2403	1:121-129	9	AYASELPDL	1.278221	0.528677	-1.164311	1.806898	0.642588	14.598586
HLA B*5801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-1.915620	2.544837	0.629217	82.341676
HLA B*5701	1:208-216	9	LSVALFFVW	1.685197	0.457260	-1.520262	2.142457	0.622195	33.133130
HLA A*0212	1:207-215	9	LLSVALFFV	1.021557	0.165031	-0.594622	1.186588	0.591966	3.932075
HLA A*0219	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-0.556179	1.141236	0.585057	3.598980
HLA A*0206	1:284-292	9	FVYNLITDL	1.173320	0.583858	-1.172985	1.757178	0.584193	14.893099
HLA A*0211	1:206-214	9	LLLSVALFF	1.278155	1.141591	-1.841235	2.419746	0.578511	69.380114
HLA A*0211	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-0.586727	1.157848	0.571121	3.861246
HLA B*1503	1:205-213	9	SLLLSVALF	1.195536	1.159378	-1.793099	2.354914	0.561815	62.101024
HLA A*0212	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-0.586041	1.141236	0.555195	3.855151
HLA A*0206	1:217-225	9	MITVAFLYL	1.461926	0.452609	-1.362645	1.914535	0.551891	23.048619
HLA B*3501	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.013903	2.544837	0.530933	103.253162
HLA A*0216	1:207-215	9	LLSVALFFV	1.021557	0.165031	-0.664096	1.186588	0.522492	4.614196
HLA B*1501	1:214-222	9	FVWMITVAF	1.324701	1.148010	-1.954414	2.472711	0.518296	90.035628
HLA B*1517	1:170-178	9	ESRDARVQL	1.767877	0.433113	-1.684266	2.200990	0.516724	48.335467
HLA A*0203	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-0.649821	1.141236	0.491416	4.464991
HLA A*0202	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-1.425174	1.914964	0.489789	26.617920
HLA A*0216	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-0.733472	1.195068	0.461596	5.413419
HLA B*1517	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-1.547568	2.003318	0.455750	35.283217
HLA A*0216	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-0.687986	1.141236	0.453251	4.875123
HLA B*1503	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-1.729681	2.176570	0.446889	53.663805
HLA A*0206	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-0.751845	1.195068	0.443223	5.647349
HLA A*0206	1:207-215	9	LLSVALFFV	1.021557	0.165031	-0.747132	1.186588	0.439456	5.586394
HLA B*3501	1:276-284	9	TALATIGAF	1.215453	1.136775	-1.935994	2.352228	0.416233	86.296750
HLA A*0250	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.405065	0.818322	0.413256	2.541355
HLA A*0219	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-0.785611	1.195068	0.409456	6.103956
HLA B*1502	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-2.081597	2.489747	0.408150	120.669280
HLA B*1501	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.143670	2.544837	0.401166	139.209898
HLA A*0250	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-0.634873	1.032607	0.397734	4.313930
HLA B*5301	1:208-216	9	LSVALFFVW	1.685197	0.457260	-1.751734	2.142457	0.390724	56.459071
HLA A*0202	1:273-281	9	VLMTALATI	1.272095	0.298918	-1.187839	1.571013	0.383175	15.411274
HLA A*0202	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.441868	0.818322	0.376454	2.766099
HLA A*0203	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-1.204745	1.580071	0.375325	16.023059
HLA B*5801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-1.628729	2.003318	0.374589	42.533272
HLA A*6802	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.070078	1.439287	0.369209	11.751076
HLA A*0203	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.457595	0.818322	0.360727	2.868105
HLA A*0201	1:273-281	9	VLMTALATI	1.272095	0.298918	-1.220073	1.571013	0.350940	16.598677
HLA A*0250	1:217-225	9	MITVAFLYL	1.461926	0.452609	-1.566834	1.914535	0.347702	36.883655
HLA B*2705	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-1.840004	2.176570	0.336566	69.183715
HLA B*1517	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.143938	2.472711	0.328773	139.295779
HLA A*0211	1:284-292	9	FVYNLITDL	1.173320	0.583858	-1.432349	1.757178	0.324828	27.061349
HLA A*0211	1:210-218	9	VALFFVWMI	1.152802	0.312235	-1.161534	1.465037	0.303503	14.505533
HLA B*1517	1:77-85	9	AADARLNRF	1.242908	1.175831	-2.126876	2.418739	0.291863	133.929423
HLA A*6801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.262798	2.544837	0.282038	183.146407
HLA A*0203	1:207-215	9	LLSVALFFV	1.021557	0.165031	-0.906897	1.186588	0.279691	8.070427
HLA A*0203	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-0.665581	0.943496	0.277915	4.629999
HLA A*3301	1:173-181	9	DARVQLSAR	0.897969	0.607997	-1.246768	1.505966	0.259197	17.650959
HLA A*6802	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-0.844649	1.101846	0.257197	6.992770
HLA A*0206	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-0.848493	1.101846	0.253353	7.054935
HLA A*0211	1:212-220	9	LFFVWMITV	1.409538	0.325913	-1.487863	1.735451	0.247588	30.751271
HLA A*0201	1:207-215	9	LLSVALFFV	1.021557	0.165031	-0.941674	1.186588	0.244914	8.743264
HLA A*0216	1:284-292	9	FVYNLITDL	1.173320	0.583858	-1.515267	1.757178	0.241910	32.754235
HLA A*0202	1:217-225	9	MITVAFLYL	1.461926	0.452609	-1.675944	1.914535	0.238591	47.418088
HLA A*0206	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.201123	1.439287	0.238165	15.889950
HLA A*2403	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.190556	2.419746	0.229190	155.080231
HLA A*0201	1:277-285	9	ALATIGAFV	1.170021	0.218155	-1.162154	1.388176	0.226022	14.526265

HLA A*0202	1:284-292	9	FVYNLITDL	1.173320	0.583858	-1.537042	1.757178	0.220135	34.438362
HLA A*0201	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-0.977531	1.195068	0.217536	9.495797
HLA A*6802	1:217-225	9	MITVAFLYL	1.461926	0.452609	-1.700670	1.914535	0.213865	50.196105
HLA B*1501	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.206415	2.419746	0.213330	160.847925
HLA A*0216	1:273-281	9	VLMTALATI	1.272095	0.298918	-1.359586	1.571013	0.211427	22.886843
HLA B*1517	1:205-213	9	SLLLSVALF	1.195536	1.159378	-2.156827	2.354914	0.198087	143.491849
HLA A*0206	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-0.957133	1.141236	0.184103	9.060104
HLA B*1501	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-2.311870	2.489747	0.177877	205.054709
HLA A*0206	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.641814	0.818322	0.176508	4.383424
HLA A*0206	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.299742	2.472711	0.172969	199.407600
HLA A*6802	1:275-283	9	MTALATIGA	1.189575	-0.192124	-0.827836	0.997451	0.169615	6.727231
HLA A*0219	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.656935	0.818322	0.161387	4.538735
HLA A*2403	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.320248	2.472711	0.152463	209.048960
HLA A*3201	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-2.208962	2.356627	0.147665	161.793960
HLA A*0201	1:284-292	9	FVYNLITDL	1.173320	0.583858	-1.613654	1.757178	0.143523	41.082276
HLA A*6801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-1.579460	1.722434	0.142974	37.971704
HLA B*5801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.277657	2.419746	0.142089	189.520654
HLA A*0203	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.020348	1.157848	0.137500	10.479690
HLA B*1503	1:276-284	9	TALATIGAF	1.215453	1.136775	-2.217312	2.352228	0.134915	164.934829
HLA A*6802	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-1.784786	1.914964	0.130177	60.923702
HLA A*0202	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-0.981596	1.101846	0.120250	9.585087
HLA B*4601	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.361392	2.472711	0.111319	229.822314
HLA B*1502	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.437172	2.544837	0.107664	273.635526
HLA A*3001	1:179-187	9	SARRSRGPV	0.654360	0.222846	-0.771646	0.877206	0.105560	5.910797
HLA A*3201	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-2.025350	2.123557	0.098207	106.010785
HLA A*0250	1:212-220	9	LFFVWMITV	1.409538	0.325913	-1.643380	1.735451	0.092071	43.992655
HLA A*0206	1:277-285	9	ALATIGAFV	1.170021	0.218155	-1.299007	1.388176	0.089169	19.907043
HLA A*6802	1:246-254	9	NASGSSAEL	1.312746	0.515179	-1.759492	1.827925	0.068434	57.476687
HLA A*0250	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-0.875066	0.943496	0.068430	7.500076
HLA A*0211	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.750435	0.818322	0.067887	5.629047
HLA A*0211	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-0.879173	0.943496	0.064323	7.571337
HLA A*0206	1:273-281	9	VLMTALATI	1.272095	0.298918	-1.509262	1.571013	0.061751	32.304437
HLA A*8001	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.382862	2.419746	0.036884	241.469224
HLA A*6802	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.787402	0.818322	0.030920	6.129171
HLA A*2403	1:215-223	9	VWMITVAFL	1.544881	0.532732	-2.052205	2.077613	0.025408	112.772878
HLA A*0211	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-2.349734	2.356627	0.006893	223.735061
HLA A*6901	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.434887	1.439287	0.004400	27.219922
HLA A*0250	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-1.580743	1.580071	-0.000672	38.084031
HLA A*6801	1:76-84	9	AAADARLNR	1.236372	0.673742	-1.923378	1.910114	-0.013263	83.825799
HLA B*1517	1:200-208	9	STLKVSLLL	1.428092	0.413469	-1.855229	1.841561	-0.013668	71.652037
HLA A*2301	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.504678	2.472711	-0.031967	319.652337
HLA A*2602	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-2.524136	2.489747	-0.034390	334.299956
HLA B*1517	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-1.577679	1.513906	-0.063773	37.816313
HLA A*0211	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-1.172821	1.101846	-0.070974	14.887461
HLA B*3901	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-2.250247	2.176570	-0.073677	177.929294
HLA A*2403	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-1.689289	1.615041	-0.074248	48.897777
HLA A*0101	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.624318	2.544837	-0.079482	421.035155
HLA A*0250	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.519027	1.439287	-0.079740	33.038980
HLA A*0211	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-1.662810	1.580071	-0.082740	46.005570
HLA A*0202	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-2.444536	2.356627	-0.087908	278.314458
HLA A*0201	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-1.215981	1.101846	-0.114134	16.442985
HLA B*1502	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.588249	2.472711	-0.115538	387.479799
HLA A*6901	1:200-208	9	STLKVSLLL	1.428092	0.413469	-1.960598	1.841561	-0.119038	91.326801
HLA A*0201	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.046505	1.914964	-0.131541	111.302473
HLA A*0206	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.552936	2.419746	-0.133190	357.220444
HLA A*0212	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.960841	0.818322	-0.142519	9.137780

HLA B*1501	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.076420	2.924422	-0.151999	1192.395589
HLA A*0211	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.069525	1.914964	-0.154561	117.361342
HLA A*0211	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.594032	1.439287	-0.154744	39.267350
HLA A*0216	1:85-93	9	FISGASAPV	0.612670	0.205652	-0.974284	0.818322	-0.155963	9.425067
HLA B*0702	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.636042	2.472711	-0.163331	432.555950
HLA B*4001	1:252-260	9	AELVSSGTI	1.198347	0.266272	-1.634936	1.464619	-0.170318	43.145562
HLA A*0203	1:288-296	9	LITDLIGGI	1.024772	0.334657	-1.548000	1.359429	-0.188571	35.318356
HLA A*6901	1:210-218	9	VALFFVWMI	1.152802	0.312235	-1.657787	1.465037	-0.192750	45.476520
HLA B*1501	1:205-213	9	SLLLSVALF	1.195536	1.159378	-2.553387	2.354914	-0.198473	357.591682
HLA A*1101	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.744025	2.544837	-0.199188	554.657156
HLA A*2402	1:215-223	9	VWMITVAFL	1.544881	0.532732	-2.277050	2.077613	-0.199437	189.256315
HLA A*6901	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-1.310458	1.101846	-0.208612	20.438930
HLA A*6901	1:85-93	9	FISGASAPV	0.612670	0.205652	-1.027552	0.818322	-0.209230	10.654963
HLA A*6901	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.128568	1.914964	-0.213604	134.452111
HLA A*1101	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-1.345940	1.126836	-0.219104	22.178904
HLA A*0201	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.678627	1.439287	-0.239340	47.711948
HLA A*0201	1:85-93	9	FISGASAPV	0.612670	0.205652	-1.060224	0.818322	-0.241902	11.487457
HLA A*8001	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.169418	2.924422	-0.244996	1477.126454
HLA B*1503	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-1.646599	1.394704	-0.251894	44.319920
HLA A*0201	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.168485	1.914535	-0.253950	147.395891
HLA A*0216	1:212-220	9	LFFVWMITV	1.409538	0.325913	-1.999473	1.735451	-0.264022	99.878687
HLA B*1502	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-2.550145	2.280423	-0.269722	354.931969
HLA A*2403	1:285-293	9	VYNLITDLI	1.083750	0.286878	-1.641440	1.370628	-0.270812	43.796510
HLA A*0250	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.429737	1.157848	-0.271889	26.899042
HLA A*3101	1:176-184	9	VQLSARRSR	1.028225	0.768884	-2.080958	1.797109	-0.283849	120.491847
HLA A*0216	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.128295	1.841561	-0.286734	134.367763
HLA B*1502	1:205-213	9	SLLLSVALF	1.195536	1.159378	-2.653673	2.354914	-0.298759	450.477211
HLA A*0216	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.460280	1.157848	-0.302432	28.858923
HLA A*6801	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.237924	2.924422	-0.313502	1729.513514
HLA A*0202	1:215-223	9	VWMITVAFL	1.544881	0.532732	-2.406197	2.077613	-0.328584	254.798502
HLA A*2602	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-2.106868	1.777358	-0.329509	127.899187
HLA B*1501	1:276-284	9	TALATIGAF	1.215453	1.136775	-2.685132	2.352228	-0.332905	484.320029
HLA B*1517	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-1.141845	0.802529	-0.339316	13.862610
HLA A*2602	1:276-284	9	TALATIGAF	1.215453	1.136775	-2.700977	2.352228	-0.348750	502.316399
HLA A*0202	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-1.494244	1.141236	-0.353008	31.206443
HLA A*0216	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-2.717518	2.356627	-0.360890	521.816408
HLA B*4801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-2.556916	2.176570	-0.380346	360.509185
HLA A*0202	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.853398	2.472711	-0.380687	713.506356
HLA A*0202	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.835596	1.439287	-0.396309	68.485124
HLA A*2601	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.874031	2.472711	-0.401320	748.222948
HLA A*3201	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.843232	1.439287	-0.403945	69.699886
HLA A*0202	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-1.985601	1.580071	-0.405531	96.738971
HLA B*2705	1:174-182	9	ARVQLSARR	0.965880	0.769663	-2.142580	1.735543	-0.407037	138.860893
HLA A*0212	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-1.995864	1.580071	-0.415793	99.052175
HLA A*0206	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.961615	2.544837	-0.416779	915.408890
HLA B*1503	1:176-184	9	VQLSARRSR	1.028225	0.768884	-2.216326	1.797109	-0.419217	164.560497
HLA B*1517	1:188-196	9	RASMQIRRI	1.055395	0.378608	-1.853236	1.434003	-0.419233	71.324080
HLA B*1517	1:216-224	9	WMITVAFLY	1.184200	1.360637	-2.974232	2.544837	-0.429395	942.392585
HLA B*1503	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.365097	2.924422	-0.440675	2317.911681
HLA B*2705	1:28-36	9	HRAATGPGR	0.868468	0.768121	-2.079078	1.636589	-0.442489	119.971496
HLA A*3201	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.288615	1.841561	-0.447054	194.363426
HLA A*0201	1:214-222	9	FVWMITVAF	1.324701	1.148010	-2.926927	2.472711	-0.454216	845.137416
HLA A*0250	1:288-296	9	LITDLIGGI	1.024772	0.334657	-1.815640	1.359429	-0.456211	65.409333
HLA B*1503	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-2.174998	1.709743	-0.465255	149.622928
HLA B*1517	1:246-254	9	NASGSSAEL	1.312746	0.515179	-2.299107	1.827925	-0.471182	199.116544
HLA A*3201	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.400173	1.914964	-0.485209	251.288603

HLA B*3501	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-2.984118	2.489747	-0.494372	964.092031
HLA B*1502	1:276-284	9	TALATIGAF	1.215453	1.136775	-2.856250	2.352228	-0.504023	718.207806
HLA A*6901	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.421835	1.914535	-0.507300	264.140529
HLA B*1517	1:29-37	9	RAATGPGRI	1.220311	0.357425	-2.086023	1.577736	-0.508287	121.905458
HLA A*0219	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.428089	1.914964	-0.513126	267.971972
HLA B*1501	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-2.230343	1.709743	-0.520600	169.958394
HLA A*0202	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-1.465670	0.943496	-0.522174	29.219302
HLA A*0211	1:205-213	9	SLLLSVALF	1.195536	1.159378	-2.877635	2.354914	-0.522721	754.458114
HLA B*0702	1:179-187	9	SARRSRGPV	0.654360	0.222846	-1.406486	0.877206	-0.529280	25.496837
HLA A*0216	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-1.969465	1.439287	-0.530178	93.210578
HLA B*1503	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-2.654458	2.123557	-0.530900	451.291915
HLA B*1501	1:208-216	9	LSVALFFVW	1.685197	0.457260	-2.674170	2.142457	-0.531712	472.247571
HLA B*2705	1:187-195	9	VRASMQIRR	1.136874	0.704701	-2.373675	1.841575	-0.532100	236.415148
HLA B*1517	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.961784	2.419746	-0.542038	915.765522
HLA A*2301	1:206-214	9	LLLSVALFF	1.278155	1.141591	-2.971817	2.419746	-0.552071	937.166141
HLA A*0301	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-1.684224	1.126836	-0.557387	48.330760
HLA A*3001	1:186-194	9	PVRASMQIR	1.283702	0.503504	-2.350223	1.787206	-0.563017	223.986963
HLA B*4501	1:252-260	9	AELVSSGTI	1.198347	0.266272	-2.028057	1.464619	-0.563438	106.673528
HLA A*3001	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.406343	1.841561	-0.564782	254.883980
HLA A*0206	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.409110	1.841561	-0.567550	256.513504
HLA A*0212	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.728765	1.157848	-0.570917	53.550701
HLA A*0211	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.045346	2.472711	-0.572635	1110.059025
HLA A*0211	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.121032	2.544837	-0.576196	1321.394157
HLA A*0201	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-1.724273	1.141236	-0.583037	52.999643
HLA A*0211	1:288-296	9	LITDLIGGI	1.024772	0.334657	-1.944044	1.359429	-0.584615	87.911112
HLA A*0206	1:288-296	9	LITDLIGGI	1.024772	0.334657	-1.946783	1.359429	-0.587354	88.467402
HLA A*6802	1:284-292	9	FVYNLITDL	1.173320	0.583858	-2.351938	1.757178	-0.594760	224.873285
HLA A*2602	1:209-217	9	SVALFFVWM	1.067963	0.243135	-1.910178	1.311098	-0.599080	81.316429
HLA A*0216	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.517515	1.914535	-0.602980	329.242181
HLA A*2602	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.077586	2.472711	-0.604875	1195.599447
HLA A*3101	1:76-84	9	AAADARLNR	1.236372	0.673742	-2.520039	1.910114	-0.609925	331.160719
HLA A*0250	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.527802	1.914964	-0.612838	337.133195
HLA A*6801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-2.267610	1.647521	-0.620089	185.186852
HLA B*5301	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.096485	2.472711	-0.623774	1248.777205
HLA A*0301	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.169859	2.544837	-0.625023	1478.629544
HLA A*6802	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.098562	2.472711	-0.625851	1254.763588
HLA B*1502	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.551834	2.924422	-0.627412	3563.148741
HLA A*0206	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.092747	1.465037	-0.627711	123.807621
HLA A*3201	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.053066	2.419746	-0.633321	1129.968872
HLA B*3501	1:246-254	9	NASGSSAEL	1.312746	0.515179	-2.461729	1.827925	-0.633804	289.553820
HLA A*0202	1:246-254	9	NASGSSAEL	1.312746	0.515179	-2.463379	1.827925	-0.635453	290.655561
HLA A*6901	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-2.739053	2.097245	-0.641808	548.344018
HLA A*3001	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-1.522509	0.879222	-0.643286	33.304934
HLA A*6802	1:277-285	9	ALATIGAFV	1.170021	0.218155	-2.037741	1.388176	-0.649565	109.079022
HLA A*3101	1:167-175	9	ITAESRDAR	0.938361	0.675089	-2.265063	1.613450	-0.651613	184.104035
HLA A*3201	1:273-281	9	VLMTALATI	1.272095	0.298918	-2.227241	1.571013	-0.656228	168.749035
HLA A*6901	1:275-283	9	MTALATIGA	1.189575	-0.192124	-1.662303	0.997451	-0.664852	45.951843
HLA A*0206	1:215-223	9	VWMITVAFL	1.544881	0.532732	-2.753216	2.077613	-0.675603	566.520730
HLA B*1503	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-2.751176	2.075252	-0.675924	563.866707
HLA A*0202	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-2.359635	1.680196	-0.679439	228.894194
HLA A*0212	1:284-292	9	FVYNLITDL	1.173320	0.583858	-2.436919	1.757178	-0.679741	273.475696
HLA A*0219	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.037940	2.356627	-0.681313	1091.290804
HLA A*2602	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-2.685720	2.003318	-0.682402	484.975502
HLA A*0202	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.843824	1.157848	-0.685976	69.794973
HLA A*0203	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-1.798709	1.101846	-0.696863	62.908500
HLA A*0216	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.124773	2.419746	-0.705027	1332.823870

HLA A*0216	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-1.746020	1.032607	-0.713413	55.721113
HLA A*2301	1:215-223	9	VWMITVAFL	1.544881	0.532732	-2.799115	2.077613	-0.721502	629.673397
HLA A*0206	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-2.500641	1.777358	-0.723283	316.695191
HLA A*0202	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.146520	2.419746	-0.726774	1401.262808
HLA A*0211	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-1.760394	1.032607	-0.727787	57.596213
HLA A*0202	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-2.831336	2.097245	-0.734091	678.166265
HLA B*5701	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.663073	2.924422	-0.738651	4603.335931
HLA A*0201	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.207844	1.465037	-0.742807	161.377859
HLA A*0201	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-1.903144	1.157848	-0.745296	80.009939
HLA A*0211	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.594189	1.841561	-0.752628	392.815453
HLA B*5701	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-2.759550	2.003318	-0.756232	574.844020
HLA A*0101	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.681610	2.924422	-0.757188	4804.078614
HLA A*0202	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-2.535076	1.777358	-0.757717	342.827397
HLA B*1502	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.196512	2.419746	-0.776766	1572.215006
HLA A*3201	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.139081	2.354914	-0.784167	1377.466754
HLA A*2501	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.266527	2.472711	-0.793816	1847.253892
HLA B*3901	1:246-254	9	NASGSSAEL	1.312746	0.515179	-2.622204	1.827925	-0.794278	418.990160
HLA A*2402	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.223024	2.419746	-0.803278	1671.181141
HLA B*2705	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-2.885736	2.075252	-0.810484	768.663321
HLA A*1101	1:76-84	9	AAADARLNR	1.236372	0.673742	-2.726615	1.910114	-0.816501	532.862229
HLA A*3001	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.734829	1.914535	-0.820293	543.036143
HLA A*0250	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-1.923086	1.101846	-0.821240	83.769586
HLA B*3501	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-3.108702	2.280423	-0.828280	1284.405879
HLA B*5801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-2.538167	1.709743	-0.828425	345.276836
HLA A*0211	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.744870	1.914535	-0.830335	555.738437
HLA A*2601	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.375731	2.544837	-0.830894	2375.366642
HLA B*5801	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.187678	2.352228	-0.835450	1540.557362
HLA A*3301	1:167-175	9	ITAESRDAR	0.938361	0.675089	-2.455170	1.613450	-0.841719	285.213144
HLA B*1801	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.767982	2.924422	-0.843560	5861.137006
HLA A*6802	1:209-217	9	SVALFFVWM	1.067963	0.243135	-2.160192	1.311098	-0.849093	144.607792
HLA A*3101	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-2.635892	1.784676	-0.851215	432.406210
HLA A*0219	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.317739	1.465037	-0.852702	207.844607
HLA A*0203	1:217-225	9	MITVAFLYL	1.461926	0.452609	-2.769037	1.914535	-0.854502	587.539728
HLA A*0203	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-2.299648	1.439287	-0.860361	199.364453
HLA B*3901	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-2.960224	2.097245	-0.862979	912.481841
HLA B*5801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-2.445753	1.577736	-0.868017	279.095478
HLA B*2705	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-2.509518	1.640132	-0.869386	323.234586
HLA A*0202	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.416696	2.544837	-0.871860	2610.335163
HLA A*0206	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-2.552791	1.680196	-0.872595	357.100648
HLA A*0201	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.292789	2.419746	-0.873043	1962.407223
HLA B*1517	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-3.362987	2.489747	-0.873240	2306.678388
HLA B*1503	1:284-292	9	FVYNLITDL	1.173320	0.583858	-2.631475	1.757178	-0.874297	428.030672
HLA A*2402	1:285-293	9	VYNLITDLI	1.083750	0.286878	-2.247071	1.370628	-0.876443	176.632636
HLA A*0216	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-2.457251	1.580071	-0.877180	286.583499
HLA A*0250	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.306228	2.419746	-0.886482	2024.082397
HLA B*4002	1:252-260	9	AELVSSGTI	1.198347	0.266272	-2.359940	1.464619	-0.895322	229.055229
HLA A*0203	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-2.992755	2.097245	-0.895510	983.456601
HLA A*6802	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-1.590493	0.687090	-0.903404	38.948727
HLA B*3901	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.029807	2.123557	-0.906249	1071.042189
HLA A*0250	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.263754	2.354914	-0.908840	1835.499193
HLA A*0203	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.827210	1.914964	-0.912247	671.754349
HLA A*0201	1:212-220	9	LFFVWMITV	1.409538	0.325913	-2.662371	1.735451	-0.926919	459.590051
HLA A*0206	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-2.332127	1.394704	-0.937423	214.845869
HLA A*0250	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-2.127506	1.182783	-0.944723	134.123741
HLA A*0206	1:212-220	9	LFFVWMITV	1.409538	0.325913	-2.689061	1.735451	-0.953609	488.720739
HLA A*6802	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.155518	2.200990	-0.954529	1430.599678

HLA A*2902	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.314348	2.354914	-0.959434	2062.281795
HLA A*6901	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-2.104636	1.141236	-0.963399	127.243549
HLA A*2601	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-3.454800	2.489747	-0.965054	2849.707080
HLA A*0212	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-1.911170	0.943496	-0.967674	81.502284
HLA B*5801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.438286	1.465037	-0.973249	274.338107
HLA B*1801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.521328	2.544837	-0.976492	3321.453974
HLA A*6801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.460072	2.472711	-0.987362	2884.512769
HLA A*6901	1:284-292	9	FVYNLITDL	1.173320	0.583858	-2.748949	1.757178	-0.991771	560.982277
HLA A*6802	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-2.077772	1.084809	-0.992963	119.611176
HLA A*0211	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.260263	2.264943	-0.995319	1820.802593
HLA A*2402	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.354397	2.354914	-0.999483	2261.503839
HLA A*2603	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-3.493078	2.489747	-1.003331	3112.275479
HLA A*2403	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.361389	2.352228	-1.009162	2298.208342
HLA A*2902	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.421527	2.412283	-1.009244	2639.531291
HLA B*1503	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.152671	2.142457	-1.010213	1421.250227
HLA A*0202	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.370966	2.354914	-1.016052	2349.448326
HLA A*0206	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-2.732061	1.709743	-1.022318	539.586460
HLA A*2602	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.572589	2.544837	-1.027753	3737.569719
HLA A*2402	1:121-129	9	AYASELPDL	1.278221	0.528677	-2.843803	1.806898	-1.036904	697.915028
HLA A*0201	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.880163	1.841561	-1.038602	758.862653
HLA A*1101	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.963525	2.924422	-1.039103	9194.430006
HLA A*6901	1:207-215	9	LLSVALFFV	1.021557	0.165031	-2.226358	1.186588	-1.039770	168.406128
HLA A*0203	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-2.822079	1.777358	-1.044721	663.864142
HLA B*4601	1:278-286	9	LATIGAFVY	1.578633	1.345789	-3.970789	2.924422	-1.046368	9349.522232
HLA B*0801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.522921	2.472711	-1.050210	3333.659121
HLA B*2705	1:164-172	9	GRSITAESR	1.007055	0.640575	-2.699201	1.647630	-1.051571	500.266182
HLA A*0212	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.408825	2.356627	-1.052198	2563.453825
HLA A*2301	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-2.669471	1.615041	-1.054430	467.165500
HLA B*5401	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-2.205678	1.150365	-1.055313	160.574924
HLA A*6802	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.897357	1.841561	-1.055796	789.508320
HLA A*2603	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.530125	2.472711	-1.057414	3389.414715
HLA A*0206	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.417021	2.356627	-1.060393	2612.284675
HLA A*0212	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.977935	1.914964	-1.062971	950.461760
HLA A*0202	1:212-220	9	LFFVWMITV	1.409538	0.325913	-2.800769	1.735451	-1.065318	632.076119
HLA A*0206	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.189017	2.123557	-1.065460	1545.315213
HLA A*0201	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.425084	2.356627	-1.068456	2661.239342
HLA A*2301	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.211929	2.142457	-1.069472	1629.030658
HLA A*0206	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.424168	2.352228	-1.071940	2655.630427
HLA A*2601	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.234835	1.157848	-1.076987	171.725517
HLA A*0216	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-2.991975	1.914964	-1.077012	981.691817
HLA A*0206	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.237889	1.157848	-1.080041	172.937495
HLA A*3001	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.281084	2.200990	-1.080094	1910.222690
HLA A*6802	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-2.481954	1.401173	-1.080781	303.356752
HLA A*6801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-2.590631	1.505966	-1.084666	389.611210
HLA A*0202	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.351446	2.264943	-1.086503	2246.189414
HLA A*2902	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-2.529225	1.439287	-1.089938	338.240263
HLA A*6802	1:207-215	9	LLSVALFFV	1.021557	0.165031	-2.277384	1.186588	-1.090796	189.401758
HLA B*5401	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.564244	2.472711	-1.091533	3666.434508
HLA A*6901	1:209-217	9	SVALFFVWM	1.067963	0.243135	-2.408217	1.311098	-1.097119	255.986716
HLA B*1801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.572773	2.472711	-1.100062	3739.147199
HLA A*6802	1:288-296	9	LITDLIGGI	1.024772	0.334657	-2.459995	1.359429	-1.100566	288.400081
HLA A*2403	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.462492	2.354914	-1.107578	2900.630674
HLA A*0250	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-1.744742	0.634444	-1.110298	55.557368
HLA B*4801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.585244	2.472711	-1.112533	3848.075893
HLA A*3101	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-2.761683	1.647521	-1.114162	577.674703
HLA A*6802	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-2.310032	1.195068	-1.114965	204.189051

HLA A*6802	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-2.894213	1.777358	-1.116855	783.814151
HLA A*2301	1:212-220	9	LFFVWMITV	1.409538	0.325913	-2.853332	1.735451	-1.117881	713.398285
HLA B*2705	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-2.483241	1.365049	-1.118192	304.257424
HLA A*2301	1:121-129	9	AYASELPDL	1.278221	0.528677	-2.925903	1.806898	-1.119004	843.146329
HLA A*0250	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.663933	2.544837	-1.119096	4612.459655
HLA A*6901	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.593678	2.472711	-1.120967	3923.541765
HLA A*2301	1:285-293	9	VYNLITDLI	1.083750	0.286878	-2.493039	1.370628	-1.122411	311.199246
HLA A*3001	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-3.199341	2.075252	-1.124089	1582.489063
HLA A*3001	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-1.435352	0.310085	-1.125267	27.249095
HLA A*8001	1:200-208	9	STLKVSLLL	1.428092	0.413469	-2.972338	1.841561	-1.130777	938.292349
HLA A*0212	1:212-220	9	LFFVWMITV	1.409538	0.325913	-2.866414	1.735451	-1.130963	735.214381
HLA B*5801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.054274	1.914535	-1.139739	1133.115330
HLA B*3501	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.563154	2.419746	-1.143408	3657.242608
HLA A*2402	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.290181	2.142457	-1.147724	1950.658324
HLA B*5401	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-1.843641	0.685107	-1.158534	69.765527
HLA B*4403	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-2.868688	1.709743	-1.158945	739.074630
HLA B*5801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.632149	2.472711	-1.159438	4286.953249
HLA A*2301	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.522207	2.354914	-1.167293	3328.181070
HLA B*5401	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-1.845445	0.676597	-1.168848	70.055992
HLA B*1502	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.329782	1.157848	-1.171934	213.689027
HLA B*0702	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-1.859533	0.676597	-1.182935	72.365705
HLA A*0206	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.538597	2.354914	-1.183683	3456.184781
HLA B*2705	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.731414	2.544837	-1.186578	5387.837500
HLA B*1503	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-3.468479	2.280423	-1.188056	2940.890965
HLA A*0212	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.735178	2.544837	-1.190342	5434.734889
HLA A*0202	1:288-296	9	LITDLIGGI	1.024772	0.334657	-2.551682	1.359429	-1.192253	356.189966
HLA A*0202	1:209-217	9	SVALFFVWM	1.067963	0.243135	-2.504593	1.311098	-1.193495	319.590089
HLA A*0301	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.623930	2.419746	-1.204184	4206.590617
HLA A*2601	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.128806	2.924422	-1.204385	13452.604736
HLA A*3101	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.131052	2.924422	-1.206631	13522.359870
HLA A*6901	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.042339	1.827925	-1.214413	1102.398799
HLA B*5101	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.140930	2.924422	-1.216508	13833.425150
HLA B*5301	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.223381	2.003318	-1.220063	1672.555923
HLA A*0202	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.066388	1.841561	-1.224827	1165.166688
HLA B*0801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.141741	1.914535	-1.227205	1385.928236
HLA A*0216	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-2.171953	0.943496	-1.228457	148.577558
HLA A*0250	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.500018	2.264943	-1.235075	3162.411712
HLA A*0216	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.785434	2.544837	-1.240597	6101.461115
HLA B*7301	1:83-91	9	NRFISGASA	0.946143	-0.055864	-2.131255	0.890279	-1.240976	135.286804
HLA B*5801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.084911	1.841561	-1.243351	1215.937912
HLA A*0203	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.091789	0.848433	-1.243356	123.534650
HLA B*5701	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.793488	2.544837	-1.248651	6215.669047
HLA A*0206	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.347471	2.097245	-1.250226	2225.722661
HLA A*0206	1:275-283	9	MTALATIGA	1.189575	-0.192124	-2.248528	0.997451	-1.251076	177.226080
HLA A*0301	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.176966	2.924422	-1.252544	15030.247273
HLA B*1503	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.457333	2.200990	-1.256343	2866.374729
HLA A*6901	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.609194	2.352228	-1.256967	4066.251897
HLA A*0216	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.723622	1.465037	-1.258585	529.202263
HLA B*4402	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.672795	2.412283	-1.260512	4707.548877
HLA A*3201	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.019741	1.757178	-1.262564	1046.505185
HLA A*3001	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.188549	2.924422	-1.264127	15436.508862
HLA A*0201	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.619433	2.354914	-1.264519	4163.258089
HLA A*2603	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.811715	2.544837	-1.266879	6482.091947
HLA B*3901	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.742593	2.472711	-1.269882	5528.322096
HLA B*3901	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.814878	2.544837	-1.270041	6529.464934
HLA B*1503	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.362362	2.087371	-1.274991	2303.361394

HLA A*2602	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.630025	2.354914	-1.275111	4266.038916
HLA B*5301	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.740374	1.465037	-1.275337	550.013717
HLA A*0212	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-2.381828	1.101846	-1.279982	240.895126
HLA B*1503	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-2.852077	1.570424	-1.281653	711.340336
HLA A*2402	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.827443	2.544837	-1.282606	6721.135325
HLA A*3201	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.426151	2.142457	-1.283693	2667.783618
HLA A*0219	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.703592	2.419746	-1.283846	5053.495546
HLA A*0202	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-2.693868	1.401173	-1.292695	494.160258
HLA B*3501	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.417415	2.123557	-1.293858	2614.659959
HLA A*0203	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.649211	2.354914	-1.294297	4458.725207
HLA B*4402	1:252-260	9	AELVSSGTI	1.198347	0.266272	-2.761787	1.464619	-1.297168	577.812226
HLA B*4601	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.650780	2.352228	-1.298553	4474.867324
HLA A*2403	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.036653	1.735451	-1.301202	1088.060333
HLA A*0206	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.569450	2.264943	-1.304507	3710.653403
HLA A*0216	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.665732	2.354914	-1.310818	4631.613232
HLA B*5301	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.858385	2.544837	-1.313549	7217.476146
HLA A*0203	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.859419	2.544837	-1.314583	7234.676737
HLA B*1503	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.231773	1.914535	-1.317238	1705.190907
HLA A*0212	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.738501	2.419746	-1.318755	5476.467762
HLA A*0206	1:77-85	9	AADARLNRF	1.242908	1.175831	-3.739276	2.418739	-1.320537	5486.253432
HLA A*0203	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-2.409500	1.084809	-1.324692	256.743967
HLA B*4403	1:252-260	9	AELVSSGTI	1.198347	0.266272	-2.793058	1.464619	-1.328440	620.952490
HLA A*0201	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.875132	2.544837	-1.330296	7501.230076
HLA A*3101	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.810489	2.472711	-1.337778	6463.812587
HLA A*0212	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.128034	1.777358	-1.350675	1342.869615
HLA B*5401	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.277073	2.924422	-1.352651	18926.616507
HLA A*0202	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.166387	1.813629	-1.352758	1466.853835
HLA A*0219	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.267838	1.914535	-1.353302	1852.838656
HLA A*2602	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.556218	2.200990	-1.355229	3599.300370
HLA B*1517	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-2.458496	1.101846	-1.356650	287.406382
HLA B*1503	1:273-281	9	VLMTALATI	1.272095	0.298918	-2.931344	1.571013	-1.360331	853.776823
HLA A*0206	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.285418	2.924422	-1.360997	19293.825808
HLA A*0203	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.718760	2.356627	-1.362133	5233.113600
HLA B*4402	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.287286	2.924422	-1.362865	19376.984586
HLA A*2602	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.289546	2.924422	-1.365125	19478.091354
HLA B*3901	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.717501	2.352228	-1.365273	5217.961117
HLA A*3201	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.462779	2.097245	-1.365534	2902.545741
HLA B*0702	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-1.884513	0.517364	-1.367148	76.650064
HLA A*6901	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.568633	2.200990	-1.367643	3703.674145
HLA B*0702	1:74-82	9	PPAAADARL	1.380529	0.144471	-2.893128	1.525000	-1.368127	781.857556
HLA A*0211	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.189137	0.820012	-1.369125	154.574322
HLA A*3101	1:186-194	9	PVRASMQIR	1.283702	0.503504	-3.160151	1.787206	-1.372946	1445.943447
HLA B*4403	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.516667	2.142457	-1.374210	3285.994714
HLA A*0203	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-2.310568	0.935815	-1.374753	204.441064
HLA A*0219	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.533478	1.157848	-1.375630	341.568547
HLA A*1101	1:167-175	9	ITAESRDAR	0.938361	0.675089	-2.990382	1.613450	-1.376932	978.097660
HLA A*6802	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-2.561935	1.182783	-1.379152	364.699220
HLA B*1517	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-3.665013	2.280423	-1.384591	4623.952281
HLA A*0211	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.065289	1.680196	-1.385093	1162.220418
HLA A*6901	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.122357	1.735451	-1.386906	1325.432122
HLA A*0206	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.563647	2.176570	-1.387077	3661.399877
HLA B*0702	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.592626	2.200990	-1.391636	3914.044064
HLA A*0211	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.064934	0.667908	-1.397026	116.127259
HLA A*2402	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.499751	2.097245	-1.402505	3160.461968
HLA A*0206	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-3.317675	1.914964	-1.402711	2078.140369
HLA A*0216	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.669266	2.264943	-1.404322	4669.451957

HLA B*2705	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.328931	2.924422	-1.404509	21327.051392
HLA A*2301	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-3.895277	2.489747	-1.405530	7857.365772
HLA A*6901	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.331440	2.924422	-1.407018	21450.630672
HLA A*2403	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.331550	2.924422	-1.407129	21456.085506
HLA A*3101	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.953812	2.544837	-1.408976	8991.083687
HLA A*0202	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.534889	2.123557	-1.411332	3426.805586
HLA A*2402	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.886147	2.472711	-1.413436	7693.905928
HLA B*3801	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.339327	2.924422	-1.414906	21843.754485
HLA A*3101	1:173-181	9	DARVQLSAR	0.897969	0.607997	-2.924761	1.505966	-1.418795	840.932435
HLA A*3002	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.839044	2.419746	-1.419298	6903.103686
HLA B*0802	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.344259	2.924422	-1.419837	22093.211780
HLA B*1501	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.833988	2.412283	-1.421705	6823.203197
HLA A*3201	1:216-224	9	WMITVAFLY	1.184200	1.360637	-3.968285	2.544837	-1.423448	9295.759254
HLA A*3301	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.897589	2.472711	-1.424878	7899.304659
HLA A*0202	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.513457	2.087371	-1.426086	3261.801019
HLA B*1501	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.691548	2.264943	-1.426605	4915.281863
HLA A*6801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-3.211953	1.784676	-1.427276	1629.118789
HLA A*0212	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.782215	2.354914	-1.427301	6056.407009
HLA A*0203	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.900634	2.472711	-1.427923	7954.883001
HLA B*3501	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.573994	2.142457	-1.431537	3749.680762
HLA B*4001	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.355976	2.924422	-1.431554	22697.380452
HLA B*1502	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.845040	2.412283	-1.432757	6999.069118
HLA A*2603	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.634851	2.200990	-1.433861	4313.707118
HLA A*0219	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.014032	1.580071	-1.433961	1032.837829
HLA B*0801	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.358983	2.924422	-1.434561	22855.097489
HLA A*0202	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-3.296436	1.861077	-1.435359	1978.953248
HLA B*1503	1:77-85	9	AADARLNRF	1.242908	1.175831	-3.859264	2.418739	-1.440525	7232.094038
HLA A*0201	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.369523	2.924422	-1.445101	23416.547721
HLA B*3901	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.532606	2.087371	-1.445234	3408.833324
HLA B*1801	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.800217	2.352228	-1.447989	6312.724082
HLA B*4801	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.372777	2.924422	-1.448355	23592.659759
HLA A*6802	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.805198	2.356627	-1.448570	6385.541264
HLA A*6802	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-2.492691	1.042623	-1.450067	310.950180
HLA A*3001	1:188-196	9	RASMQIRRI	1.055395	0.378608	-2.888086	1.434003	-1.454082	772.832973
HLA A*6802	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.379177	2.924422	-1.454755	23942.908273
HLA A*3002	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-3.735662	2.280423	-1.455240	5440.794935
HLA B*3501	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.812091	2.354914	-1.457177	6487.705159
HLA A*0203	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.881392	2.419746	-1.461646	7610.120163
HLA A*6802	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.007629	2.544837	-1.462793	10177.224236
HLA B*7301	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.645062	2.176570	-1.468491	4416.329993
HLA B*3901	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.393840	2.924422	-1.469418	24765.097242
HLA A*3301	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-3.255738	1.784676	-1.471061	1801.929333
HLA A*6801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-3.962693	2.489747	-1.472946	9176.838596
HLA B*1502	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-2.617030	1.141236	-1.475794	414.028519
HLA A*3201	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.058536	1.580071	-1.478465	1144.289943
HLA A*0216	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.403628	2.924422	-1.479206	25329.580204
HLA A*2301	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.832179	2.352228	-1.479952	6794.839479
HLA A*2301	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.024823	2.544837	-1.479986	10588.218008
HLA B*0803	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.406081	2.924422	-1.481659	25473.044511
HLA B*0702	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.406212	2.924422	-1.481791	25480.762836
HLA A*0212	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.406219	2.924422	-1.481798	25481.176383
HLA B*1501	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-3.763156	2.280423	-1.482733	5796.369080
HLA B*1509	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.407502	2.924422	-1.483081	25556.553939
HLA A*0219	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.407874	2.924422	-1.483452	25578.408061
HLA A*3002	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.563511	2.077613	-1.485898	3660.251207
HLA A*0202	1:285-293	9	VYNLITDLI	1.083750	0.286878	-2.862213	1.370628	-1.491586	728.137024

HLA A*2501	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.418237	2.924422	-1.493815	26196.127159
HLA B*3901	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-2.933666	1.439287	-1.494379	858.352452
HLA B*1501	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.594299	2.097245	-1.497053	3929.149413
HLA A*0201	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.764932	2.264943	-1.499989	5820.124056
HLA A*0202	1:275-283	9	MTALATIGA	1.189575	-0.192124	-2.498687	0.997451	-1.501236	315.272941
HLA B*2705	1:183-191	9	SRGPVRASM	1.037490	0.231097	-2.769864	1.268587	-1.501277	588.659635
HLA A*0203	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.426991	2.924422	-1.502570	26729.526837
HLA B*3501	1:74-82	9	PPAAADARL	1.380529	0.144471	-3.029398	1.525000	-1.504397	1070.034469
HLA B*5701	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.858005	2.352228	-1.505777	7211.153506
HLA B*0801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.861458	2.354914	-1.506544	7268.729104
HLA A*2402	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.431460	2.924422	-1.507038	27005.983096
HLA B*1503	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.923071	2.412283	-1.510788	8376.669451
HLA B*0702	1:185-193	9	GPVRASMQI	1.134441	0.112255	-2.758540	1.246696	-1.511844	573.508342
HLA A*2601	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.867323	2.352228	-1.515095	7367.545017
HLA B*1517	1:210-218	9	VALFFVWMI	1.152802	0.312235	-2.982615	1.465037	-1.517578	960.759799
HLA A*2602	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.325151	1.806898	-1.518252	2114.223715
HLA A*2603	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.872186	2.352228	-1.519959	7450.513948
HLA A*0219	1:214-222	9	FVWMITVAF	1.324701	1.148010	-3.993678	2.472711	-1.520967	9855.487275
HLA B*5301	1:276-284	9	TALATIGAF	1.215453	1.136775	-3.877778	2.352228	-1.525550	7547.063540
HLA A*3201	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.791293	2.264943	-1.526350	6184.341501
HLA B*1501	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.099098	1.571013	-1.528084	1256.312237
HLA A*0212	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.003029	2.472711	-1.530318	10069.990291
HLA A*3201	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.456285	2.924422	-1.531863	28594.641103
HLA A*2603	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.674778	2.142457	-1.532320	4729.092439
HLA A*0202	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.457544	2.924422	-1.533122	28677.677333
HLA A*3002	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.005985	2.472711	-1.533274	10138.756760
HLA A*0219	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.078584	2.544837	-1.533747	11983.503044
HLA A*3301	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.458855	2.924422	-1.534433	28764.377954
HLA A*6901	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-2.729693	1.195068	-1.534625	536.652012
HLA B*4801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-3.320898	1.784644	-1.536254	2093.622477
HLA A*0211	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.465528	2.924422	-1.541106	29209.728750
HLA A*8001	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.015458	2.472711	-1.542747	10362.339753
HLA B*1501	1:85-93	9	FISGASAPV	0.612670	0.205652	-2.363436	0.818322	-1.545115	230.906546
HLA A*0219	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-2.986341	1.439287	-1.547054	969.038665
HLA B*3501	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-3.903961	2.356627	-1.547333	8016.054611
HLA A*0202	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.012406	1.465037	-1.547370	1028.978481
HLA A*0250	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.020974	2.472711	-1.548264	10494.806082
HLA A*2603	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.551637	2.003318	-1.548319	3561.529905
HLA B*4801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.671949	2.123557	-1.548392	4698.389565
HLA A*6802	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.815094	2.264943	-1.550150	6532.715522
HLA A*0206	1:209-217	9	SVALFFVWM	1.067963	0.243135	-2.864798	1.311098	-1.553699	732.482997
HLA B*4403	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.480014	2.924422	-1.555593	30200.521927
HLA B*0702	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-2.241202	0.685107	-1.556095	174.261696
HLA A*2403	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.699006	2.142457	-1.556548	5000.410893
HLA A*6901	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.714600	1.157848	-1.556752	518.322033
HLA A*3002	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-3.969173	2.412283	-1.556890	9314.787956
HLA A*0211	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.634635	2.077613	-1.557022	4311.560678
HLA A*0212	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.824910	2.264943	-1.559966	6682.052675
HLA A*0203	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.381753	0.820012	-1.561741	240.853427
HLA A*0202	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-2.597450	1.032607	-1.564843	395.776177
HLA B*5801	1:77-85	9	AADARLNRF	1.242908	1.175831	-3.987034	2.418739	-1.568295	9705.854085
HLA A*0250	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.493975	2.924422	-1.569553	31187.106864
HLA B*5701	1:206-214	9	LLLSVALFF	1.278155	1.141591	-3.992564	2.419746	-1.572819	9830.247348
HLA B*5701	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.282743	1.709743	-1.573000	1917.532510
HLA A*6901	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.118464	2.544837	-1.573627	13136.024476
HLA A*0216	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.049704	2.472711	-1.576993	11212.537819

HLA A*3001	1:275-283	9	MTALATIGA	1.189575	-0.192124	-2.575068	0.997451	-1.577617	375.896650
HLA A*2902	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.492204	1.914535	-1.577669	3106.018389
HLA A*0101	1:77-85	9	AADARLNRF	1.242908	1.175831	-3.996582	2.418739	-1.577843	9921.608019
HLA A*0203	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.845275	2.264943	-1.580332	7002.856562
HLA A*2301	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.506559	2.924422	-1.582137	32103.983985
HLA A*2403	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.585629	2.003318	-1.582311	3851.491505
HLA A*3201	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.292268	1.709743	-1.582525	1960.051795
HLA A*0203	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.321650	1.735451	-1.586199	2097.250021
HLA A*3201	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.051657	1.465037	-1.586620	1126.307015
HLA A*2603	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.511718	2.924422	-1.587297	32487.657588
HLA A*2402	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.158319	1.571013	-1.587305	1439.854835
HLA B*4601	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.132730	2.544837	-1.587893	13574.693168
HLA A*2402	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.053433	1.465037	-1.588396	1130.922904
HLA A*0219	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.946364	2.354914	-1.591450	8838.207073
HLA A*6802	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.058809	1.465037	-1.593772	1145.008264
HLA A*0211	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.371784	1.777358	-1.594425	2353.875661
HLA A*0202	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-2.990063	1.394704	-1.595358	977.378295
HLA B*5801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-3.954522	2.354914	-1.599608	9005.785205
HLA B*2705	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.073866	2.472711	-1.601155	11854.030072
HLA A*3101	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.336645	1.735451	-1.601193	2170.924004
HLA A*0202	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.091177	2.489747	-1.601430	12336.075825
HLA A*0202	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-2.993446	1.391116	-1.602330	985.022041
HLA A*3201	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.094946	2.489747	-1.605199	12443.587446
HLA B*3501	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.703169	2.097245	-1.605924	5048.576948
HLA A*0250	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.426586	0.820012	-1.606574	267.045769
HLA B*0801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.026608	2.419746	-1.606863	10631.841251
HLA A*2402	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-3.010372	1.401173	-1.609199	1024.169029
HLA B*2705	1:176-184	9	VQLSARRSR	1.028225	0.768884	-3.408163	1.797109	-1.611054	2559.546030
HLA A*2301	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.712402	2.097245	-1.615157	5157.063227
HLA B*1501	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-2.775033	1.157848	-1.617185	595.707576
HLA A*2403	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.164011	2.544837	-1.619175	14588.514293
HLA A*0206	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.432974	1.813629	-1.619345	2710.026301
HLA A*3001	1:76-84	9	AAADARLNR	1.236372	0.673742	-3.534039	1.910114	-1.623925	3420.101166
HLA A*2602	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-3.542901	1.914964	-1.627938	3490.609048
HLA A*0216	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-2.729942	1.101846	-1.628096	536.959843
HLA A*2902	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.363819	1.735451	-1.628367	2311.100142
HLA B*1502	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.632078	2.003318	-1.628760	4286.257547
HLA B*5401	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.772371	2.142457	-1.629913	5920.668033
HLA B*1501	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.388310	1.757178	-1.631132	2445.174150
HLA A*3001	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-2.435631	0.802529	-1.633102	272.666146
HLA B*1517	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.392811	1.757178	-1.635634	2470.651040
HLA A*1101	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-3.284077	1.647521	-1.636556	1923.433799
HLA B*1517	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.813444	2.176570	-1.636874	6507.953003
HLA B*5701	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.102528	1.465037	-1.637491	1266.274433
HLA A*2902	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.129507	2.489747	-1.639760	13474.309803
HLA A*2402	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.131057	2.489747	-1.641311	13522.506180
HLA B*4801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.456172	1.813629	-1.642543	2858.724612
HLA A*0201	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.722745	2.077613	-1.645132	5281.349264
HLA B*0801	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.064905	2.418739	-1.646166	11611.948175
HLA B*7301	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.573500	2.924422	-1.649079	37454.194096
HLA A*3101	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.069534	2.419746	-1.649788	11736.364101
HLA B*1501	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.775350	2.123557	-1.651793	5961.421894
HLA A*3001	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.729455	2.077613	-1.651842	5363.583156
HLA B*4801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.197529	2.544837	-1.652692	15759.005905
HLA B*1501	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.010063	2.356627	-1.653436	10234.424109
HLA A*1101	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.495047	1.841561	-1.653486	3126.416971

HLA A*0201	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.755205	2.097245	-1.657960	5691.219997
HLA A*0219	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-3.925059	2.264943	-1.660116	8415.095375
HLA A*3101	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.016426	2.354914	-1.661512	10385.461864
HLA A*0216	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.439637	1.777358	-1.662278	2751.925327
HLA B*4501	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.586904	2.924422	-1.662483	38628.181978
HLA A*6901	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.787036	2.123557	-1.663479	6124.014307
HLA A*3101	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-2.793693	1.126836	-1.666857	621.860159
HLA A*2902	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.766727	2.097245	-1.669482	5844.229313
HLA B*0803	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.144341	2.472711	-1.671630	13942.516810
HLA A*3201	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.026251	2.352228	-1.674024	10623.102248
HLA A*0203	1:275-283	9	MTALATIGA	1.189575	-0.192124	-2.672220	0.997451	-1.674768	470.131835
HLA A*3001	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.094866	2.419746	-1.675120	12441.298830
HLA B*0803	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.227391	2.544837	-1.682554	16880.712472
HLA B*0801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.780039	2.097245	-1.682794	6026.142959
HLA A*0203	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.512170	1.827925	-1.684245	3252.145340
HLA A*2601	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.442644	1.757178	-1.685466	2771.047600
HLA B*4002	1:278-286	9	LATIGAFVY	1.578633	1.345789	-4.610167	2.924422	-1.685745	40753.650786
HLA A*0202	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.492744	1.806898	-1.685846	3109.885534
HLA B*1501	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.690017	2.003318	-1.686699	4897.974987
HLA A*6801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-3.529025	1.841575	-1.687450	3380.844154
HLA B*1501	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.106670	2.418739	-1.687931	12784.081606
HLA A*0203	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-2.721705	1.032607	-1.689098	526.871265
HLA A*0216	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.510401	0.820012	-1.690389	323.892752
HLA B*1503	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.271630	1.580071	-1.691559	1869.087666
HLA A*2403	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.789315	2.097245	-1.692070	6156.235105
HLA B*3901	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-2.887385	1.195068	-1.692318	771.588056
HLA A*3101	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.835342	2.142457	-1.692884	6844.498116
HLA B*3501	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.113272	2.418739	-1.694533	12979.907189
HLA B*1801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.114348	2.419746	-1.694602	13012.107760
HLA A*2402	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.430469	1.735451	-1.695018	2694.442715
HLA A*2902	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.049023	2.352228	-1.696795	11194.960621
HLA B*0801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.187548	2.489747	-1.697802	15400.974649
HLA A*6901	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.087566	1.388176	-1.699391	1223.393920
HLA A*0211	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.878685	2.176570	-1.702115	7562.839914
HLA A*3301	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.248111	2.544837	-1.703274	17705.609472
HLA A*2501	1:170-178	9	ESRDARVQL	1.767877	0.433113	-3.905272	2.200990	-1.704282	8040.289381
HLA A*2602	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.124103	2.419746	-1.704357	13307.691148
HLA B*1501	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.482548	1.777358	-1.705189	3037.719292
HLA A*6901	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.126504	2.419746	-1.706758	13381.471906
HLA A*0203	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.197153	2.489747	-1.707406	15745.371091
HLA A*3001	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.253221	2.544837	-1.708384	17915.173182
HLA A*2602	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.806382	2.097245	-1.709136	6402.975737
HLA B*0802	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.182736	2.472711	-1.710026	15231.282061
HLA B*4801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.066677	2.356627	-1.710049	11659.410702
HLA A*0206	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-2.653739	0.943496	-1.710243	450.545453
HLA B*1517	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.421179	1.709743	-1.711436	2637.418760
HLA A*3001	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.491485	1.777358	-1.714127	3100.880859
HLA A*0216	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.385155	0.667908	-1.717247	242.747566
HLA A*2403	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.136066	2.418739	-1.717328	13679.376113
HLA B*1503	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.796284	2.077613	-1.718671	6255.813164
HLA B*3501	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.477816	1.757178	-1.720638	3004.801425
HLA B*4002	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.808318	2.087371	-1.720946	6431.582306
HLA A*2403	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.635696	1.914535	-1.721161	4322.116508
HLA A*0202	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-2.764197	1.042623	-1.721574	581.028317
HLA B*5701	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.194926	2.472711	-1.722215	15664.826492
HLA A*3002	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.076812	2.352228	-1.724585	11934.721219

HLA A*0216	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.084545	1.359429	-1.725116	1214.912163
HLA B*0702	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.077705	2.352228	-1.725477	11959.281352
HLA A*2402	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.568022	1.841561	-1.726461	3698.468326
HLA B*1503	1:28-36	9	HRAATGPGR	0.868468	0.768121	-3.364336	1.636589	-1.727747	2313.852394
HLA A*3001	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.083071	2.354914	-1.728157	12107.969182
HLA B*0802	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.273175	2.544837	-1.728339	18757.510010
HLA B*3501	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.141780	2.412283	-1.729497	13860.542796
HLA B*1509	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.202853	2.472711	-1.730142	15953.381518
HLA A*3001	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-2.674395	0.943496	-1.730899	472.492896
HLA B*7301	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-3.096419	1.365049	-1.731370	1248.588059
HLA A*2301	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.199134	1.465037	-1.734097	1581.735866
HLA B*5801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.857657	2.123557	-1.734100	7205.382108
HLA A*6901	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-2.916947	1.182783	-1.734164	825.936610
HLA A*3002	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.089269	2.354914	-1.734355	12282.004392
HLA A*0301	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.207289	2.472711	-1.734578	16117.162288
HLA A*1101	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.156098	2.419746	-1.736352	14325.111128
HLA B*5801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.833955	2.097245	-1.736710	6822.686438
HLA A*0201	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-2.684376	0.943496	-1.740880	483.477085
HLA A*2403	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.582664	1.841561	-1.741103	3825.285852
HLA A*0203	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.819741	2.077613	-1.742128	6602.995904
HLA A*2301	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.314541	1.571013	-1.743527	2063.196849
HLA B*4501	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-2.626550	0.882547	-1.744003	423.204591
HLA A*6901	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.103886	1.359429	-1.744457	1270.240163
HLA A*2501	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.234298	2.489747	-1.744552	17151.347989
HLA B*1801	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.887209	2.142457	-1.744752	7712.742625
HLA A*0212	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.660653	1.914535	-1.746117	4577.756620
HLA A*0201	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.426461	1.680196	-1.746265	2669.689377
HLA A*0250	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.236093	2.489747	-1.746347	17222.383874
HLA A*3001	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.220563	2.472711	-1.747852	16617.403645
HLA A*0203	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.143254	1.394704	-1.748549	1390.765187
HLA A*0101	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.222245	2.472711	-1.749535	16681.895660
HLA A*2601	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.170449	2.419746	-1.750703	14806.371918
HLA B*0702	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.927893	2.176570	-1.751322	8470.177696
HLA B*1503	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.108643	2.356627	-1.752016	12842.308597
HLA A*2501	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.104813	2.352228	-1.752586	12729.561427
HLA A*2403	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.109263	2.356627	-1.752636	12860.663224
HLA B*4402	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.300159	2.544837	-1.755322	19959.930379
HLA A*0101	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.175204	2.419746	-1.755458	14969.386846
HLA A*3001	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.880527	2.123557	-1.756970	7594.984709
HLA B*1801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.248484	2.489747	-1.758738	17720.845900
HLA A*0301	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.113887	2.354914	-1.758973	12998.317837
HLA B*2705	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.181190	2.419746	-1.761445	15177.159546
HLA B*4403	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.306322	2.544837	-1.761485	20245.183676
HLA B*0801	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.114235	2.352228	-1.762007	13008.729284
HLA B*0803	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.116974	2.354914	-1.762060	13091.046801
HLA B*4001	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.235489	2.472711	-1.762779	17198.455516
HLA B*4002	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.237393	2.472711	-1.764682	17273.984688
HLA B*3901	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.255418	2.489747	-1.765671	18006.022116
HLA B*5801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.255773	2.489747	-1.766026	18020.737124
HLA A*0206	1:103-111	9	PQPDPDASL	1.546426	0.238218	-3.550683	1.784644	-1.766038	3553.715892
HLA B*4001	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.313109	2.544837	-1.768273	20564.084675
HLA A*2403	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.233700	1.465037	-1.768663	1712.772123
HLA B*0801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.125343	2.356627	-1.768716	13345.757864
HLA B*4601	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.259102	2.489747	-1.769355	18159.411570
HLA B*4002	1:78-86	9	ADARLNRFI	1.288538	0.234644	-3.293268	1.523182	-1.770087	1964.574165
HLA B*0801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.893736	2.123557	-1.770179	7829.530288

HLA A*3101	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.685806	1.914535	-1.771271	4850.720887
HLA A*6801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-3.408074	1.636589	-1.771485	2559.019903
HLA B*5301	1:74-82	9	PPAAADARL	1.380529	0.144471	-3.297662	1.525000	-1.772662	1984.549636
HLA B*5101	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.247871	2.472711	-1.775160	17695.842058
HLA B*4403	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.188206	2.412283	-1.775923	15424.321245
HLA B*4001	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.955612	2.176570	-1.779042	9028.419821
HLA B*3901	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.622845	1.841561	-1.781284	4196.089924
HLA B*0702	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.200701	2.418739	-1.781962	15874.520756
HLA A*2603	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-3.697079	1.914964	-1.782116	4978.277654
HLA B*4601	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.202284	2.419746	-1.782538	15932.509126
HLA A*6801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.202580	2.419746	-1.782834	15943.373160
HLA A*3301	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.520097	1.735451	-1.784646	3312.051710
HLA A*3001	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-2.810896	1.025655	-1.785240	646.987161
HLA A*6901	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.142988	2.356627	-1.786360	13899.138208
HLA A*3002	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.563826	1.777358	-1.786467	3662.905577
HLA A*3301	1:76-84	9	AAADARLNR	1.236372	0.673742	-3.696971	1.910114	-1.786857	4977.038939
HLA B*0801	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.358044	1.571013	-1.787030	2280.571696
HLA A*0206	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.277573	2.489747	-1.787827	18948.438338
HLA B*5701	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.207011	2.418739	-1.788273	16106.876908
HLA A*0203	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-2.832906	1.042623	-1.790282	680.621460
HLA A*0201	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.370877	1.580071	-1.790806	2348.965386
HLA A*8001	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.204709	2.412283	-1.792426	16021.709184
HLA A*3001	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.145037	2.352228	-1.792809	13964.861227
HLA A*0250	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.461400	0.667908	-1.793492	289.334599
HLA A*1101	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.149482	2.354914	-1.794568	14108.532729
HLA A*6901	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.284678	2.489747	-1.794932	19260.974907
HLA B*0702	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.341174	2.544837	-1.796337	21936.835664
HLA A*6802	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.884056	2.087371	-1.796684	7656.950338
HLA A*2902	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.574459	1.777358	-1.797101	3753.699414
HLA B*0803	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.216964	2.419746	-1.797218	16480.248584
HLA B*0802	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.218204	2.418739	-1.799466	16527.390416
HLA A*3001	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.291132	2.489747	-1.801386	19549.349042
HLA A*3002	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.222288	2.418739	-1.803549	16683.520189
HLA B*1503	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.271249	1.465037	-1.806212	1867.450312
HLA B*1501	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.896564	2.087371	-1.809193	7880.694433
HLA A*6901	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.380293	1.571013	-1.809280	2400.453807
HLA B*0801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.356136	2.544837	-1.811299	22705.731729
HLA A*3001	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.908721	2.097245	-1.811475	8104.397312
HLA B*4601	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.569887	1.757178	-1.812710	3714.389088
HLA A*0212	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.280140	1.465037	-1.815103	1906.072898
HLA A*2403	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.305032	2.489747	-1.815285	20185.144094
HLA A*1101	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.289739	2.472711	-1.817028	19486.733964
HLA A*3101	1:215-223	9	VWMITVAFL	1.544881	0.532732	-3.895404	2.077613	-1.817791	7859.661511
HLA A*0250	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.915280	2.097245	-1.818035	8227.738610
HLA A*2603	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-3.995130	2.176570	-1.818560	9888.492381
HLA A*2902	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.961937	2.142457	-1.819479	9160.866603
HLA A*6802	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-2.961188	1.141236	-1.819951	914.508022
HLA A*6901	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.500352	1.680196	-1.820156	3164.842024
HLA B*5801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.177831	2.356627	-1.821203	15060.199884
HLA A*3002	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.629780	1.806898	-1.822882	4263.639396
HLA B*5301	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.535688	1.709743	-1.825945	3433.114524
HLA B*0702	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.654676	1.827925	-1.826750	4515.185626
HLA A*0202	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-2.978090	1.150365	-1.827725	950.801185
HLA A*6802	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.563191	1.735451	-1.827740	3657.559186
HLA B*4601	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.109226	2.280423	-1.828803	12859.550075
HLA B*3901	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.094335	2.264943	-1.829391	12426.096958

HLA B*3501	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.094617	2.264943	-1.829673	12434.166434
HLA A*0202	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-2.765128	0.935291	-1.829837	582.274398
HLA A*2902	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.248921	2.418739	-1.830183	17738.686288
HLA B*3901	1:280-288	9	TIGAFVVYNL	1.455838	0.459126	-3.745286	1.914964	-1.830322	5562.702681
HLA B*4402	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.322002	2.489747	-1.832256	20989.504398
HLA B*2705	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.322409	2.489747	-1.832662	21009.157898
HLA A*3001	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.251696	2.418739	-1.832958	17852.382979
HLA A*6802	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.682590	0.848433	-1.834157	481.493343
HLA A*3201	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.253313	2.418739	-1.834574	17918.953426
HLA B*0801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.035654	2.200990	-1.834664	10855.604205
HLA B*1501	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.749360	1.914535	-1.834824	5615.130514
HLA A*2501	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.380154	2.544837	-1.835318	23996.852799
HLA B*4402	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.187713	2.352228	-1.835485	15406.807983
HLA B*1503	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.677193	1.841561	-1.835632	4755.465922
HLA B*4001	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.326252	2.489747	-1.836506	21195.926388
HLA A*2402	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.193351	2.356627	-1.836724	15608.150136
HLA B*1501	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.038107	2.200990	-1.837117	10917.089304
HLA A*3101	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-3.912814	2.075252	-1.837561	8181.134389
HLA A*6802	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.327352	2.489747	-1.837605	21249.658822
HLA B*2705	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.193422	2.354914	-1.838508	15610.683493
HLA A*0202	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.658776	0.820012	-1.838764	455.801665
HLA A*6801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.279059	1.439287	-1.839772	1901.335440
HLA B*1517	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.197712	2.356627	-1.841085	15765.657158
HLA B*1517	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.756643	1.914535	-1.842108	5710.094012
HLA A*8001	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.197397	2.354914	-1.842483	15754.232378
HLA A*2902	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.123290	2.280423	-1.842867	13282.804822
HLA A*2501	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.846826	2.003318	-1.843508	7027.905141
HLA A*2403	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.123934	2.280423	-1.843511	13302.508652
HLA A*0301	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.334184	2.489747	-1.844438	21586.600985
HLA A*6802	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.967998	2.123557	-1.844441	9289.626017
HLA A*3101	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.334844	2.489747	-1.845098	21619.441434
HLA B*0702	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.336191	2.489747	-1.846444	21686.562796
HLA B*1509	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.337053	2.489747	-1.847306	21729.662705
HLA A*0202	1:208-216	9	LSVALFFVW	1.685197	0.457260	-3.990793	2.142457	-1.848336	9790.230884
HLA A*0206	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-2.998963	1.150365	-1.848598	997.614009
HLA A*3002	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.338785	2.489747	-1.849038	21816.473736
HLA B*0801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.115170	2.264943	-1.850226	13036.769022
HLA B*3901	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.207303	2.356627	-1.850675	16117.685449
HLA A*0211	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.340523	2.489747	-1.850777	21903.987072
HLA B*3801	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.395661	2.544837	-1.850824	24869.146947
HLA B*4402	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.324335	2.472711	-1.851624	21102.563841
HLA A*0216	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.341562	2.489747	-1.851815	21956.425921
HLA A*6901	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.116866	2.264943	-1.851923	13087.789435
HLA B*4403	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.272052	2.419746	-1.852306	18709.067120
HLA A*0206	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.939997	2.087371	-1.852626	8709.577104
HLA A*2403	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-3.606032	1.752306	-1.853726	4036.750168
HLA B*3901	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.273767	2.419746	-1.854021	18783.099413
HLA A*2601	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.209243	2.354914	-1.854329	16189.869589
HLA A*0202	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.206635	2.352228	-1.854408	16092.941113
HLA B*5101	1:185-193	9	GPVRASMQI	1.134441	0.112255	-3.101663	1.246696	-1.854967	1263.755992
HLA A*0203	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-3.979666	2.123557	-1.856109	9542.579197
HLA A*2902	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.860791	2.003318	-1.857473	7257.569941
HLA B*1517	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.957628	2.097245	-1.860382	9070.424311
HLA B*0803	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.350403	2.489747	-1.860656	22407.982616
HLA A*0250	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.326946	1.465037	-1.861909	2122.980214
HLA A*0206	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.004453	2.142457	-1.861996	10103.057850

HLA A*6801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.960865	2.097245	-1.863620	9138.295427
HLA B*1509	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.408752	2.544837	-1.863916	25630.213208
HLA B*3901	1:85-93	9	FISGASAPV	0.612670	0.205652	-2.683102	0.818322	-1.864781	482.061530
HLA A*6802	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.218176	2.352228	-1.865948	16526.317515
HLA A*0101	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.356582	2.489747	-1.866835	22729.082471
HLA A*2402	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.285646	2.418739	-1.866908	19303.953078
HLA A*0216	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.964685	2.097245	-1.867440	9219.034848
HLA B*4601	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.286469	2.418739	-1.867730	19340.538990
HLA B*7301	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.340880	2.472711	-1.868169	21922.006197
HLA B*5101	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.415427	2.544837	-1.870591	26027.179414
HLA B*1503	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-3.236641	1.365049	-1.871592	1724.412416
HLA A*6802	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.386651	1.513906	-1.872745	2435.852909
HLA A*0203	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.451309	1.577736	-1.873573	2826.889851
HLA B*5701	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.363456	2.489747	-1.873710	23091.731420
HLA A*3001	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.489013	1.615041	-1.873972	3083.283239
HLA B*1801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.229369	2.354914	-1.874455	16957.781653
HLA A*3001	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.232440	2.356627	-1.875812	17078.110369
HLA A*6802	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-3.701703	1.824948	-1.876755	5031.562844
HLA B*1503	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.141808	2.264943	-1.876865	13861.442634
HLA A*0201	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.001055	2.123557	-1.877498	10024.332984
HLA A*3001	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.290712	2.412283	-1.878429	19530.427199
HLA A*2402	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.055042	2.176570	-1.878472	11351.204577
HLA B*3801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.368287	2.489747	-1.878540	23350.008271
HLA A*0219	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.368567	2.489747	-1.878820	23365.045304
HLA A*0216	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.494488	1.615041	-1.879447	3122.394132
HLA A*3002	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.460909	1.580071	-1.880838	2890.073464
HLA A*2603	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.293364	2.412283	-1.881081	19650.079488
HLA B*4002	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.057683	2.176570	-1.881113	11420.438304
HLA B*1503	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.978688	2.097245	-1.881443	9521.127637
HLA B*5301	1:185-193	9	GPVRASMQI	1.134441	0.112255	-3.128241	1.246696	-1.881545	1343.509068
HLA B*4402	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.300685	2.418739	-1.881947	19984.132787
HLA B*4801	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.371976	2.489747	-1.882229	23549.176796
HLA A*3301	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.083480	2.200990	-1.882491	12119.372030
HLA A*0202	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.302262	2.418739	-1.883523	20056.807728
HLA B*4402	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.304343	2.419746	-1.884598	20153.174017
HLA A*3001	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.061249	2.176570	-1.884679	11514.611517
HLA B*5701	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.240405	2.354914	-1.885491	17394.204436
HLA B*3801	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.358842	2.472711	-1.886131	22847.680080
HLA A*2603	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.305913	2.419746	-1.886167	20226.135432
HLA B*0802	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.306122	2.419746	-1.886376	20235.876259
HLA A*3001	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.622069	1.735451	-1.886618	4188.605481
HLA A*8001	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.376449	2.489747	-1.886703	23792.996989
HLA A*2402	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.239331	2.352228	-1.887103	17351.253524
HLA B*5301	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.715866	1.827925	-1.887940	5198.350959
HLA B*0802	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.378355	2.489747	-1.888608	23897.616198
HLA B*5301	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.308380	2.419746	-1.888634	20341.354574
HLA A*0212	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.379158	2.489747	-1.889411	23941.872068
HLA A*2301	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.804902	1.914535	-1.890366	6381.190068
HLA B*5701	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-2.992281	1.101846	-1.890434	982.382469
HLA B*0702	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.468188	1.577736	-1.890452	2938.918800
HLA A*3101	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.243522	2.352228	-1.891295	17519.525384
HLA A*3001	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.157729	2.264943	-1.892785	14378.995319
HLA B*1503	1:183-191	9	SRGPVRASM	1.037490	0.231097	-3.161801	1.268587	-1.893214	1451.445208
HLA A*0202	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-2.978292	1.084809	-1.893483	951.243649
HLA A*0201	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.205572	1.311098	-1.894473	1605.356724
HLA B*1503	1:187-195	9	VRASMQIRR	1.136874	0.704701	-3.736565	1.841575	-1.894990	5452.109377

HLA A*3101	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-3.618071	1.722434	-1.895636	4150.215358
HLA A*6802	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.316704	2.419746	-1.896958	20735.002665
HLA A*0201	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.389103	2.489747	-1.899357	24496.468300
HLA A*6901	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.254652	2.354914	-1.899738	17974.294252
HLA A*2601	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-3.997329	2.097245	-1.900084	9938.691295
HLA A*6901	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-2.942791	1.042623	-1.900168	876.578979
HLA A*6901	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.679322	1.777358	-1.901963	4778.831384
HLA A*0211	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.025814	2.123557	-1.902257	10612.418240
HLA B*1502	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.321182	2.418739	-1.902444	20949.912525
HLA A*0203	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.744351	1.841561	-1.902790	5550.738312
HLA A*2602	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.322021	2.418739	-1.903282	20990.412825
HLA A*2902	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.260429	2.356627	-1.903802	18215.002314
HLA B*4601	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.316497	2.412283	-1.904214	20725.133696
HLA B*3901	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.259250	2.354914	-1.904336	18165.601770
HLA B*1501	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.732312	1.827925	-1.904387	5398.983397
HLA B*1509	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.261064	2.356627	-1.904436	18241.627863
HLA B*3901	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.662067	1.757178	-1.904889	4592.689547
HLA B*4601	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.992673	2.087371	-1.905301	9832.693957
HLA A*0211	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.003978	2.097245	-1.906733	10092.023283
HLA B*1801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.187276	2.280423	-1.906853	15391.312843
HLA A*2602	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-3.994289	2.087371	-1.906918	9869.359473
HLA A*6801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.821757	1.914535	-1.907221	6633.716172
HLA A*3101	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.326457	2.418739	-1.907718	21205.904818
HLA A*0201	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.685679	1.777358	-1.908321	4849.304033
HLA B*1503	1:83-91	9	NRFISGASA	0.946143	-0.055864	-2.800633	0.890279	-1.910354	631.877822
HLA A*0201	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.271789	1.359429	-1.912360	1869.775379
HLA A*0219	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.669957	1.757178	-1.912779	4676.884664
HLA B*5701	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.269893	2.356627	-1.913266	18616.282313
HLA B*1801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.325999	2.412283	-1.913716	21183.545903
HLA A*0211	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.762539	0.848433	-1.914106	578.813381
HLA B*5401	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.460208	2.544837	-1.915372	28854.150318
HLA B*1502	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.093155	2.176570	-1.916585	12392.396389
HLA A*2501	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.272278	2.354914	-1.917364	18718.786185
HLA B*4001	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.339010	2.419746	-1.919264	21827.807050
HLA B*3901	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.338155	2.418739	-1.919416	21784.866034
HLA A*3101	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.017516	2.097245	-1.920271	10411.564079
HLA A*0219	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.022340	1.101846	-1.920494	1052.785549
HLA A*3301	1:186-194	9	PVRASMQIR	1.283702	0.503504	-3.710589	1.787206	-1.923383	5135.570005
HLA A*0211	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.275804	2.352228	-1.923577	18871.406106
HLA A*2601	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.342889	2.418739	-1.924150	22023.640326
HLA A*0203	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.592920	0.667908	-1.925012	391.669580
HLA B*4403	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.414945	2.489747	-1.925199	25998.330562
HLA B*5401	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.661442	1.735451	-1.925991	4586.085280
HLA A*6802	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.281006	2.354914	-1.926092	19098.797340
HLA A*0203	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.013512	2.087371	-1.926141	10316.026615
HLA A*2501	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.683964	1.757178	-1.926787	4830.190835
HLA B*4402	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.282395	2.354914	-1.927481	19159.958586
HLA B*2705	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.346585	2.418739	-1.927846	22211.855821
HLA A*2603	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.283252	2.354914	-1.928338	19197.829401
HLA A*8001	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.026270	2.097245	-1.929025	10623.562016
HLA B*5801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.341334	2.412283	-1.929051	21944.907106
HLA A*2902	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.770848	1.841561	-1.929288	5899.948829
HLA A*0206	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.757780	1.827925	-1.929855	5725.064836
HLA A*6901	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.349938	2.418739	-1.931199	22383.992976
HLA A*0301	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.351979	2.418739	-1.933241	22489.472207
HLA B*5301	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.352184	2.418739	-1.933445	22500.059601

HLA A*2301	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.290832	2.356627	-1.934204	19535.816472
HLA B*3801	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.353570	2.418739	-1.934831	22571.990805
HLA A*3101	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.291722	2.356627	-1.935095	19575.912786
HLA A*3101	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.201415	2.264943	-1.936471	15900.649572
HLA B*4801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.356258	2.419746	-1.936512	22712.120073
HLA A*0201	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.605095	0.667908	-1.937187	402.805019
HLA A*8001	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.356573	2.418739	-1.937834	22728.590629
HLA A*0301	1:76-84	9	AAADARLNR	1.236372	0.673742	-3.848832	1.910114	-1.938718	7060.449501
HLA B*0702	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.358577	2.419746	-1.938831	22833.717163
HLA B*0803	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.358022	2.418739	-1.939283	22804.583186
HLA A*0219	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-2.573978	0.634444	-1.939535	374.954262
HLA A*0101	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.352322	2.412283	-1.940039	22507.242394
HLA B*4801	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.292464	2.352228	-1.940237	19609.406919
HLA B*4001	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.360043	2.418739	-1.941304	22910.928810
HLA A*0212	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.380956	1.439287	-1.941669	2404.118707
HLA A*0301	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.355085	2.412283	-1.942802	22650.890600
HLA A*0211	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.126422	1.182783	-1.943639	1337.895215
HLA B*5101	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.364751	2.419746	-1.945005	23160.667075
HLA A*0201	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.365738	2.418739	-1.946999	23213.351495
HLA B*5101	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.437893	2.489747	-1.948146	27408.980470
HLA B*5801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.213313	2.264943	-1.948369	16342.280426
HLA B*0702	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.046128	2.097245	-1.948883	11120.594494
HLA A*2603	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.306348	2.356627	-1.949720	20246.388478
HLA B*3901	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.027605	2.077613	-1.949992	10656.256485
HLA A*2501	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.370399	2.418739	-1.951661	23463.847414
HLA A*2501	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.310163	2.356627	-1.953536	20425.050043
HLA B*4402	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.096008	2.142457	-1.953550	12474.052608
HLA A*0203	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.372568	2.418739	-1.953829	23581.303096
HLA A*0216	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.031594	2.077613	-1.953981	10754.595750
HLA A*0250	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.131316	2.176570	-1.954745	13530.555653
HLA B*4801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.042552	2.087371	-1.955181	11029.405107
HLA A*1101	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.053426	2.097245	-1.956180	11309.033880
HLA A*0206	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-2.892249	0.935815	-1.956434	780.277224
HLA A*1101	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.376043	2.418739	-1.957304	23770.739283
HLA B*0802	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.310377	2.352228	-1.958149	20435.107769
HLA A*1101	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.448449	2.489747	-1.958703	28083.363254
HLA A*2603	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.800414	1.841561	-1.958853	6315.593429
HLA B*3501	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.873930	1.914535	-1.959394	7480.481444
HLA B*4801	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.378200	2.418739	-1.959461	23889.085013
HLA B*3501	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-3.963271	2.003318	-1.959953	9189.059564
HLA A*0250	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.767517	1.806898	-1.960618	5854.862163
HLA B*1503	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.696769	1.735451	-1.961318	4974.723908
HLA A*6801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.163612	2.200990	-1.962622	14575.103679
HLA B*7301	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.038229	2.075252	-1.962977	10920.160868
HLA B*4001	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.375284	2.412283	-1.963001	23729.238700
HLA B*1503	1:252-260	9	AELVSSGTI	1.198347	0.266272	-3.428242	1.464619	-1.963623	2680.659438
HLA A*3301	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.383378	2.419746	-1.963632	24175.628920
HLA A*6801	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.315941	2.352228	-1.963713	20698.578124
HLA A*2602	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.106312	2.142457	-1.963855	12773.573536
HLA A*6901	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.377624	2.412283	-1.965341	23857.442849
HLA A*0101	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.321713	2.354914	-1.966799	20975.542284
HLA A*1101	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-3.689890	1.722434	-1.967455	4896.544331
HLA A*8001	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.319845	2.352228	-1.967618	20885.523093
HLA A*3001	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.250738	2.280423	-1.970315	17813.022034
HLA A*3101	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-3.676836	1.706509	-1.970327	4751.557094
HLA A*2601	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.382769	2.412283	-1.970486	24141.778685

HLA A*2603	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.390196	2.418739	-1.971457	24558.169152
HLA B*5101	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.324345	2.352228	-1.972117	21103.020496
HLA A*0212	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.391331	2.418739	-1.972592	24622.422980
HLA A*0212	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.332364	1.359429	-1.972935	2149.630716
HLA B*0801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.060559	2.087371	-1.973187	11496.311998
HLA A*6801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.328442	2.354914	-1.973528	21303.066476
HLA B*2705	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.326126	2.352228	-1.973898	21189.735241
HLA A*0206	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.254715	2.280423	-1.974293	17976.919895
HLA A*6802	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.545307	1.571013	-1.974294	3509.999727
HLA A*3301	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-3.623747	1.647521	-1.976226	4204.815931
HLA A*2601	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.177962	2.200990	-1.976973	15064.763120
HLA B*4601	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.333296	2.354914	-1.978382	21542.502826
HLA A*3002	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.367319	1.388176	-1.979144	2329.804592
HLA A*0301	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.335805	2.356627	-1.979178	21667.330537
HLA B*0702	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.336005	2.356627	-1.979378	21677.296346
HLA A*2501	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.076925	2.097245	-1.979680	11937.820766
HLA B*4801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.335206	2.354914	-1.980292	21637.460592
HLA A*0212	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.058110	2.077613	-1.980497	11431.688403
HLA B*1502	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.737702	1.757178	-1.980524	5466.403812
HLA B*4801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.393199	2.412283	-1.980916	24728.548673
HLA B*1509	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.157522	2.176570	-1.980952	14372.151536
HLA B*4601	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.337899	2.356627	-1.981271	21772.023766
HLA A*0101	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.334158	2.352228	-1.981931	21585.316431
HLA A*0203	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.447869	1.465037	-1.982832	2804.589093
HLA A*0201	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.395948	2.412283	-1.983664	24885.566162
HLA B*4001	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.335998	2.352228	-1.983770	21676.944534
HLA B*5101	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.126231	2.142457	-1.983774	13373.077036
HLA A*0203	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.336097	2.352228	-1.983869	21681.870428
HLA A*0211	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.402749	2.418739	-1.984011	25278.382713
HLA A*0301	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.336524	2.352228	-1.984297	21703.228907
HLA B*4002	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.108991	2.123557	-1.985434	12852.595083
HLA A*1101	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.338688	2.352228	-1.986461	21811.635260
HLA B*5301	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.476387	2.489747	-1.986640	29949.311553
HLA B*3901	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.187793	2.200990	-1.986803	15409.642113
HLA A*3101	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.110988	2.123557	-1.987431	12911.832625
HLA A*3101	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.400172	2.412283	-1.987889	25128.808673
HLA B*5101	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.406673	2.418739	-1.987934	25507.795393
HLA A*0250	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.816757	1.827925	-1.988832	6557.785119
HLA B*0801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.746634	1.757178	-1.989457	5580.003258
HLA A*3201	1:285-293	9	VYNLITDLI	1.083750	0.286878	-3.360097	1.370628	-1.989470	2291.380326
HLA A*3201	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.725630	1.735451	-1.990179	5316.551885
HLA A*0211	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.803990	1.813629	-1.990361	6367.809762
HLA B*1501	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.168113	2.176570	-1.991543	14726.965385
HLA B*1517	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.403872	2.412283	-1.991589	25343.835357
HLA A*2301	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.410430	2.418739	-1.991691	25729.405479
HLA B*1517	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-3.639568	1.647521	-1.992047	4360.822612
HLA B*1509	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.257201	2.264943	-1.992258	18080.108749
HLA A*3101	1:295-303	9	GIEVTLADR	0.657184	0.545986	-3.196512	1.203170	-1.993342	1572.215006
HLA B*4001	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.350248	2.356627	-1.993620	22399.983214
HLA A*8001	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.274566	2.280423	-1.994143	18817.680132
HLA B*2705	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-2.892987	0.898490	-1.994496	781.603812
HLA A*2602	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.751714	1.757178	-1.994536	5645.651149
HLA A*1101	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.407357	2.412283	-1.995074	25547.983373
HLA A*2501	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.414967	2.419746	-1.995221	25999.596426
HLA B*0802	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.352066	2.356627	-1.995439	22493.974283
HLA B*7301	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.541331	2.544837	-1.996495	34780.138581

HLA A*3001	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-2.651511	0.654994	-1.996517	448.240712
HLA B*3501	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-3.821663	1.824948	-1.996715	6632.280820
HLA B*0801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.278520	2.280423	-1.998098	18989.794511
HLA B*3501	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.199319	2.200990	-1.998330	15824.103901
HLA B*5301	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.913443	1.914535	-1.998908	8193.004412
HLA A*0216	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.418841	2.418739	-2.000102	26232.574053
HLA A*0212	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.412711	2.412283	-2.000428	25864.917718
HLA B*0802	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.357284	2.354914	-2.002370	22765.877806
HLA A*0101	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.359101	2.356627	-2.002473	22861.280503
HLA A*3001	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-2.938924	0.935815	-2.003109	868.807977
HLA B*5701	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.415939	2.412283	-2.003656	26057.892827
HLA B*2705	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.081638	2.077613	-2.004025	12068.078349
HLA A*0219	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-2.947894	0.943496	-2.004398	886.939779
HLA A*2601	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.361866	2.356627	-2.005238	23007.312756
HLA A*0219	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.425224	2.418739	-2.006486	26621.005692
HLA A*6801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.763692	1.757178	-2.006514	5803.523050
HLA B*4403	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.480017	2.472711	-2.007306	30200.685309
HLA B*1517	1:118-126	9	PAEAYASEL	1.515766	0.191360	-3.714559	1.707126	-2.007434	5182.738340
HLA A*3301	1:176-184	9	VQLSARRSR	1.028225	0.768884	-3.804718	1.797109	-2.007610	6378.497957
HLA B*5301	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.764843	1.757178	-2.007665	5818.927702
HLA A*6802	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.426653	2.418739	-2.007914	26708.712002
HLA B*0702	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.363092	2.354914	-2.008178	23072.376361
HLA B*1801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.132124	2.123557	-2.008567	13555.759487
HLA A*8001	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.365228	2.356627	-2.008601	23186.116265
HLA A*2402	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.624099	1.615041	-2.009058	4208.229454
HLA B*0702	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.012455	2.003318	-2.009137	10290.943307
HLA B*0802	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.210240	2.200990	-2.009250	16227.048423
HLA A*0212	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.362343	2.352228	-2.010115	23032.593438
HLA A*1101	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.924758	1.914535	-2.010223	8409.270227
HLA A*0219	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.746320	1.735451	-2.010868	5575.959639
HLA B*1509	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.430718	2.418739	-2.011979	26959.855133
HLA A*3301	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.090049	2.077613	-2.012436	12304.083715
HLA B*3501	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-2.697881	0.685107	-2.012773	498.747504
HLA A*0219	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.090585	2.077613	-2.012972	12319.269609
HLA B*0702	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.293712	2.280423	-2.013289	19665.818891
HLA A*2403	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.426594	2.412283	-2.014311	26705.099967
HLA B*1517	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.585652	1.571013	-2.014639	3851.699872
HLA B*2705	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.371637	2.356627	-2.015010	23530.838565
HLA A*0301	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.280306	2.264943	-2.015362	19068.032078
HLA A*6802	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.093367	2.077613	-2.015754	12398.431592
HLA A*2402	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.282933	2.264943	-2.017989	19183.709890
HLA B*0702	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.282956	2.264943	-2.018013	19184.747736
HLA B*1509	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.370477	2.352228	-2.018249	23468.036703
HLA A*0250	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.699908	1.680196	-2.019712	5010.809531
HLA B*0802	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.432715	2.412283	-2.020432	27084.112961
HLA B*5701	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.221606	2.200990	-2.020617	16657.366471
HLA B*0702	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.144355	2.123557	-2.020798	13942.969382
HLA B*1509	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.433128	2.412283	-2.020845	27109.913123
HLA A*0212	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.862666	1.841561	-2.021105	7288.969263
HLA A*2403	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.778451	1.757178	-2.021274	6004.145090
HLA A*6801	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.163739	2.142457	-2.021281	14579.362185
HLA B*1501	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-2.866259	0.844974	-2.021285	734.951918
HLA A*0201	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.375129	2.352228	-2.022901	23720.767624
HLA A*3101	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.125012	1.101846	-2.023166	1333.559537
HLA A*0219	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.435522	2.412283	-2.023239	27259.774006

HLA A*0203	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.435781	2.412283	-2.023498	27276.000793
HLA B*0702	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.110903	2.087371	-2.023532	12909.318213
HLA B*3801	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.444030	2.419746	-2.024284	27799.036018
HLA A*2403	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.148246	2.123557	-2.024689	14068.442531
HLA A*0101	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.289798	2.264943	-2.024854	19489.369669
HLA B*1503	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-3.940862	1.914964	-2.025898	8726.933743
HLA B*1509	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.446774	2.419746	-2.027028	27975.247323
HLA B*5301	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.384198	2.356627	-2.027570	24221.316865
HLA A*2403	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.292627	2.264943	-2.027683	19616.728131
HLA B*4402	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.737951	1.709743	-2.028208	5469.539410
HLA A*0250	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.424722	1.394704	-2.030018	2659.023126
HLA A*0219	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.382370	2.352228	-2.030142	24119.586152
HLA A*6802	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.443774	2.412283	-2.031491	27782.648373
HLA B*0801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-3.946477	1.914964	-2.031513	8840.502430
HLA B*1509	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.128966	2.097245	-2.031721	13457.554489
HLA B*0801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.444610	2.412283	-2.032327	27836.207104
HLA B*0702	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.444728	2.412283	-2.032444	27843.737662
HLA A*2602	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.445989	2.412283	-2.033706	27924.744406
HLA B*0801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-2.911346	0.877206	-2.034139	815.352758
HLA B*5801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.315160	2.280423	-2.034738	20661.435121
HLA B*1517	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.123440	2.087371	-2.036069	13287.404563
HLA A*0250	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.877816	1.841561	-2.036255	7547.716828
HLA B*1503	1:103-111	9	PQPDPDASL	1.546426	0.238218	-3.821644	1.784644	-2.037000	6631.993787
HLA A*0203	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.215225	2.176570	-2.038655	16414.404794
HLA A*3301	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.528771	2.489747	-2.039024	33788.659420
HLA B*0803	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.391761	2.352228	-2.039533	24646.811489
HLA A*8001	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.185349	2.142457	-2.042892	15323.186520
HLA A*0211	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.657970	1.615041	-2.042928	4549.561997
HLA B*3901	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.455737	2.412283	-2.043454	28558.620146
HLA B*5101	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.400658	2.356627	-2.044031	25156.964858
HLA A*0202	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.557990	1.513906	-2.044084	3614.012104
HLA B*1503	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.851215	1.806898	-2.044316	7099.286924
HLA B*1503	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-3.905784	1.861077	-2.044707	8049.777337
HLA A*3002	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.401469	2.356627	-2.044841	25203.961957
HLA B*4601	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.168503	2.123557	-2.044946	14740.196753
HLA B*1503	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.872947	1.827925	-2.045022	7463.584691
HLA A*2601	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.823505	1.777358	-2.046147	6660.470404
HLA A*0216	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.459579	2.412283	-2.047296	28812.346432
HLA A*2902	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.312266	2.264943	-2.047322	20524.184892
HLA B*4001	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.402587	2.354914	-2.047673	25268.948500
HLA A*2902	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.125301	2.077613	-2.047688	13344.458344
HLA A*2301	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.225859	2.176570	-2.049289	16821.274905
HLA A*0219	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-3.081913	1.032607	-2.049307	1207.573174
HLA B*3501	1:73-81	9	NPPAAADAR	0.833991	0.526025	-3.409878	1.360016	-2.049862	2569.674224
HLA B*4402	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.331259	2.280423	-2.050837	21441.697027
HLA B*1509	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.405853	2.354914	-2.050939	25459.680802
HLA A*3002	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.193868	2.142457	-2.051411	15626.737635
HLA B*3801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.409025	2.356627	-2.052397	25646.302423
HLA B*1801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.410463	2.356627	-2.053835	25731.354258
HLA B*2705	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.466136	2.412283	-2.053853	29250.684977
HLA B*4801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.254974	2.200990	-2.053984	17987.620925
HLA B*4801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.319176	2.264943	-2.054232	20853.346221
HLA B*5701	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.334941	2.280423	-2.054518	21624.237276
HLA A*2602	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.231942	2.176570	-2.055372	17058.534772
HLA B*3501	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.232571	2.176570	-2.056001	17083.285031
HLA B*5301	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.469369	2.412283	-2.057086	29469.239747

HLA A*6802	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-2.851161	0.793787	-2.057374	709.841092
HLA B*3801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.470999	2.412283	-2.058716	29580.088878
HLA A*3001	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.636956	1.577736	-2.059220	4334.667541
HLA B*0801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.137335	2.077613	-2.059722	13719.396652
HLA B*0803	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.472383	2.412283	-2.060100	29674.493932
HLA A*6801	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.416731	2.356627	-2.060104	26105.443154
HLA A*6901	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.340824	2.280423	-2.060401	21919.160087
HLA A*2601	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.341273	2.280423	-2.060850	21941.820616
HLA B*4001	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.184804	2.123557	-2.061247	15303.966540
HLA B*1801	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.481069	2.418739	-2.062331	30273.969377
HLA B*2705	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.343613	2.280423	-2.063190	22060.367715
HLA A*3101	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.343646	2.280423	-2.063223	22062.038597
HLA A*2601	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.904985	1.841561	-2.063424	8034.984489
HLA B*5401	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-2.754799	0.691047	-2.063752	568.590185
HLA A*2602	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.221830	1.157848	-2.063982	1666.594666
HLA B*5401	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.554103	2.489747	-2.064356	35818.146513
HLA B*4001	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.345062	2.280423	-2.064640	22134.126083
HLA A*0216	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.878539	1.813629	-2.064910	7560.303664
HLA A*2601	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.330463	2.264943	-2.065519	21402.410011
HLA B*4002	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.611085	2.544837	-2.066249	40839.946862
HLA B*4402	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.425448	2.356627	-2.068820	26634.690793
HLA B*5101	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.481201	2.412283	-2.068918	30283.142381
HLA A*2301	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-3.471110	1.401173	-2.069938	2958.764139
HLA B*4801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.351526	2.280423	-2.071103	22466.003010
HLA A*0101	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.351610	2.280423	-2.071188	22470.378825
HLA A*0250	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.222107	1.150365	-2.071742	1667.658905
HLA B*3801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.248454	2.176570	-2.071884	17719.599663
HLA A*3301	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.427814	2.354914	-2.072900	26780.186105
HLA B*5701	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.337948	2.264943	-2.073005	21774.497376
HLA B*0803	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.431655	2.356627	-2.075028	27018.112066
HLA B*1801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.340239	2.264943	-2.075295	21889.653489
HLA A*0202	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.692502	1.615041	-2.077461	4926.089727
HLA A*0250	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.926063	0.848433	-2.077630	843.456557
HLA B*3801	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.430158	2.352228	-2.077931	26925.165211
HLA B*1503	1:174-182	9	ARVQLSARR	0.965880	0.769663	-3.813877	1.735543	-2.078334	6514.434373
HLA A*6801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-3.439886	1.360016	-2.079870	2753.503866
HLA A*1101	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.360745	2.280423	-2.080323	22948.018529
HLA B*4801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-3.837644	1.757178	-2.080466	6880.881895
HLA B*1801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.281833	2.200990	-2.080844	19135.201467
HLA A*3201	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.084260	2.003318	-2.080942	12141.158991
HLA A*0301	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.361699	2.280423	-2.081276	22998.477295
HLA A*0301	1:217-225	9	MITVAFLYL	1.461926	0.452609	-3.995957	1.914535	-2.081422	9907.340790
HLA B*4601	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.346998	2.264943	-2.082055	22233.014700
HLA A*1101	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-3.788836	1.706509	-2.082326	6149.444725
HLA B*5401	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.278495	1.195068	-2.083427	1898.868398
HLA B*4001	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.284460	2.200990	-2.083470	19251.286769
HLA A*0216	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.436488	2.352228	-2.084260	27320.452577
HLA A*2501	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.496668	2.412283	-2.084384	31381.059204
HLA B*1509	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.286682	2.200990	-2.085693	19350.062680
HLA A*3101	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.864034	1.777358	-2.086675	7311.955154
HLA B*4501	1:216-224	9	WMITVAFLY	1.184200	1.360637	-4.631667	2.544837	-2.086830	42821.971388
HLA A*3101	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.001826	1.914964	-2.086863	10042.136389
HLA B*5701	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.928475	1.841561	-2.086914	8481.549357
HLA B*1503	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-3.209547	1.120296	-2.089251	1620.118869
HLA B*1517	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.354491	2.264943	-2.089547	22619.909488

HLA B*4403	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.508396	2.418739	-2.089658	32240.088654
HLA A*0201	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-2.910171	0.820012	-2.090159	813.150254
HLA A*3001	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.232766	2.142457	-2.090309	17090.957504
HLA B*4501	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.502635	2.412283	-2.090352	31815.246331
HLA A*3301	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.447606	2.356627	-2.090978	28028.874074
HLA B*4002	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-3.253454	1.162375	-2.091079	1792.478915
HLA B*4001	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.356281	2.264943	-2.091338	22713.348807
HLA B*4002	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.503885	2.412283	-2.091602	31906.944444
HLA A*0250	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.510476	2.418739	-2.091737	32394.816302
HLA A*0301	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.189160	2.097245	-2.091915	15458.236688
HLA B*1502	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.448701	2.356627	-2.092073	28099.624243
HLA A*3101	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-3.663716	1.570424	-2.093292	4610.164560
HLA B*5301	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.190847	2.097245	-2.093601	15518.397889
HLA A*0216	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.217481	2.123557	-2.093924	16499.874651
HLA B*5401	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.942612	0.848433	-2.094180	876.218646
HLA A*0212	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.191575	2.097245	-2.094330	15544.445096
HLA A*2602	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.451478	2.356627	-2.094850	28279.882696
HLA A*0216	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.272585	2.176570	-2.096015	18732.056806
HLA A*2301	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.361939	2.264943	-2.096995	23011.171557
HLA A*3201	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.300262	2.200990	-2.099273	19964.682109
HLA A*0212	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.277491	2.176570	-2.100921	18944.850865
HLA A*0211	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.514542	2.412283	-2.102259	32699.603009
HLA A*2402	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.225831	2.123557	-2.102274	16820.182926
HLA A*8001	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.368012	2.264943	-2.103069	23335.233395
HLA A*0219	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.463818	1.359429	-2.104388	2909.494529
HLA B*3901	1:183-191	9	SRGPVRASM	1.037490	0.231097	-3.373184	1.268587	-2.104597	2361.477497
HLA A*1101	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.461658	2.356627	-2.105030	28950.623552
HLA B*4403	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.457575	2.352228	-2.105347	28679.694263
HLA A*0212	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.229296	2.123557	-2.105739	16954.937960
HLA A*3101	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.306914	2.200990	-2.105924	20272.802596
HLA B*5101	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.462043	2.354914	-2.107129	28976.320575
HLA A*3001	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.127428	1.020231	-2.107197	1340.996611
HLA A*3001	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.678288	1.571013	-2.107275	4767.469615
HLA A*6901	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.185156	2.077613	-2.107543	15316.390494
HLA A*0206	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.724079	1.615041	-2.109038	5297.602843
HLA A*3002	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.112496	2.003318	-2.109178	12956.755308
HLA A*3001	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-3.236655	1.126836	-2.109819	1724.468390
HLA A*0219	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.207782	2.097245	-2.110537	16135.483026
HLA A*3201	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.287286	2.176570	-2.110716	19376.984586
HLA B*4601	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.253494	2.142457	-2.111036	17926.419326
HLA B*4002	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.600806	2.489747	-2.111060	39884.685461
HLA B*2705	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.376677	2.264943	-2.111734	23805.485860
HLA A*0206	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.524542	2.412283	-2.112259	33461.229010
HLA A*0250	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.190884	2.077613	-2.113272	15519.741192
HLA A*0101	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.255923	2.142457	-2.113466	18026.977576
HLA B*0801	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.256242	2.142457	-2.113785	18040.245714
HLA B*1503	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.023958	1.910114	-2.113844	10567.159538
HLA A*0201	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.394846	2.280423	-2.114423	24822.505592
HLA B*3801	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.469966	2.354914	-2.115052	29509.761613
HLA A*2402	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.554343	1.439287	-2.115056	3583.795353
HLA A*3201	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.527425	2.412283	-2.115142	33684.081260
HLA A*2902	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.218066	1.101846	-2.116220	1652.213295
HLA B*0802	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.397688	2.280423	-2.117266	24985.525846
HLA A*6901	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.259952	2.142457	-2.117495	18195.009442
HLA A*0206	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-3.160170	1.042623	-2.117547	1446.006027

HLA B*0702	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-2.399971	0.281226	-2.118745	251.171718
HLA B*4501	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.609600	2.489747	-2.119854	40700.551480
HLA B*4403	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.475562	2.354914	-2.120648	29892.495632
HLA B*1801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.218059	2.097245	-2.120813	16521.847842
HLA B*4402	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.298244	2.176570	-2.121674	19872.119580
HLA B*3501	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.209361	2.087371	-2.121989	16194.249451
HLA A*6802	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.298620	2.176570	-2.122050	19889.327980
HLA B*7301	1:253-261	9	ELVSSGTIF	1.369450	1.120297	-4.611938	2.489747	-2.122191	40920.226732
HLA B*1801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.209859	2.087371	-2.122488	16212.833234
HLA A*6802	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.403062	2.280423	-2.122639	25296.577440
HLA B*4801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.220051	2.097245	-2.122806	16597.817365
HLA B*5401	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.543714	2.419746	-2.123968	34971.453731
HLA B*1509	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-3.985286	1.861077	-2.124209	9666.866948
HLA B*0802	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.389510	2.264943	-2.124566	24519.405541
HLA A*2301	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.537130	2.412283	-2.124847	34445.336274
HLA B*1509	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.405519	2.280423	-2.125097	25440.130077
HLA B*5301	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.480830	2.354914	-2.125916	30257.268546
HLA A*0216	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.806307	1.680196	-2.126111	6401.867372
HLA B*3801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.327859	2.200990	-2.126870	21274.504328
HLA B*2705	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.250594	2.123557	-2.127037	17807.144649
HLA A*0203	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.407603	2.280423	-2.127181	25562.499730
HLA B*4002	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.547116	2.419746	-2.127370	35246.479097
HLA B*5401	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.546225	2.418739	-2.127487	35174.285586
HLA B*4601	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.329452	2.200990	-2.128463	21352.680469
HLA A*0206	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.935594	1.806898	-2.128696	8621.724343
HLA A*3002	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.700119	1.571013	-2.129106	5013.249838
HLA B*4601	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.306406	2.176570	-2.129836	20249.126931
HLA A*0301	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.971772	1.841561	-2.130211	9370.688544
HLA A*0211	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.525102	1.394704	-2.130397	3350.437429
HLA B*4002	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.550478	2.418739	-2.131739	35520.400445
HLA A*0206	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-2.980364	0.848433	-2.131931	955.793375
HLA B*5801	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.333202	2.200990	-2.132213	21537.841629
HLA B*5101	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.397613	2.264943	-2.132670	24981.200815
HLA A*2501	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.414205	2.280423	-2.133783	25954.064143
HLA B*0803	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.334868	2.200990	-2.133878	21620.611054
HLA B*4001	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.221837	2.087371	-2.134465	16666.200034
HLA A*2603	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.446159	1.311098	-2.135060	2793.565223
HLA A*0250	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.912419	1.777358	-2.135060	8173.702250
HLA A*0202	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.416059	2.280423	-2.135636	26065.083305
HLA B*1517	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-3.949630	1.813629	-2.136001	8904.918657
HLA A*2301	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.051823	1.914964	-2.136860	11267.385576
HLA A*0212	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.417389	2.280423	-2.136966	26145.016834
HLA A*6802	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.279951	2.142457	-2.137494	19052.461891
HLA A*1101	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-3.924072	1.784676	-2.139396	8395.996693
HLA A*2602	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.849175	1.709743	-2.139433	7066.028357
HLA B*5801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.316540	2.176570	-2.139969	20727.151967
HLA A*0206	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.340988	2.200990	-2.139999	21927.462275
HLA B*4002	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.494497	2.352228	-2.142269	31224.584937
HLA B*4801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.852051	1.709743	-2.142308	7112.972761
HLA B*5401	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.496057	2.352228	-2.143829	31336.950539
HLA A*3301	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.496249	2.352228	-2.144022	31350.855036
HLA A*0203	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.824666	1.680196	-2.144470	6678.294219
HLA A*2501	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.409593	2.264943	-2.144650	25679.900375
HLA B*0801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.321248	2.176570	-2.144678	20953.086193
HLA A*0202	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.382586	1.236873	-2.145714	2413.161847
HLA B*4501	1:214-222	9	FVWMITVAF	1.324701	1.148010	-4.620126	2.472711	-2.147415	41699.033271

HLA B*5401	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.559951	2.412283	-2.147668	36303.707276
HLA B*3901	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.290270	2.142457	-2.147813	19510.573697
HLA A*3101	1:200-208	9	STLKVSLLL	1.428092	0.413469	-3.990422	1.841561	-2.148861	9781.866138
HLA B*4402	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.413867	2.264943	-2.148924	25933.853177
HLA B*1517	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-3.871491	1.722434	-2.149056	7438.592785
HLA B*1502	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.859165	1.709743	-2.149423	7230.450982
HLA A*3002	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.414584	2.264943	-2.149640	25976.679777
HLA B*3901	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.431014	2.280423	-2.150591	26978.238476
HLA B*5701	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.274745	2.123557	-2.151188	18825.418641
HLA A*0203	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.462530	1.311098	-2.151432	2900.881759
HLA A*0203	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.352729	2.200990	-2.151739	22528.317026
HLA A*2402	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.543319	1.391116	-2.152204	3493.971984
HLA A*3001	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-3.723393	1.570424	-2.152969	5289.240892
HLA A*8001	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.067753	1.914535	-2.153217	11688.335383
HLA B*1501	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.068641	1.914964	-2.153677	11712.261761
HLA A*6901	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.330387	2.176570	-2.153817	21398.705223
HLA A*3002	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.331005	2.176570	-2.154435	21429.172988
HLA A*0219	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.278137	2.123557	-2.154580	18973.056465
HLA B*4002	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.509667	2.354914	-2.154753	32334.585551
HLA A*0301	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.356784	2.200990	-2.155794	22739.659648
HLA B*3901	1:118-126	9	PAEAYASEL	1.515766	0.191360	-3.863117	1.707126	-2.155992	7296.544239
HLA B*1509	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.244354	2.087371	-2.156983	17553.109189
HLA B*5401	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.514947	2.356627	-2.158319	32730.044181
HLA A*2403	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.335502	2.176570	-2.158932	21652.214709
HLA A*6801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-3.987071	1.827925	-2.159146	9706.694242
HLA B*1501	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.237094	2.077613	-2.159481	17262.120571
HLA A*0101	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.361032	2.200990	-2.160042	22963.169369
HLA A*2603	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.425401	2.264943	-2.160457	26631.809135
HLA A*6802	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.840915	1.680196	-2.160719	6932.894424
HLA A*2403	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.076634	1.914964	-2.161670	11929.815248
HLA A*0206	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-3.246730	1.084809	-2.161921	1764.939527
HLA A*1101	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.427085	2.264943	-2.162142	26735.311614
HLA A*3301	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.076873	1.914535	-2.162338	11936.400040
HLA A*2501	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.250768	2.087371	-2.163397	17814.274842
HLA A*6801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-3.818698	1.653369	-2.165329	6587.154601
HLA A*3101	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.342029	2.176570	-2.165459	21980.076233
HLA A*3101	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.253209	2.087371	-2.165838	17914.688593
HLA A*3001	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.253524	2.087371	-2.166153	17927.680110
HLA B*2705	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.367439	2.200990	-2.166449	23304.450906
HLA A*0202	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.579059	2.412283	-2.166776	37936.681487
HLA B*5701	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.343688	2.176570	-2.167118	22064.187059
HLA A*3201	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.783446	1.615041	-2.168405	6073.599960
HLA B*0803	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.449051	2.280423	-2.168628	28122.283736
HLA A*2603	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-3.946087	1.777358	-2.168729	8832.566854
HLA A*6901	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.258251	2.087371	-2.170880	18123.883344
HLA A*0216	1:121-129	9	AYASELPDL	1.278221	0.528677	-3.978143	1.806898	-2.171245	9509.185221
HLA A*0203	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-3.996601	1.824948	-2.171653	9922.037426
HLA B*1501	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.013263	1.841561	-2.171703	10310.112603
HLA B*5101	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.637022	1.465037	-2.171985	4335.324192
HLA A*0203	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.322557	1.150365	-2.172192	2101.634110
HLA B*1503	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-3.314141	1.141236	-2.172905	2061.300238
HLA B*4801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.036801	1.861077	-2.175724	10884.301145
HLA B*7301	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.595506	2.419746	-2.175760	39400.862908
HLA A*0206	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.179090	2.003318	-2.175772	15103.933331
HLA A*2603	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.299630	2.123557	-2.176073	19935.649433

HLA A*0101	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.273929	2.097245	-2.176684	18790.112121
HLA A*2402	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.589073	2.412283	-2.176790	38821.547515
HLA A*0216	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.457231	2.280423	-2.176809	28657.050728
HLA B*0801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.252483	2.075252	-2.177231	17884.766418
HLA B*3801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.457950	2.280423	-2.177528	28704.529645
HLA A*2403	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.379027	2.200990	-2.178037	23934.619885
HLA A*3201	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.280736	1.101846	-2.178890	1908.693856
HLA B*1503	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.567369	1.388176	-2.179193	3692.910198
HLA A*0201	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.355882	2.176570	-2.179312	22692.469371
HLA A*0250	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.591883	2.412283	-2.179600	39073.546121
HLA B*0803	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.276967	2.097245	-2.179722	18922.009477
HLA B*3901	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.095096	1.914535	-2.180561	12447.896571
HLA A*0219	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.008621	1.827925	-2.180695	10200.485108
HLA B*4402	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.381740	2.200990	-2.180751	24084.641702
HLA A*0219	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.383676	2.200990	-2.182687	24192.244636
HLA B*0803	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.448482	2.264943	-2.183539	28085.490324
HLA A*2402	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.464132	2.280423	-2.183709	29116.014696
HLA B*1501	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.764246	1.580071	-2.184175	5810.937336
HLA B*1503	1:164-172	9	GRSITAESR	1.007055	0.640575	-3.832602	1.647630	-2.184972	6801.459381
HLA B*0803	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.362054	2.176570	-2.185484	23017.272272
HLA B*5801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.263155	2.077613	-2.185542	18329.669459
HLA B*4001	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.328538	2.142457	-2.186081	21307.792137
HLA A*0301	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-3.909064	1.722434	-2.186629	8110.801049
HLA B*4501	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.605479	2.418739	-2.186741	40316.172722
HLA A*1101	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.329288	2.142457	-2.186831	21344.595906
HLA A*0219	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.467292	2.280423	-2.186869	29328.644220
HLA A*3002	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.028582	1.841561	-2.187021	10680.265544
HLA A*3002	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.310680	2.123557	-2.187123	20449.373912
HLA A*3201	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.274909	2.087371	-2.187538	18832.549031
HLA A*0250	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.388540	2.200990	-2.187550	24464.683376
HLA B*0801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.898500	1.709743	-2.188758	7915.903005
HLA B*1502	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.453780	2.264943	-2.188837	28430.212054
HLA A*0101	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.312489	2.123557	-2.188932	20534.735792
HLA A*0250	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.542043	2.352228	-2.189816	34837.196812
HLA A*6801	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.602253	2.412283	-2.189970	40017.822560
HLA A*0301	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.367230	2.176570	-2.190660	23293.232977
HLA A*0301	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-3.975366	1.784676	-2.190690	9448.572840
HLA A*2301	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.471540	2.280423	-2.191117	29616.917537
HLA B*0802	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.316027	2.123557	-2.192470	20702.721688
HLA A*0301	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.336726	2.142457	-2.194269	21713.328693
HLA A*6801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-3.397468	1.203170	-2.194298	2497.284884
HLA A*6801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-3.929965	1.735543	-2.194422	8510.689912
HLA A*2501	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.337008	2.142457	-2.194551	21727.429274
HLA A*0201	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.395856	2.200990	-2.194866	24880.316218
HLA A*0202	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-3.130759	0.935815	-2.194944	1351.323253
HLA A*8001	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.318866	2.123557	-2.195309	20838.460050
HLA A*6801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.192809	0.997451	-2.195358	1558.867306
HLA A*0219	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.372363	2.176570	-2.195793	23570.206923
HLA B*3501	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.507288	1.311098	-2.196189	3215.790267
HLA B*4601	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.199695	2.003318	-2.196377	15837.806894
HLA A*6801	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.615270	2.418739	-2.196531	41235.342023
HLA A*2602	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.111162	1.914535	-2.196626	12917.002677
HLA B*5101	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.320318	2.123557	-2.196760	20908.246107
HLA A*3301	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.615613	2.418739	-2.196874	41267.924369
HLA A*2601	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.200569	2.003318	-2.197251	

									15869.712238
HLA A*0301	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.320999	2.123557	-2.197442	20941.074126
HLA A*2301	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.907269	1.709743	-2.197526	8077.347032
HLA A*2601	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.374471	2.176570	-2.197901	23684.863342
HLA A*2902	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.322801	2.123557	-2.199244	21028.147230
HLA B*1517	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.276937	2.077613	-2.199324	18920.678767
HLA B*4801	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.341888	2.142457	-2.199431	21972.942805
HLA A*6801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-3.839575	1.640132	-2.199443	6911.548823
HLA A*0216	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.400508	2.200990	-2.199518	25148.256197
HLA B*3801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.465976	2.264943	-2.201033	29239.926435
HLA A*0101	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.378113	2.176570	-2.201542	23884.303712
HLA B*4801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.043365	1.841561	-2.201804	11050.069521
HLA B*5101	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.482254	2.280423	-2.201831	30356.626536
HLA A*8001	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.116946	1.914964	-2.201983	13090.196975
HLA B*4001	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.299922	2.097245	-2.202676	19949.027276
HLA A*3201	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.483266	2.280423	-2.202843	30427.490519
HLA B*3501	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.022269	0.818322	-2.203948	1052.614699
HLA A*2601	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.118840	1.914535	-2.204304	13147.399708
HLA B*5401	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.559516	2.354914	-2.204602	36267.391631
HLA A*2902	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.381726	2.176570	-2.205156	24083.859943
HLA B*1509	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.329192	2.123557	-2.205634	21339.862083
HLA A*0211	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.033596	1.827925	-2.205670	10804.280523
HLA A*2402	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-3.958516	1.752306	-2.206210	9088.991745
HLA B*0801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.048529	1.841561	-2.206968	11182.249508
HLA B*4801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.284951	2.077613	-2.207338	19273.065870
HLA B*0802	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.383921	2.176570	-2.207350	24205.859711
HLA A*0202	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.384484	2.176570	-2.207914	24237.308367
HLA B*2705	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.350828	2.142457	-2.208371	22429.935033
HLA A*0211	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.488825	2.280423	-2.208402	30819.459452
HLA A*0203	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.351173	2.142457	-2.208716	22447.779617
HLA A*0211	1:103-111	9	PQPDPDASL	1.546426	0.238218	-3.993396	1.784644	-2.208752	9849.091300
HLA A*0201	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.351265	2.142457	-2.208808	22452.516277
HLA B*7301	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.621547	2.412283	-2.209264	41835.737088
HLA A*1101	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.124559	1.914964	-2.209595	13321.665148
HLA B*3501	1:118-126	9	PAEAYASEL	1.515766	0.191360	-3.916761	1.707126	-2.209635	8255.828478
HLA B*1503	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-3.108355	0.898490	-2.209864	1283.377913
HLA B*5401	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-2.700385	0.489523	-2.210863	501.632061
HLA A*2301	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.334708	2.123557	-2.211151	21612.658889
HLA A*2402	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.126104	1.914535	-2.211569	13369.170876
HLA A*6901	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.214957	2.003318	-2.211639	16404.284702
HLA B*3501	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-2.493452	0.281226	-2.212226	311.495692
HLA A*3301	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.477179	2.264943	-2.212235	30003.962924
HLA B*4402	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.337495	2.123557	-2.213938	21751.774300
HLA B*5301	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.478955	2.264943	-2.214011	30126.926699
HLA B*1503	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.409930	1.195068	-2.214862	2569.980079
HLA B*0802	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.357336	2.142457	-2.214879	22768.587506
HLA A*2902	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.129939	1.914964	-2.214975	13487.729073
HLA A*3002	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.607827	1.391116	-2.216711	4053.469211
HLA A*6801	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.481706	2.264943	-2.216763	30318.385988
HLA B*7301	1:77-85	9	AADARLNRF	1.242908	1.175831	-4.635600	2.418739	-2.216861	43211.535086
HLA B*5801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.304282	2.087371	-2.216911	20150.339529
HLA B*1509	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.294927	2.077613	-2.217314	19720.899461
HLA B*1801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.221052	2.003318	-2.217734	16636.113018
HLA A*8001	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.394550	2.176570	-2.217979	24805.591195

HLA B*3901	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.043191	1.824948	-2.218243	11045.646712
HLA A*2601	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.360919	2.142457	-2.218462	22957.207190
HLA B*0802	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.134281	1.914535	-2.219745	13623.248607
HLA B*5101	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.421388	2.200990	-2.220398	26386.862213
HLA A*2602	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.485778	2.264943	-2.220834	30603.967722
HLA A*2402	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.224294	2.003318	-2.220976	16760.777136
HLA A*8001	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.422830	2.200990	-2.221841	26474.656444
HLA A*6802	1:168-176	9	TAESRDARV	0.917270	0.090109	-3.229386	1.007379	-2.222007	1695.844126
HLA B*4501	1:206-214	9	LLLSVALFF	1.278155	1.141591	-4.641762	2.419746	-2.222016	43829.083975
HLA B*7301	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.579130	2.356627	-2.222502	37942.838984
HLA A*3101	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.064360	1.841575	-2.222785	11597.383227
HLA A*3001	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.020415	1.797109	-2.223307	10481.302151
HLA A*0212	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.424736	2.200990	-2.223746	26591.067068
HLA A*2301	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.424994	2.200990	-2.224005	26606.895797
HLA B*2705	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.311716	2.087371	-2.224345	20498.219476
HLA B*2705	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.321824	2.097245	-2.224578	20980.876304
HLA A*3001	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.229289	2.003318	-2.225971	16954.662789
HLA A*0219	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.068058	1.841561	-2.226497	11696.558512
HLA B*4001	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.304257	2.077613	-2.226644	20149.140442
HLA A*3301	1:114-122	9	GDGSPAEAY	1.427881	0.984402	-4.639366	2.412283	-2.227083	43587.897336
HLA A*2603	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.508359	2.280423	-2.227936	32237.298129
HLA B*4402	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.316133	2.087371	-2.228762	20707.762276
HLA A*0212	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.371372	2.142457	-2.228915	23516.458149
HLA A*2501	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.406781	2.176570	-2.230211	25514.143923
HLA B*1509	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.305814	2.075252	-2.230562	20221.540266
HLA B*5701	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.328257	2.097245	-2.231011	21293.963890
HLA B*5301	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.511869	2.280423	-2.231446	32498.907832
HLA A*0206	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-2.901370	0.669638	-2.231732	796.837256
HLA A*6801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-3.827941	1.596160	-2.231780	6728.848194
HLA B*5101	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.329429	2.097245	-2.232184	21351.525344
HLA A*1101	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.355797	2.123557	-2.232240	22688.050306
HLA A*2902	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.433344	2.200990	-2.232355	27123.409350
HLA B*4801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.060845	1.827925	-2.232920	11503.902143
HLA A*0301	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-3.880626	1.647521	-2.233104	7596.710602
HLA B*0803	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.310891	2.077613	-2.233279	20459.332932
HLA B*1503	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-3.007439	0.773810	-2.233629	1017.277599
HLA A*3001	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.149740	1.914964	-2.234777	14116.931043
HLA A*3002	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.814177	1.577736	-2.236442	6518.946958
HLA B*5101	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.413075	2.176570	-2.236505	25886.615396
HLA A*3002	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.151944	1.914535	-2.237409	14188.749136
HLA B*0803	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.361466	2.123557	-2.237909	22986.163091
HLA A*0201	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.066005	1.827925	-2.238079	11641.384880
HLA A*0201	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.326941	2.087371	-2.239569	21229.550640
HLA A*1101	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.416200	2.176570	-2.239630	26073.545231
HLA A*3002	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.338594	2.097245	-2.241349	21806.915829
HLA A*6802	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.055502	1.813629	-2.241873	11363.247077
HLA A*2602	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.522439	2.280423	-2.242016	33299.606325
HLA B*1801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.319850	2.077613	-2.242237	20885.749071
HLA B*4501	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.594498	2.352228	-2.242270	39309.525743
HLA A*0211	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.445054	2.200990	-2.244065	27864.683320
HLA B*1801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.421651	2.176570	-2.245081	26402.855057
HLA A*2902	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.002460	1.757178	-2.245283	10056.815355
HLA B*1503	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-3.650837	1.405388	-2.245449	4475.448367

HLA B*5801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.347297	1.101846	-2.245451	2224.831812
HLA A*6802	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.107999	1.861077	-2.246922	12823.286421
HLA B*0702	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.389710	2.142457	-2.247252	24530.683152
HLA B*5801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.075374	1.827925	-2.247449	11895.272462
HLA B*5401	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.251116	2.003318	-2.247798	17828.543795
HLA A*0219	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.391180	2.142457	-2.248723	24613.899363
HLA B*5701	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.682733	1.434003	-2.248730	4816.517687
HLA B*5301	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.372335	2.123557	-2.248778	23568.676826
HLA A*3002	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.350746	1.101846	-2.248900	2242.571144
HLA B*4601	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.347031	2.097245	-2.249786	22234.698658
HLA B*4403	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.530293	2.280423	-2.249871	33907.317083
HLA B*0702	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.164885	1.914535	-2.250350	14617.902930
HLA A*6801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.027727	1.777358	-2.250368	10659.254663
HLA B*1517	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-2.561554	0.310085	-2.251470	364.379736
HLA B*5401	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.518236	2.264943	-2.253292	32978.877579
HLA B*4002	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.533992	2.280423	-2.253569	34197.276273
HLA B*0801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.081751	1.827925	-2.253826	12071.212530
HLA B*4501	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.608745	2.354914	-2.253831	40620.482830
HLA B*4001	1:119-127	9	AEAYASELP	0.543268	-0.008008	-2.789929	0.535260	-2.254669	616.494006
HLA B*1801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.990671	1.735451	-2.255219	9787.477140
HLA B*1503	1:167-175	9	ITAESRDAR	0.938361	0.675089	-3.868723	1.613450	-2.255273	7391.338485
HLA B*4601	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.333649	2.077613	-2.256036	21559.991304
HLA A*2501	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.379755	2.123557	-2.256198	23974.793491
HLA B*7301	1:205-213	9	SLLLSVALF	1.195536	1.159378	-4.611905	2.354914	-2.256991	40917.127615
HLA A*2402	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.172408	1.914964	-2.257445	14873.326943
HLA A*0301	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.333118	2.075252	-2.257865	21533.647413
HLA A*3002	1:212-220	9	LFFVWMITV	1.409538	0.325913	-3.993636	1.735451	-2.258185	9854.527614
HLA A*0202	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.107062	0.848433	-2.258629	1279.564976
HLA A*0101	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.346918	2.087371	-2.259547	22228.925619
HLA B*1801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.969441	1.709743	-2.259698	9320.534412
HLA A*0212	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-3.292446	1.032607	-2.259839	1960.857839
HLA B*4002	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.616717	2.356627	-2.260089	41372.987683
HLA A*0202	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.462086	2.200990	-2.261096	28979.142369
HLA A*2601	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.385354	2.123557	-2.261797	24285.871781
HLA A*1101	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.059102	1.797109	-2.261993	11457.816455
HLA B*1501	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.047326	1.784644	-2.262682	11151.319063
HLA A*1101	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.463707	2.200990	-2.262717	29087.518541
HLA A*0212	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.350389	2.087371	-2.263017	22407.255280
HLA B*7301	1:276-284	9	TALATIGAF	1.215453	1.136775	-4.615418	2.352228	-2.263190	41249.398372
HLA A*2601	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.350703	2.087371	-2.263332	22423.504752
HLA A*2602	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.365788	1.101846	-2.263941	2321.601270
HLA A*2902	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.352202	2.087371	-2.264831	22501.033405
HLA B*1509	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.092911	1.827925	-2.264986	12385.426035
HLA A*0301	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.342856	2.077613	-2.265243	22021.972353
HLA B*3501	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.975117	1.709743	-2.265374	9443.156125
HLA A*2402	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-3.975211	1.709743	-2.265468	9445.199804
HLA B*5401	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.545929	2.280423	-2.265507	35150.317344
HLA A*6801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.053999	1.787206	-2.266793	11323.971808
HLA A*6801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.578017	1.311098	-2.266918	3784.570614
HLA A*8001	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.354317	2.087371	-2.266946	22610.855832
HLA A*0203	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.784043	1.513906	-2.270137	6081.951502
HLA B*0802	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.368259	2.097245	-2.271013	23348.492469
HLA A*2301	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.029367	1.757178	-2.272189	10699.581193
HLA A*0301	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.360353	2.087371	-2.272981	22927.295470
HLA B*4002	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.415803	2.142457	-2.273346	26049.717832

HLA A*3001	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.081817	1.806898	-2.274918	12073.041178
HLA A*0211	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.362669	2.087371	-2.275298	23049.919877
HLA A*6802	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.853367	1.577736	-2.275631	7134.554457
HLA B*4402	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.353565	2.077613	-2.275952	22571.746582
HLA A*3301	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.418989	2.142457	-2.276532	26241.516242
HLA B*3501	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.354324	2.077613	-2.276711	22611.222801
HLA A*2603	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.364718	2.087371	-2.277347	23158.912988
HLA A*0202	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-2.946278	0.667908	-2.278369	883.644722
HLA B*5801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.355379	2.075252	-2.280127	22666.213131
HLA B*4501	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.636878	2.356627	-2.280250	43338.893070
HLA A*2301	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.284453	2.003318	-2.281135	19250.974329
HLA A*2301	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.369022	2.087371	-2.281651	23389.580224
HLA A*0216	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.425044	2.142457	-2.282586	26609.918716
HLA A*0101	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.360517	2.077613	-2.282904	22935.979503
HLA A*2603	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.042087	1.757178	-2.284909	11017.597197
HLA B*1502	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.855979	1.571013	-2.284966	7177.603845
HLA A*8001	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.363783	2.077613	-2.286170	23109.102345
HLA A*6801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.127918	1.841561	-2.286358	13425.123101
HLA B*4001	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.064867	1.777358	-2.287509	11610.943108
HLA B*5101	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.375225	2.087371	-2.287854	23726.029604
HLA B*1503	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.075186	1.787206	-2.287981	11890.125407
HLA A*2603	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.090898	0.802529	-2.288369	1232.814936
HLA B*1503	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.066000	1.777358	-2.288642	11641.258924
HLA B*3901	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.102281	1.813629	-2.288652	12655.540450
HLA A*0201	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-3.322111	1.032607	-2.289504	2099.474995
HLA B*4002	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.554977	2.264943	-2.290034	35890.302353
HLA B*4403	1:292-300	9	LIGGIEVTL	2.013476	0.343151	-4.646753	2.356627	-2.290125	44335.611225
HLA A*3002	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.491315	2.200990	-2.290326	30996.700811
HLA A*2403	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.378286	2.087371	-2.290915	23893.867272
HLA B*1517	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.730658	1.439287	-2.291371	5378.460141
HLA A*3001	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.140843	0.848433	-2.292410	1383.067065
HLA A*2402	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.494534	2.200990	-2.293545	31227.287799
HLA A*1101	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.733759	1.439287	-2.294472	5417.005477
HLA A*2601	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.372457	2.077613	-2.294844	23575.307963
HLA A*0216	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.382405	2.087371	-2.295034	24121.543496
HLA B*1503	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.300617	2.003318	-2.297299	19980.997787
HLA A*3201	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.212227	1.914535	-2.297692	16301.486041
HLA A*3002	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.386195	2.087371	-2.298823	24332.952785
HLA B*1501	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.374666	2.075252	-2.299414	23695.500726
HLA B*4403	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.476044	2.176570	-2.299474	29925.665614
HLA B*5101	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.215225	1.914535	-2.300690	16414.404794
HLA A*0250	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-2.890233	0.589436	-2.300797	776.663816
HLA B*1503	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.244319	0.943496	-2.300823	1755.170286
HLA A*0216	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.304534	2.003318	-2.301216	20162.007093
HLA A*3001	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.690322	1.388176	-2.302146	4901.420874
HLA B*1501	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-3.443664	1.141236	-2.302427	2777.561364
HLA B*1517	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.213115	1.910114	-2.303001	16334.855679
HLA B*5701	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.390990	2.087371	-2.303619	24603.115890
HLA A*0101	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.380284	2.075252	-2.305031	24003.993979
HLA B*0803	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.447765	2.142457	-2.305308	28039.187022
HLA A*3301	1:44-52	9	PPWQRAATR	0.944487	0.314914	-3.565343	1.259401	-2.305942	3675.729051
HLA B*7301	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.507677	2.200990	-2.306688	32186.761722

HLA A*0250	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.587290	2.280423	-2.306867	38662.468951
HLA A*0211	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-2.941466	0.634444	-2.307022	873.908457
HLA B*3901	1:28-36	9	HRAATGPGR	0.868468	0.768121	-3.943925	1.636589	-2.307337	8788.715520
HLA B*4001	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.168423	1.861077	-2.307346	14737.485746
HLA B*1502	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.125694	0.818322	-2.307372	1335.653358
HLA A*0301	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.104574	1.797109	-2.307465	12722.539082
HLA B*1503	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.489526	1.181941	-2.307585	3086.921672
HLA B*5801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.223270	1.914964	-2.308306	16721.289883
HLA B*5301	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.509851	2.200990	-2.308861	32348.232699
HLA B*5701	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.386606	2.077613	-2.308993	24356.000444
HLA B*4402	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.384470	2.075252	-2.309218	24236.521653
HLA A*6801	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.589658	2.280423	-2.309235	38873.877800
HLA A*2602	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.150906	1.841561	-2.309345	14154.861942
HLA B*0702	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.387487	2.077613	-2.309874	24405.461822
HLA B*7301	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.152099	1.841575	-2.310524	14193.816172
HLA B*1502	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.095209	1.784644	-2.310564	12451.129395
HLA B*1503	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-3.991986	1.680196	-2.311791	9817.173634
HLA B*0803	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.399260	2.087371	-2.311889	25076.117694
HLA B*3801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.387781	2.075252	-2.312529	24421.971259
HLA A*6901	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.137979	1.824948	-2.313031	13739.748126
HLA A*0202	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.097788	1.784644	-2.313144	12525.309929
HLA B*7301	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.578242	2.264943	-2.313298	37865.327507
HLA B*5101	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.316970	2.003318	-2.313652	20747.682209
HLA A*6901	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.389343	2.075252	-2.314091	24509.989394
HLA B*0702	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.389482	2.075252	-2.314230	24517.813826
HLA B*1517	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.229273	1.914964	-2.314309	16954.020741
HLA B*0801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.828392	1.513906	-2.314486	6735.841071
HLA B*2705	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.128163	1.813629	-2.314534	13432.678582
HLA A*3101	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.318457	2.003318	-2.315139	20818.853606
HLA A*0203	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.129384	1.813629	-2.315755	13470.519821
HLA A*2501	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.230365	1.914535	-2.315830	16996.723939
HLA A*1101	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.403400	2.087371	-2.316029	25316.291760
HLA A*3301	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.391519	2.075252	-2.316267	24633.081653
HLA B*1509	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.073697	1.757178	-2.316519	11849.413684
HLA B*1509	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.459057	2.142457	-2.316600	28777.763708
HLA B*4601	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.391906	2.075252	-2.316654	24655.079739
HLA B*4402	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.414633	2.097245	-2.317388	25979.631095
HLA B*5801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.757010	1.439287	-2.317723	5714.915039
HLA B*4501	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.598706	2.280423	-2.318283	39692.251260
HLA B*0802	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.393701	2.075252	-2.318449	24757.193894
HLA A*3301	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.442183	2.123557	-2.318626	27681.080673
HLA A*2602	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.442486	2.123557	-2.318929	27700.405369
HLA B*3801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.407657	2.087371	-2.320286	25565.680604
HLA B*0802	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.398180	2.077613	-2.320567	25013.792129
HLA B*5801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.134915	1.813629	-2.321286	13643.162218
HLA A*2601	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.397146	2.075252	-2.321894	24954.321327
HLA A*3301	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.419529	2.097245	-2.322284	26274.188214
HLA A*3002	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.237268	1.914964	-2.322304	17269.032530
HLA B*3801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.446010	2.123557	-2.322453	27926.104067
HLA B*0803	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.398060	2.075252	-2.322808	25006.891667
HLA B*3501	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.481476	1.157848	-2.323628	3030.234749

HLA B*1501	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.059116	1.735451	-2.323665	11458.188374
HLA B*4801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.101590	1.777358	-2.324232	12635.427718
HLA B*2705	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.034197	1.709743	-2.324454	10819.254079
HLA A*6801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.239662	1.914964	-2.324699	17364.494011
HLA B*0802	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.412345	2.087371	-2.324973	25843.098418
HLA B*5801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.759218	1.434003	-2.325215	5744.051092
HLA B*4002	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.526290	2.200990	-2.325300	33596.180441
HLA B*1501	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.186754	1.861077	-2.325677	15372.839043
HLA A*0201	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.400994	2.075252	-2.325742	25176.434172
HLA B*1502	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.526833	2.200990	-2.325843	33638.191308
HLA B*5301	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.502483	2.176570	-2.325912	31804.060696
HLA A*0201	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.139633	1.813629	-2.326004	13792.176583
HLA B*5101	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.063317	1.735451	-2.327866	11569.559849
HLA B*3901	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.403626	2.075252	-2.328373	25329.443174
HLA B*4002	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.427313	2.097245	-2.330068	26749.344898
HLA B*1501	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.525299	1.195068	-2.330231	3351.960316
HLA B*4801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.405609	2.075252	-2.330356	25445.360490
HLA A*3001	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.144327	1.813629	-2.330698	13942.064253
HLA B*5401	1:185-193	9	GPVRASMQI	1.134441	0.112255	-3.577923	1.246696	-2.331227	3783.751738
HLA B*1503	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.765407	1.434003	-2.331404	5826.487750
HLA B*5701	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.145065	1.813629	-2.331436	13965.767837
HLA A*0301	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.335209	2.003318	-2.331891	21637.577648
HLA A*8001	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.335925	2.003318	-2.332607	21673.309473
HLA B*1502	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.420154	2.087371	-2.332783	26312.024790
HLA B*2705	1:83-91	9	NRFISGASA	0.946143	-0.055864	-3.225086	0.890279	-2.334807	1679.137937
HLA B*5401	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-2.852712	0.517364	-2.335347	712.380129
HLA A*2301	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.774974	1.439287	-2.335687	5956.264025
HLA B*4801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.250902	1.914535	-2.336367	17819.768965
HLA A*3001	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.164302	1.827925	-2.336377	14598.303935
HLA A*2402	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.423871	2.087371	-2.336500	26538.181190
HLA B*5701	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.251184	1.914535	-2.336649	17831.341077
HLA B*4001	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.412145	2.075252	-2.336893	25831.217444
HLA B*2705	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.178897	1.841561	-2.337337	15097.234547
HLA A*6801	1:164-172	9	GRSITAESR	1.007055	0.640575	-3.987381	1.647630	-2.339751	9713.628320
HLA A*3301	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.620241	2.280423	-2.339818	41710.088507
HLA A*0101	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.181383	1.841561	-2.339822	15183.893793
HLA B*2705	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-3.460589	1.120296	-2.340293	2887.947889
HLA A*0212	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.168621	1.827925	-2.340695	14744.184434
HLA A*3001	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.527860	1.186588	-2.341272	3371.784478
HLA A*2403	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.417243	2.075252	-2.341991	26136.248923
HLA A*0250	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.465666	2.123557	-2.342109	29219.053500
HLA A*0301	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.129394	1.787206	-2.342188	13470.811320
HLA B*5701	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.418700	2.075252	-2.343448	26224.060516
HLA A*0212	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.023728	1.680196	-2.343532	10561.558641
HLA B*0801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.363997	1.020231	-2.343767	2312.050550
HLA A*6801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.140930	1.797109	-2.343821	13833.425150
HLA A*2301	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.185509	1.841561	-2.343948	15328.824535
HLA B*7301	1:257-265	9	SGTIFGGAF	1.266168	1.014255	-4.625161	2.280423	-2.344738	42185.279705
HLA A*2501	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.186890	1.841561	-2.345330	15377.663390
HLA B*5401	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.546319	2.200990	-2.345330	35181.897969
HLA A*1101	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.423190	2.077613	-2.345577	26496.578933

HLA A*6901	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-2.980030	0.634444	-2.345587	955.059413
HLA A*0211	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.488355	2.142457	-2.345898	30786.131514
HLA B*3801	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.443541	2.097245	-2.346296	27767.772553
HLA B*5801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.123703	1.777358	-2.346345	13295.457941
HLA A*0101	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.261096	1.914535	-2.346561	18243.009508
HLA A*0219	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.435273	2.087371	-2.347902	27244.146417
HLA B*5101	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.425685	2.077613	-2.348072	26649.247933
HLA A*2403	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.060131	1.709743	-2.350388	11484.998302
HLA A*0203	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-3.966838	1.615041	-2.351796	9264.832773
HLA B*1503	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.165590	1.813629	-2.351961	14641.646563
HLA B*0801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.355294	2.003318	-2.351976	22661.799180
HLA B*4001	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.267003	1.914535	-2.352468	18492.817756
HLA B*3801	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.494967	2.142457	-2.352509	31258.387529
HLA A*0203	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.356119	2.003318	-2.352801	22704.871897
HLA B*5401	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.476514	2.123557	-2.352957	29958.062044
HLA B*3801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.431166	2.077613	-2.353553	26987.726847
HLA A*0203	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.429345	2.075252	-2.354093	26874.813244
HLA A*3001	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-2.844954	0.490659	-2.354295	699.767547
HLA A*0203	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.789498	1.434003	-2.355495	6158.833408
HLA B*3501	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.216616	1.861077	-2.355539	16467.058730
HLA A*2602	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.433295	2.077613	-2.355682	27120.328098
HLA B*1502	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.479455	2.123557	-2.355898	30161.662159
HLA A*3001	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.004866	1.647521	-2.357345	10112.681961
HLA B*1502	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.185814	1.827925	-2.357889	15339.608868
HLA A*2902	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.166610	1.806898	-2.359711	14676.063955
HLA B*5301	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.447180	2.087371	-2.359809	28001.441916
HLA B*1517	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.542709	1.181941	-2.360768	3489.060919
HLA A*3002	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.826305	1.465037	-2.361269	6703.559816
HLA A*0212	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.436803	2.075252	-2.361551	27340.265041
HLA A*0301	1:167-175	9	ITAESRDAR	0.938361	0.675089	-3.975047	1.613450	-2.361596	9441.623657
HLA A*2603	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.459308	2.097245	-2.362063	28794.426773
HLA B*4402	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.365782	2.003318	-2.362464	23215.737669
HLA A*0201	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.365844	2.003318	-2.362526	23219.003358
HLA B*5401	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.539236	2.176570	-2.362665	34612.707116
HLA B*4501	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.628142	2.264943	-2.363199	42475.884330
HLA B*1503	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.878323	1.513906	-2.364417	7556.541763
HLA B*1502	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.803755	1.439287	-2.364468	6364.365779
HLA B*1501	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.162099	1.797109	-2.364990	14524.412829
HLA A*3001	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-3.304584	0.939568	-2.365015	2016.431849
HLA A*0206	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.033909	0.667908	-2.366001	1081.206827
HLA B*1502	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.509294	2.142457	-2.366836	32306.784192
HLA A*3101	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.020631	1.653369	-2.367262	10486.520097
HLA B*4001	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.180998	1.813629	-2.367369	15170.428285
HLA A*0203	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.055181	0.687090	-2.368092	1135.483993
HLA B*0702	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.680045	1.311098	-2.368947	4786.800730
HLA A*3001	1:173-181	9	DARVQLSAR	0.897969	0.607997	-3.876490	1.505966	-2.370525	7524.722502
HLA B*5801	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.941947	1.571013	-2.370934	8748.772849
HLA A*0101	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.374617	2.003318	-2.371299	23692.808889
HLA A*3001	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-3.951791	1.580071	-2.371721	8949.349787

HLA B*1801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.286513	1.914535	-2.371978	19342.527066
HLA A*6802	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.447585	2.075252	-2.372332	28027.509409
HLA A*2403	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.149891	1.777358	-2.372532	14121.819635
HLA A*0202	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.079665	1.707126	-2.372539	12013.361716
HLA B*1502	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.470083	2.097245	-2.372838	29517.744919
HLA A*2902	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.448896	2.075252	-2.373643	28112.244392
HLA A*3301	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.097253	1.722434	-2.374818	12509.870050
HLA B*4601	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.202994	1.827925	-2.375068	15958.560720
HLA B*1517	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.450566	2.075252	-2.375314	28220.584433
HLA A*0219	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.378803	2.003318	-2.375485	23922.322100
HLA B*4001	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.103742	1.727210	-2.376532	12698.197453
HLA A*2501	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.291816	1.914964	-2.376852	19580.149385
HLA A*2403	1:273-281	9	VLMTALATI	1.272095	0.298918	-3.948201	1.571013	-2.377188	8875.676605
HLA A*2301	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.190842	1.813629	-2.377213	15518.229985
HLA B*4403	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.579090	2.200990	-2.378100	37939.349613
HLA A*3002	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.453649	2.075252	-2.378396	28421.600318
HLA A*3101	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.192327	1.813629	-2.378698	15571.378395
HLA B*3901	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.239855	1.861077	-2.378778	17372.198799
HLA A*0206	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.615904	1.236873	-2.379032	4129.565967
HLA A*2603	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.060408	1.680196	-2.380212	11492.332286
HLA A*2501	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.458183	2.077613	-2.380570	28719.907307
HLA B*1503	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.484014	1.101846	-2.382168	3047.991264
HLA B*3901	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.092098	1.709743	-2.382355	12362.264411
HLA B*5701	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.297481	1.914964	-2.382517	19837.210839
HLA B*4001	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.386449	2.003318	-2.383131	24347.173905
HLA B*4601	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.208148	1.824948	-2.383200	16149.106197
HLA A*0201	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.380928	0.997451	-2.383477	2403.962640
HLA B*3501	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.197350	1.813629	-2.383721	15752.527897
HLA A*0211	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.387175	2.003318	-2.383857	24387.908035
HLA B*4801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.299609	1.914964	-2.384646	19934.678809
HLA A*0211	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.210573	1.824948	-2.385625	16239.518900
HLA B*4403	1:266-274	9	LIGLVNIVL	1.906993	0.357950	-4.650613	2.264943	-2.385669	44731.442550
HLA A*0301	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.300885	1.914964	-2.385921	19993.324416
HLA A*8001	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.461674	2.075252	-2.386422	28951.719911
HLA A*6901	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-3.471585	1.084809	-2.386776	2961.999237
HLA B*2705	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.301985	1.914535	-2.387449	20044.008211
HLA A*0250	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.173188	1.784644	-2.388544	14900.064680
HLA B*4801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.392776	2.003318	-2.389458	24704.480226
HLA A*2403	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.215056	1.824948	-2.390108	16408.012431
HLA B*7301	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.127176	1.735543	-2.391633	13402.192124
HLA B*3501	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.128412	1.735451	-2.392960	13440.383737
HLA A*0219	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.468850	2.075252	-2.393598	29434.027805
HLA A*2603	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.471761	2.077613	-2.394148	29631.982445
HLA A*3201	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.171684	1.777358	-2.394326	14848.564959
HLA A*1101	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.469858	2.075252	-2.394605	29502.418878
HLA A*0216	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.223345	1.827925	-2.395420	16724.184864
HLA A*3001	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.180490	1.784676	-2.395814	15152.711446
HLA B*0801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.829947	1.434003	-2.395944	6760.007701
HLA B*5401	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.493446	2.097245	-2.396201	31149.168231

HLA B*4501	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.538878	2.142457	-2.396421	34584.256677
HLA B*4002	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.123642	1.727210	-2.396432	13293.587972
HLA B*5301	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.474091	2.077613	-2.396478	29791.433212
HLA B*3501	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.472059	2.075252	-2.396807	29652.348270
HLA A*3201	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.975338	1.577736	-2.397602	9447.959471
HLA B*3901	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.078537	1.680196	-2.398341	11982.206526
HLA B*1502	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.212218	1.813629	-2.398589	16301.133288
HLA A*6901	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.977415	1.577736	-2.399679	9493.251058
HLA A*0219	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.177098	1.777358	-2.399739	15034.801433
HLA B*4501	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.576595	2.176570	-2.400025	37722.001544
HLA A*0203	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.109771	1.709743	-2.400028	12875.700156
HLA A*3001	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.123144	1.722434	-2.400710	13278.350342
HLA B*3501	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.242333	1.841561	-2.400773	17471.632948
HLA A*3201	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.478438	2.077613	-2.400825	30091.091695
HLA B*3901	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.404274	2.003318	-2.400956	25367.291560
HLA B*3501	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.316187	1.914964	-2.401224	20710.339050
HLA A*3001	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.262520	1.861077	-2.401443	18302.915403
HLA A*0212	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.405028	2.003318	-2.401710	25411.382022
HLA A*0216	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.477305	2.075252	-2.402053	30012.729383
HLA B*7301	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-3.590521	1.187527	-2.402993	3895.117580
HLA A*0203	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-3.338285	0.935291	-2.402994	2179.137133
HLA B*4403	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.526605	2.123557	-2.403048	33620.543986
HLA B*0803	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.160633	1.757178	-2.403455	14475.464406
HLA B*4801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.228815	1.824948	-2.403866	16936.144894
HLA A*3001	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.843306	1.439287	-2.404019	6971.181056
HLA B*0702	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.111679	1.707126	-2.404553	12932.385331
HLA A*2501	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.480181	2.075252	-2.404929	30212.124240
HLA A*0211	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.556162	1.150365	-2.405797	3598.833077
HLA B*4501	1:170-178	9	ESRDARVQL	1.767877	0.433113	-4.607035	2.200990	-2.406045	40460.817768
HLA A*0250	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.493942	2.087371	-2.406571	31184.744891
HLA B*7301	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.549190	2.142457	-2.406733	35415.251922
HLA A*0219	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.589585	1.182783	-2.406803	3886.739885
HLA A*2601	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.236777	1.827925	-2.408852	17249.518042
HLA B*5401	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.496646	2.087371	-2.409275	31379.531328
HLA B*1502	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.324378	1.914535	-2.409842	21104.618866
HLA A*0202	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.413204	2.003318	-2.409886	25894.318947
HLA A*0211	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.988570	1.577736	-2.410834	9740.254872
HLA A*2402	1:29-37	9	RAATGPGRI	1.220311	0.357425	-3.988829	1.577736	-2.411093	9746.052904
HLA B*0702	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.321373	1.910114	-2.411258	20959.094809
HLA B*1501	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.225008	1.813629	-2.411379	16788.364695
HLA A*3301	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.588048	2.176570	-2.411478	38730.086585
HLA A*0212	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.196147	1.784644	-2.411503	15708.955921
HLA A*2403	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.240130	1.827925	-2.412204	17383.198135
HLA A*6901	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.323170	1.910114	-2.413056	21046.015128
HLA B*1801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.488543	2.075252	-2.413291	30799.458362
HLA A*6801	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.489159	2.075252	-2.413906	30843.144189
HLA A*3001	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.101428	0.687090	-2.414339	1263.072499
HLA B*4601	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.329344	1.914535	-2.414809	21347.367411
HLA B*1501	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.803257	1.388176	-2.415081	6357.070695
HLA B*3901	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.151789	1.735451	-2.416338	14183.683910
HLA B*4501	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.514040	2.097245	-2.416794	32661.768052

HLA B*5301	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.332161	1.914964	-2.417198	21486.286252
HLA A*6802	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.420605	2.003318	-2.417287	26339.369255
HLA B*0802	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.245505	1.827925	-2.417580	17599.701500
HLA B*0803	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.332190	1.914535	-2.417654	21487.681158
HLA B*1502	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.332911	1.914964	-2.417947	21523.398324
HLA B*3901	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.225370	1.806898	-2.418472	16802.357294
HLA A*3001	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.260218	1.841575	-2.418643	18206.135769
HLA B*2705	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-2.921829	0.502834	-2.418995	835.273968
HLA B*4002	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-3.279975	0.860615	-2.419360	1905.351220
HLA A*2603	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.334097	1.914535	-2.419562	21582.280516
HLA B*1501	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.329779	1.910114	-2.419665	21368.743181
HLA B*2705	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.423068	2.003318	-2.419750	26489.126117
HLA B*4403	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-3.302319	0.882547	-2.419771	2005.943262
HLA B*1502	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.497849	2.077613	-2.420236	31466.568824
HLA A*3201	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.731513	1.311098	-2.420415	5389.061838
HLA A*0206	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-3.821837	1.401173	-2.420664	6634.936465
HLA B*3501	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.102497	1.680196	-2.422301	12661.840804
HLA B*5401	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-3.483624	1.060834	-2.422789	3045.255270
HLA A*3101	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.609871	1.186588	-2.423283	4072.592251
HLA B*2705	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.333463	1.910114	-2.423349	21550.778937
HLA B*1503	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.248412	1.824948	-2.423463	17717.874247
HLA A*0219	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.237512	1.813629	-2.423883	17278.751313
HLA A*0203	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.209737	1.784644	-2.425092	16208.272975
HLA B*4403	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.512576	2.087371	-2.425205	32551.871404
HLA B*5801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-3.826559	1.401173	-2.425387	6707.477636
HLA B*5101	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.500770	2.075252	-2.425518	31678.878558
HLA A*2601	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.736696	1.311098	-2.425598	5453.761364
HLA B*1801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.340709	1.914964	-2.425745	21913.350426
HLA B*0702	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.183775	1.757178	-2.426597	15267.746239
HLA B*4001	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.268615	1.841561	-2.427054	18561.575512
HLA A*3101	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.163203	1.735543	-2.427660	14561.390288
HLA B*7301	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.553210	2.123557	-2.429653	35744.588710
HLA A*3201	1:188-196	9	RASMQIRRI	1.055395	0.378608	-3.863803	1.434003	-2.429800	7308.079609
HLA A*0101	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.345685	1.914964	-2.430721	22165.880779
HLA B*0802	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.434131	2.003318	-2.430813	27172.610024
HLA A*2601	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.255852	1.824948	-2.430904	18024.052095
HLA A*0216	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.215695	1.784644	-2.431051	16432.174427
HLA A*0250	1:208-216	9	LSVALFFVW	1.685197	0.457260	-4.573752	2.142457	-2.431295	37475.881037
HLA A*0206	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.012150	1.580071	-2.432079	10283.708379
HLA A*3001	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.257062	1.824948	-2.432114	18074.338798
HLA A*0206	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.124829	0.692679	-2.432150	1332.996932
HLA B*5801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.190654	1.757178	-2.433477	15511.515285
HLA A*0206	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.258573	1.824948	-2.433625	18137.320927
HLA A*0203	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.295810	1.861077	-2.434733	19761.054931
HLA B*5801	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.344931	1.910114	-2.434817	22127.421481
HLA A*2602	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.630269	1.195068	-2.435201	4268.439786
HLA B*5101	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.192463	1.757178	-2.435286	15576.265048
HLA B*1517	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.260309	1.824948	-2.435361	18209.977409
HLA A*2601	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.350579	1.914964	-2.435615	22417.076314
HLA A*1101	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.746714	1.311098	-2.435616	5581.029717
HLA B*3901	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.830600	1.394704	-2.435896	6770.182058
HLA A*0250	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.250517	1.813629	-2.436888	

									17803.965888
HLA B*1503	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.748007	1.311098	-2.436908	5597.660461
HLA A*2602	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.224374	1.787206	-2.437168	16763.860334
HLA B*1509	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.074153	1.636589	-2.437564	11861.856391
HLA A*0203	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.244464	1.806898	-2.437566	17557.572894
HLA A*0206	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.300194	1.861077	-2.439117	19961.550160
HLA B*1502	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.634437	1.195068	-2.439369	4309.601818
HLA B*1517	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.053397	1.613450	-2.439947	11308.299736
HLA B*5801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.301367	1.861077	-2.440290	20015.509858
HLA A*2902	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.351392	1.910114	-2.441278	22459.076378
HLA B*0801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.266237	1.824948	-2.441289	18460.232124
HLA A*2602	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.266500	1.824948	-2.441552	18471.420708
HLA A*2301	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.193915	1.752306	-2.441609	15628.428505
HLA A*0203	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.462023	1.020231	-2.441792	2897.493953
HLA B*1517	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.439416	0.997451	-2.441965	2750.526247
HLA B*3901	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.195269	1.752306	-2.442963	15677.204146
HLA A*2603	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.152997	1.709743	-2.443254	14223.179125
HLA A*0201	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.250566	1.806898	-2.443668	17805.988670
HLA B*5701	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.271702	1.827925	-2.443777	18693.992313
HLA A*2601	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.166506	1.722434	-2.444072	14672.570952
HLA B*1503	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.602479	1.157848	-2.444631	4003.865230
HLA A*1101	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.222095	1.777358	-2.444737	16676.120838
HLA A*3001	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.910314	1.465037	-2.445277	8134.178054
HLA A*3101	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.202651	1.757178	-2.445473	15945.960926
HLA B*1503	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.198022	1.752306	-2.445716	15776.919519
HLA B*5401	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.523973	2.077613	-2.446360	33417.450461
HLA B*1801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.289133	1.841561	-2.447572	19459.554300
HLA A*2602	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.019043	1.571013	-2.448030	10448.240040
HLA B*5101	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.309475	1.861077	-2.448398	20392.699993
HLA A*3001	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.550274	1.101846	-2.448428	3550.372279
HLA A*3101	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.063627	1.615041	-2.448586	11577.824684
HLA A*1101	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.453066	2.003318	-2.449748	28383.493975
HLA A*2301	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.840868	1.391116	-2.449752	6932.144341
HLA B*1509	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.256952	1.806898	-2.450054	18069.743714
HLA A*3301	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.538115	2.087371	-2.450743	34523.503577
HLA B*0801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-3.915877	1.465037	-2.450841	8239.052214
HLA A*3301	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.208106	1.757178	-2.450929	16147.533706
HLA B*1509	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.292977	1.841561	-2.451416	19632.547030
HLA B*5801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-3.965531	1.513906	-2.451625	9237.006967
HLA B*4403	1:78-86	9	ADARLNRFI	1.288538	0.234644	-3.974976	1.523182	-2.451795	9440.091437
HLA B*2705	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.209591	1.757178	-2.452413	16202.837419
HLA A*6801	1:194-202	9	RRIDPWSTL	1.530353	0.646217	-4.629021	2.176570	-2.452451	42561.912726
HLA A*2601	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.362867	1.910114	-2.452753	23060.396848
HLA B*0702	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.294711	1.841561	-2.453150	19711.086618
HLA A*0201	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.068551	1.615041	-2.453510	11709.854251
HLA B*2705	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.368574	1.914964	-2.453610	23365.424514
HLA B*1801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.250836	1.797109	-2.453728	17817.069886
HLA A*2902	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.070459	1.615041	-2.455418	11761.406798
HLA B*0702	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.269082	1.813629	-2.455453	18581.569069
HLA B*4001	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.284260	1.827925	-2.456335	19242.436281
HLA A*0101	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.317531	1.861077	-2.456454	20774.525555
HLA B*1509	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.460034	2.003318	-2.456716	28842.601396
HLA B*0803	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.460199	2.003318	-2.456881	

28853.525934

HLA A*6901	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.318015	1.861077	-2.456938	20797.690364
HLA A*0203	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-3.859447	1.401173	-2.458275	7235.146418
HLA B*2705	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.853033	1.394704	-2.458329	7129.075766
HLA B*1517	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.695956	1.236873	-2.459083	4965.420821
HLA A*0206	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-3.520022	1.060834	-2.459188	3311.478389
HLA B*7301	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.547026	2.087371	-2.459655	35239.234019
HLA B*4402	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.369810	1.910114	-2.459695	23432.007896
HLA A*2603	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.284815	1.824948	-2.459866	19267.019440
HLA B*0802	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.374938	1.914964	-2.459975	23710.375437
HLA A*2301	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.536012	2.075252	-2.460760	34356.749948
HLA B*4601	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.376132	1.914964	-2.461168	23775.626473
HLA A*0250	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.076309	1.615041	-2.461268	11920.912193
HLA B*1503	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.039263	1.577736	-2.461527	10946.185648
HLA B*4501	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.536820	2.075252	-2.461568	34420.747455
HLA B*1509	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.376416	1.914535	-2.461881	23791.195012
HLA A*0301	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.219919	1.757178	-2.462742	16592.789755
HLA B*0802	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.372963	1.910114	-2.462848	23602.744974
HLA B*4601	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.276800	1.813629	-2.463171	18914.742889
HLA B*0803	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.305445	1.841561	-2.463885	20204.372340
HLA B*2705	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.241375	1.777358	-2.464017	17433.111480
HLA B*1502	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.199935	1.735451	-2.464483	15846.548745
HLA A*0206	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.540610	2.075252	-2.465358	34722.422418
HLA A*3101	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.175251	1.709743	-2.465508	14971.006588
HLA A*0203	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.375965	1.910114	-2.465851	23766.495958
HLA A*0206	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.193290	1.727210	-2.466080	15605.954893
HLA B*4501	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.589902	2.123557	-2.466345	38895.755504
HLA A*6801	1:204-212	9	VSLLLSVAL	1.611099	0.512458	-4.590412	2.123557	-2.466855	38941.443831
HLA A*0211	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.542412	2.075252	-2.467160	34866.798445
HLA B*0801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.174321	1.707126	-2.467195	14938.968290
HLA A*3301	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.308885	1.841575	-2.467310	20365.027901
HLA B*7301	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.564648	2.097245	-2.467402	36698.439484
HLA A*0101	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.377772	1.910114	-2.467658	23865.575400
HLA B*4601	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.378446	1.910114	-2.468332	23902.658785
HLA B*0801	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.378575	1.910114	-2.468461	23909.771933
HLA B*1502	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.544165	2.075252	-2.468913	35007.797407
HLA B*3901	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.246553	1.777358	-2.469195	17642.217516
HLA A*3301	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.384390	1.914964	-2.469427	24232.064089
HLA A*0211	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.278391	1.806898	-2.471493	18984.145054
HLA B*1501	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.296973	1.824948	-2.472025	19814.043881
HLA B*5301	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.179184	1.707126	-2.472058	15107.202109
HLA A*0211	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.783244	1.311098	-2.472146	6070.774872
HLA B*4402	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.387233	1.914964	-2.472270	24391.206655
HLA A*2602	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.548187	2.075252	-2.472935	35333.536306
HLA B*4001	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.383718	1.910114	-2.473604	24194.600543
HLA B*0803	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.388612	1.914964	-2.473649	24468.786608
HLA A*2602	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.657260	1.182783	-2.474477	4542.135052
HLA A*6802	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.384597	1.910114	-2.474483	24243.603000
HLA A*0250	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.477808	2.003318	-2.474490	30047.495729
HLA A*0211	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.336202	1.861077	-2.475125	21687.149413
HLA B*5301	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.300533	1.824948	-2.475584	19977.106746
HLA A*6901	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.182971	1.707126	-2.475846	15239.524245
HLA B*1503	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.091121	1.615041	-2.476080	12334.474246
HLA A*0202	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.186106	1.709743	-2.476363	15349.902533

HLA A*2403	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.337549	1.861077	-2.476472	21754.480986
HLA B*1501	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.157268	1.680196	-2.477072	14363.756800
HLA B*0702	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-3.882585	1.405388	-2.477197	7631.063241
HLA B*4001	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.392256	1.914964	-2.477293	24674.961557
HLA B*5401	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.391850	1.914535	-2.477315	24651.878797
HLA A*0202	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.302725	1.824948	-2.477777	20078.194628
HLA B*3901	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.048839	1.571013	-2.477826	11190.237665
HLA B*1517	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.058275	1.580071	-2.478204	11436.018314
HLA B*0702	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-2.471170	-0.007282	-2.478451	295.916737
HLA B*4601	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.320125	1.841561	-2.478564	20898.973038
HLA A*2403	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.292528	1.813629	-2.478899	19612.271415
HLA B*0801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.293141	1.813629	-2.479512	19639.983131
HLA B*5701	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.257022	1.777358	-2.479664	18072.676611
HLA B*0702	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.499901	1.020231	-2.479670	3161.556413
HLA A*0212	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.189672	1.709743	-2.479929	15476.478204
HLA B*4403	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.557667	2.077613	-2.480054	36113.308454
HLA B*1801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.308067	1.827925	-2.480142	20326.723924
HLA A*3301	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.257605	1.777358	-2.480247	18096.940136
HLA B*2705	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.341388	1.861077	-2.480311	21947.637825
HLA A*0216	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.342534	1.861077	-2.481457	22005.656709
HLA B*4601	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.343545	1.861077	-2.482468	22056.907007
HLA B*5401	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.557721	2.075252	-2.482469	36117.802220
HLA A*6801	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.570044	2.087371	-2.482673	37157.318434
HLA B*0702	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.062786	1.580071	-2.482715	11555.423144
HLA A*0206	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.665812	1.182783	-2.483029	4632.465232
HLA A*3001	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.235384	1.752306	-2.483078	17194.269148
HLA A*0301	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.324688	1.841575	-2.483113	21119.695170
HLA A*3001	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.096943	1.613450	-2.483492	12500.939874
HLA A*3001	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.241253	1.757178	-2.484075	17428.207988
HLA B*1509	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.297732	1.813629	-2.484103	19848.697094
HLA B*3801	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.399467	1.914964	-2.484503	25088.058530
HLA A*0201	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.394648	1.910114	-2.484534	24811.228046
HLA A*6901	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.298590	1.813629	-2.484961	19887.929242
HLA A*0212	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.298984	1.813629	-2.485355	19906.012829
HLA A*6801	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.563041	2.077613	-2.485428	36562.892834
HLA B*4402	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.400407	1.914535	-2.485871	25142.406758
HLA A*2902	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.348777	1.861077	-2.487700	22324.251949
HLA B*0801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.349773	1.861077	-2.488696	22375.517936
HLA B*5701	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.398917	1.910114	-2.488803	25056.319297
HLA A*0212	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.104400	1.615041	-2.489359	12717.446864
HLA A*2402	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.564859	2.075252	-2.489607	36716.311938
HLA A*3002	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.677141	1.186588	-2.490553	4754.899971
HLA B*4002	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.568508	2.077613	-2.490895	37026.085625
HLA B*4402	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.333017	1.841561	-2.491456	21528.638726
HLA B*4801	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.401901	1.910114	-2.491787	25229.062966
HLA B*4501	1:270-278	9	VNIVLMTAL	1.658984	0.428387	-4.580095	2.087371	-2.492724	38027.297397
HLA B*3501	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.402987	1.910114	-2.492872	25292.198565
HLA A*0250	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.804183	1.311098	-2.493084	6370.635219
HLA A*2902	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.651800	1.157848	-2.493952	4485.386173
HLA B*1517	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.175575	1.680196	-2.495379	14982.187586
HLA A*2603	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.571031	2.075252	-2.495779	37241.841551

HLA B*0802	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.337579	1.841561	-2.496019	21756.011002
HLA B*1509	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.321356	1.824948	-2.496408	20958.301120
HLA A*3101	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.324822	1.827925	-2.496896	21126.208722
HLA B*3501	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.274700	1.777358	-2.497342	18823.483716
HLA B*0802	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.207274	1.709743	-2.497532	16116.639144
HLA A*2403	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.407744	1.910114	-2.497630	25570.798494
HLA A*3101	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.359303	1.861077	-2.498226	22871.919199
HLA A*0203	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.206048	1.707126	-2.498922	16071.190568
HLA B*1509	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.234827	1.735451	-2.499376	17172.237750
HLA A*6802	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.222386	1.722434	-2.499952	16687.311371
HLA B*4002	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.575826	2.075252	-2.500574	37655.329041
HLA B*4402	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.361817	1.861077	-2.500740	23004.699097
HLA B*1501	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.444834	0.943496	-2.501338	2785.054550
HLA B*4403	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.504971	2.003318	-2.501653	31986.791407
HLA A*3101	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.141973	1.640132	-2.501841	13866.692848
HLA B*3501	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.287509	1.784644	-2.502865	19386.945743
HLA B*1503	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.143157	1.640132	-2.503025	13904.553144
HLA B*1517	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.196531	0.692679	-2.503852	1572.283052
HLA A*0301	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.364972	1.861077	-2.503895	23172.447954
HLA A*0250	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.579273	2.075252	-2.504021	37955.362310
HLA B*1509	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.419247	1.914964	-2.504284	26257.136896
HLA A*2601	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.365531	1.861077	-2.504454	23202.302939
HLA B*7301	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.582764	2.077613	-2.505152	38261.718848
HLA B*1517	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-3.200985	0.695802	-2.505184	1588.493188
HLA B*4801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.257748	1.752306	-2.505443	18102.913171
HLA A*0216	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.290169	1.784676	-2.505493	19506.035573
HLA B*1503	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.383728	0.877206	-2.506522	2419.514895
HLA A*2402	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.320898	1.813629	-2.507269	20936.203271
HLA A*0301	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.284746	1.777358	-2.507388	19263.996937
HLA B*7301	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.144097	1.636589	-2.507508	13934.674560
HLA B*0702	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.285049	1.777358	-2.507691	19277.445504
HLA B*0702	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.423573	1.914964	-2.508609	26519.954238
HLA A*3001	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.293310	1.784644	-2.508666	19647.634630
HLA A*0201	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.369779	1.861077	-2.508702	23430.360014
HLA A*2402	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.335476	1.824948	-2.510528	21650.926250
HLA B*1502	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.352400	1.841561	-2.510839	22511.260889
HLA B*4002	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.269470	1.757178	-2.512292	18598.162972
HLA B*4403	1:219-227	9	TVAFLYLVL	1.618736	0.478509	-4.609741	2.097245	-2.512496	40713.764753
HLA B*3801	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.427062	1.914535	-2.512526	26733.865303
HLA A*0101	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.297311	1.784676	-2.512635	19829.485511
HLA B*3501	1:185-193	9	GPVRASMQI	1.134441	0.112255	-3.759524	1.246696	-2.512828	5748.092221
HLA A*3301	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.516302	2.003318	-2.512984	32832.370835
HLA B*0802	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.270262	1.757178	-2.513084	18632.100817
HLA B*5101	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.354698	1.841561	-2.513137	22630.680718
HLA A*3001	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.248823	1.735543	-2.513280	17734.656244
HLA A*2501	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.338632	1.824948	-2.513684	21808.803479
HLA B*0801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.266660	1.752306	-2.514354	18478.217085
HLA B*5101	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.342306	1.827925	-2.514381	21994.112066
HLA A*0212	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.375711	1.861077	-2.514634	23752.614010
HLA A*0219	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.299309	1.784644	-2.514664	19920.879504
HLA B*1503	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.221874	1.707126	-2.514749	16667.642694
HLA B*3501	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.665417	1.150365	-2.515052	4628.256876
HLA B*3901	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.250799	1.735543	-2.515256	17815.527738

HLA A*6901	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.238868	1.722434	-2.516434	17332.771308
HLA A*3001	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.226315	1.709743	-2.516572	16838.938412
HLA B*4001	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.223885	1.707126	-2.516760	16745.007293
HLA A*1101	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.330735	1.813629	-2.517106	21415.845248
HLA B*3901	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.302147	1.784644	-2.517502	20051.491682
HLA A*0219	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.427663	1.910114	-2.517549	26770.915528
HLA A*8001	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.427846	1.910114	-2.517732	26782.214471
HLA B*5701	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.379041	1.861077	-2.517964	23935.396800
HLA B*3901	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.360435	1.841575	-2.518860	22931.637076
HLA A*0201	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.344071	1.824948	-2.519123	22083.652103
HLA A*0216	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.367865	0.848433	-2.519432	2332.730552
HLA B*4601	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.255004	1.735451	-2.519553	17988.886013
HLA B*4001	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.229649	1.709743	-2.519906	16968.702194
HLA B*5301	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.098526	1.577736	-2.520790	12546.604820
HLA B*5401	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.230551	1.709743	-2.520808	17003.989572
HLA B*5801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.362564	1.841575	-2.520989	23044.309172
HLA B*1501	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-3.214485	0.693390	-2.521095	1638.647341
HLA B*3801	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.349400	1.827925	-2.521474	22356.279409
HLA A*2603	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.679430	1.157848	-2.521582	4780.020768
HLA B*3801	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.363229	1.841561	-2.521668	23079.616999
HLA A*6901	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.328581	1.806898	-2.521682	21309.867148
HLA B*4002	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.258075	1.735451	-2.522624	18116.531221
HLA A*0219	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.384045	1.861077	-2.522968	24212.801110
HLA A*2902	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-3.664496	1.141236	-2.523260	4618.452240
HLA B*4001	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.330886	1.806898	-2.523987	21423.261402
HLA A*3001	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.160726	1.636589	-2.524138	14478.597171
HLA A*2902	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.338247	1.813629	-2.524618	21789.462813
HLA A*6801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.528510	2.003318	-2.525192	33768.375499
HLA B*4501	1:119-127	9	AEAYASELP	0.543268	-0.008008	-3.060637	0.535260	-2.525376	1149.837638
HLA B*0702	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.350412	1.824948	-2.525464	22408.467520
HLA A*0202	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.601102	2.075252	-2.525850	39911.881966
HLA B*3901	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.051715	1.525000	-2.526715	11264.581981
HLA B*5401	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.180561	1.653369	-2.527192	15155.170881
HLA A*0301	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.355231	1.827925	-2.527306	22658.489280
HLA A*0216	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-3.161791	0.634444	-2.527348	1451.413799
HLA B*3801	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.530841	2.003318	-2.527523	33950.084346
HLA A*2603	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.312268	1.784644	-2.527624	20524.295926
HLA B*4001	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.312679	1.784644	-2.528035	20543.736106
HLA B*0803	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.438774	1.910114	-2.528660	27464.641740
HLA B*1503	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.765914	1.236873	-2.529042	5833.300190
HLA A*0212	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.336240	1.806898	-2.529342	21689.026696
HLA B*0801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.264853	1.735451	-2.529402	18401.503601
HLA B*1509	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.371170	1.841575	-2.529595	23505.519650
HLA A*0201	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.314343	1.784644	-2.529698	20622.573640
HLA B*0801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.210146	1.680196	-2.529950	16223.537341
HLA A*1101	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.371539	1.841575	-2.529964	23525.492605
HLA A*0216	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.355630	1.824948	-2.530682	22679.337451
HLA A*0101	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.372429	1.841575	-2.530854	23573.777535
HLA B*1502	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.308375	1.777358	-2.531017	20341.134487
HLA A*0101	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.359117	1.827925	-2.531192	22862.146258
HLA A*2501	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.441499	1.910114	-2.531385	27637.537247
HLA B*0801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.373042	1.841575	-2.531467	23607.086773

HLA A*8001	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.393069	1.861077	-2.531992	24721.191938
HLA A*0219	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.339710	1.806898	-2.532812	21863.025064
HLA A*0212	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.442944	1.910114	-2.532830	27729.642731
HLA A*0301	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.268370	1.735451	-2.532919	18551.135178
HLA B*4402	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.340018	1.806898	-2.533120	21878.524782
HLA B*1501	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.317844	1.784676	-2.533167	20789.478522
HLA A*3002	1:285-293	9	VYNLITDLI	1.083750	0.286878	-3.904088	1.370628	-2.533460	8018.396715
HLA B*1509	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.318969	1.784644	-2.534325	20843.420926
HLA B*5301	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.395471	1.861077	-2.534394	24858.251648
HLA B*5301	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.609647	2.075252	-2.534395	40704.955428
HLA B*4402	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.057763	1.523182	-2.534581	11422.539129
HLA A*1101	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.396105	1.861077	-2.535028	24894.587884
HLA A*0301	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.348880	1.813629	-2.535251	22329.566538
HLA A*2402	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.312729	1.777358	-2.535370	20546.070165
HLA A*0206	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.926774	1.391116	-2.535659	8448.394139
HLA A*2403	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.926774	1.391116	-2.535659	8448.394139
HLA A*0202	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.288226	1.752306	-2.535920	19418.960923
HLA B*4402	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.364352	1.827925	-2.536426	23139.376438
HLA A*3201	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.611886	2.075252	-2.536634	40915.356796
HLA A*0301	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.362216	1.824948	-2.537268	23025.865817
HLA B*3901	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.447389	1.910114	-2.537275	28014.927300
HLA A*6901	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.379095	1.841575	-2.537520	23938.375206
HLA A*2601	1:288-296	9	LITDLIGGI	1.024772	0.334657	-3.896950	1.359429	-2.537521	7887.689460
HLA B*1517	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.695406	1.157848	-2.537558	4959.139002
HLA B*1503	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-3.928715	1.391116	-2.537599	8486.230842
HLA B*4001	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.294863	1.757178	-2.537686	19718.019099
HLA B*1801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.398882	1.861077	-2.537805	25054.286101
HLA B*5401	1:73-81	9	NPPAAADAR	0.833991	0.526025	-3.897908	1.360016	-2.537893	7905.118670
HLA A*6802	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.151404	1.613450	-2.537953	14171.105417
HLA B*5101	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.453646	1.914964	-2.538683	28421.446560
HLA B*3801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.399812	1.861077	-2.538735	25108.017836
HLA B*4402	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.323567	1.784644	-2.538923	21065.265694
HLA B*5801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.364608	1.824948	-2.539660	23153.025241
HLA A*2902	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.367857	1.827925	-2.539932	23326.902975
HLA B*5801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.347104	1.806898	-2.540206	22238.427875
HLA B*4801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.337328	1.797109	-2.540219	21743.421002
HLA A*0101	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.365623	1.824948	-2.540675	23207.198809
HLA B*4501	1:215-223	9	VWMITVAFL	1.544881	0.532732	-4.619052	2.077613	-2.541439	41596.067280
HLA B*1501	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.852906	1.311098	-2.541808	7126.993425
HLA A*0219	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.222081	1.680196	-2.541885	16675.579551
HLA A*0216	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.452161	1.910114	-2.542047	28324.438148
HLA A*2501	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.327272	1.784644	-2.542628	21245.750599
HLA B*1501	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.349543	1.806898	-2.542644	22363.658272
HLA A*6802	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.700730	1.157848	-2.542882	5020.306292
HLA A*1101	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.330895	1.787206	-2.543689	21423.724997
HLA A*0212	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.271119	1.727210	-2.543909	18668.928289
HLA B*0702	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.405188	1.861077	-2.544111	25420.731889
HLA B*5101	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.369076	1.824948	-2.544128	23392.490711
HLA A*3001	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-3.909209	1.365049	-2.544160	8113.521975
HLA A*3201	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.369290	1.824948	-2.544342	23404.009667
HLA B*0801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.341498	1.797109	-2.544390	21953.219046
HLA A*3101	1:277-285	9	ALATIGAFV	1.170021	0.218155	-3.933245	1.388176	-2.545069	8575.207708
HLA A*2301	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.406175	1.861077	-2.545098	25478.557362
HLA A*0101	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.358910	1.813629	-2.545281	22851.264861

HLA B*1502	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.406490	1.861077	-2.545413	25497.034105
HLA A*0250	1:168-176	9	TAESRDARV	0.917270	0.090109	-3.553638	1.007379	-2.546260	3577.983690
HLA A*8001	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.325073	1.777358	-2.547715	21138.441340
HLA B*4402	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.345469	1.797109	-2.548360	22154.851348
HLA B*4001	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.373353	1.824948	-2.548404	23623.950741
HLA B*0801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.356013	1.806898	-2.549115	22699.345182
HLA B*4403	1:180-188	9	ARRSRGPVR	1.234616	0.840636	-4.624512	2.075252	-2.549260	42122.338624
HLA B*0803	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.377438	1.827925	-2.549513	23847.248804
HLA A*3101	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.302290	1.752306	-2.549984	20058.109831
HLA A*3201	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.357005	1.806898	-2.550106	22751.226378
HLA A*0212	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.375406	1.824948	-2.550458	23735.915012
HLA B*5401	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.548540	0.997451	-2.551089	3536.225683
HLA A*2601	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.364758	1.813629	-2.551129	23161.042968
HLA A*3001	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.258528	1.707126	-2.551403	18135.456725
HLA B*5801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.336181	1.784676	-2.551505	21686.093514
HLA A*0301	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.131800	1.580071	-2.551729	13545.643012
HLA A*0301	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.495385	0.943496	-2.551889	3128.853474
HLA B*4801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.232188	1.680196	-2.551993	17068.227427
HLA A*3101	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.377537	1.824948	-2.552589	23852.667880
HLA B*7301	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.555980	2.003318	-2.552662	35973.305598
HLA A*2402	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.413804	1.861077	-2.552727	25930.065373
HLA B*1501	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-3.958347	1.405388	-2.552959	9085.452163
HLA B*5801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.133891	1.580071	-2.553820	13611.019854
HLA A*2601	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.395750	1.841575	-2.554175	24874.259967
HLA A*2501	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.331680	1.777358	-2.554321	21462.470583
HLA A*0301	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.361356	1.806898	-2.554458	22980.319262
HLA B*5101	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.464811	1.910114	-2.554697	29161.571965
HLA B*4601	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.396702	1.841575	-2.555127	24928.819345
HLA A*0201	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.396836	1.841575	-2.555261	24936.507673
HLA B*4402	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.282773	1.727210	-2.555563	19176.654030
HLA A*2601	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.343382	1.787206	-2.556177	22048.675089
HLA B*4001	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.292192	1.735451	-2.556741	19597.104952
HLA B*3501	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.738909	1.181941	-2.556969	5481.625301
HLA B*1517	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.418230	1.861077	-2.557153	26195.702008
HLA B*4801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.399629	1.841575	-2.558054	25097.425207
HLA B*5701	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.135977	1.577736	-2.558241	13676.564254
HLA B*4402	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.399984	1.841575	-2.558409	25117.935501
HLA A*3002	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-3.998170	1.439287	-2.558883	9957.958611
HLA A*0206	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.356185	1.797109	-2.559076	22708.311421
HLA A*2602	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.387064	1.827925	-2.559139	24381.707837
HLA B*4403	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.400839	1.841561	-2.559278	25167.446463
HLA A*3002	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.373404	1.813629	-2.559775	23626.762573
HLA A*6802	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.344529	1.784644	-2.559885	22106.961067
HLA A*3101	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.366929	1.806898	-2.560031	23277.108793
HLA A*0101	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.337640	1.777358	-2.560282	21759.071355
HLA A*2902	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.401995	1.841575	-2.560420	25234.523014
HLA B*2705	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.345676	1.784676	-2.560999	22165.401124
HLA B*3501	1:44-52	9	PPWQRAATR	0.944487	0.314914	-3.820512	1.259401	-2.561110	6614.722949
HLA B*5801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.358269	1.797109	-2.561160	22817.540743
HLA B*1509	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.338723	1.777358	-2.561365	21813.405309
HLA B*0803	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.348634	1.787206	-2.561428	22316.886089
HLA B*1502	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.358593	1.797109	-2.561485	22834.581874
HLA B*1502	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.241824	1.680196	-2.561628	17451.134230

HLA A*2402	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.320033	1.757178	-2.562856	20894.564119
HLA A*6901	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.178146	1.615041	-2.563104	15071.121360
HLA B*1517	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.348302	1.784676	-2.563626	22299.869385
HLA B*3801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.370951	1.806898	-2.564053	23493.696535
HLA B*3901	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.078330	1.513906	-2.564424	11976.503512
HLA A*2902	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.349327	1.784676	-2.564650	22352.530429
HLA B*1801	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.475355	1.910114	-2.565241	29878.268091
HLA A*2602	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.178973	1.613450	-2.565522	15099.848353
HLA A*6901	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.350255	1.784676	-2.565578	22400.346761
HLA B*0702	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.407852	1.841575	-2.566277	25577.162704
HLA A*3002	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.391418	1.824948	-2.566470	24627.352043
HLA A*3002	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.476854	1.910114	-2.566740	29981.571384
HLA A*3001	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.247042	1.680196	-2.566846	17662.080717
HLA B*4001	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.408433	1.841575	-2.566858	25611.362844
HLA B*5801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.354272	1.787206	-2.567067	22608.531829
HLA B*4601	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.276963	1.709743	-2.567220	18921.804747
HLA B*1501	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.409530	1.841575	-2.567955	25676.149663
HLA A*0219	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.183032	1.615041	-2.567991	15241.667943
HLA B*5801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.352651	1.784644	-2.568007	22524.295487
HLA A*3002	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.215892	1.647521	-2.568371	16439.643408
HLA B*4601	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.345929	1.777358	-2.568571	22178.355443
HLA B*4402	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.382631	1.813629	-2.569002	24134.074258
HLA B*1801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.326682	1.757178	-2.569505	21216.920951
HLA B*0803	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.430750	1.861077	-2.569673	26961.897108
HLA A*0206	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.479826	1.910114	-2.569712	30187.454237
HLA A*3002	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.430790	1.861077	-2.569713	26964.376857
HLA B*4801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.376945	1.806898	-2.570046	23820.171883
HLA A*2501	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.398438	1.827925	-2.570513	25028.681961
HLA B*5701	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.412958	1.841575	-2.571383	25879.614157
HLA B*4601	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.379264	1.806898	-2.572365	23947.701307
HLA B*5701	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.397902	1.824948	-2.572954	24997.829247
HLA A*3301	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.415192	1.841561	-2.573631	26013.102806
HLA A*8001	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.331135	1.757178	-2.573957	21435.550056
HLA A*6801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.280489	1.706509	-2.573980	19076.079939
HLA B*1502	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-3.341734	0.767455	-2.574279	2196.512126
HLA B*3901	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.372190	1.797109	-2.575081	23560.772908
HLA A*8001	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.403012	1.827925	-2.575087	25293.703718
HLA A*0250	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.282735	1.707126	-2.575610	19174.994204
HLA A*3001	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.302976	1.727210	-2.575766	20089.820419
HLA B*0802	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.418087	1.841575	-2.576512	26187.058768
HLA B*5301	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.418117	1.841561	-2.576557	26188.900531
HLA A*2301	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.353962	1.777358	-2.576604	22592.392718
HLA A*6901	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.373985	1.797109	-2.576876	23658.354763
HLA A*8001	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.384184	1.806898	-2.577285	24220.530669
HLA A*3101	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.214455	1.636589	-2.577866	16385.304184
HLA A*6802	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-3.513227	0.935291	-2.577937	3260.072171
HLA A*2501	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.889126	1.311098	-2.578028	7746.865555
HLA A*2601	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.313669	1.735451	-2.578217	20590.579090
HLA A*0219	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.403193	1.824948	-2.578245	25304.242295
HLA A*0250	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.403576	1.824948	-2.578628	25326.565719
HLA B*1502	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.158805	1.580071	-2.578734	14414.666750
HLA B*5801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.314517	1.735451	-2.579065	20630.831165
HLA B*0801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.890169	1.311098	-2.579071	7765.495820
HLA B*1501	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.302309	1.722434	-2.579874	20058.977947
HLA A*6901	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.364612	1.784644	-2.579968	23153.275753

HLA A*0202	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.307424	1.727210	-2.580213	20296.615745
HLA A*0202	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.490441	1.910114	-2.580327	30934.383336
HLA B*4001	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.365376	1.784676	-2.580700	23194.019973
HLA B*0801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.365595	1.784676	-2.580918	23205.692278
HLA B*1517	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.368452	1.787206	-2.581246	23358.852412
HLA B*1501	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.368543	1.787206	-2.581338	23363.781316
HLA A*0203	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.422962	1.841575	-2.581387	26482.678256
HLA B*3801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.423180	1.841575	-2.581605	26496.005565
HLA B*0801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.359244	1.777358	-2.581885	22868.826044
HLA A*2501	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.292222	1.709743	-2.582480	19598.483237
HLA B*0802	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.443720	1.861077	-2.582643	27779.191664
HLA B*0802	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.407646	1.824948	-2.582697	25564.989076
HLA A*2603	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.411071	1.827925	-2.583146	25767.433306
HLA B*4402	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.318600	1.735451	-2.583149	20825.725029
HLA A*0101	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.340765	1.757178	-2.583588	21916.195782
HLA A*8001	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.408583	1.824948	-2.583635	25620.231876
HLA A*2601	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.368435	1.784644	-2.583791	23357.967847
HLA A*0301	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.368517	1.784644	-2.583873	23362.391007
HLA A*3001	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.290512	1.706509	-2.584003	19521.448381
HLA B*4001	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.381120	1.797109	-2.584011	24050.268310
HLA A*6801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-3.991615	1.407576	-2.584039	9808.785868
HLA A*2601	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.391138	1.806898	-2.584240	24611.502627
HLA A*3002	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.412192	1.827925	-2.584266	25834.012476
HLA A*0211	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.019931	1.434003	-2.585928	10469.627905
HLA B*1502	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.308481	1.722434	-2.586047	20346.087037
HLA B*0801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.373331	1.787206	-2.586126	23622.800543
HLA A*2403	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.371283	1.784644	-2.586638	23511.624231
HLA A*0206	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.274040	0.687090	-2.586951	1879.490969
HLA A*3002	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.384113	1.797109	-2.587005	24216.600077
HLA B*1503	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.093254	1.505966	-2.587288	12395.212452
HLA A*6802	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.429249	1.841575	-2.587674	26868.852925
HLA A*0201	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.385361	1.797109	-2.588252	24286.265935
HLA A*0216	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.315588	1.727210	-2.588378	20681.788385
HLA A*0211	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.825314	1.236873	-2.588441	6688.273225
HLA B*0702	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.385824	1.797109	-2.588715	24312.162776
HLA A*8001	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.430323	1.841575	-2.588748	26935.363493
HLA B*3801	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.499358	1.910114	-2.589244	31576.046908
HLA B*5401	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.346597	1.757178	-2.589419	22212.456648
HLA A*6901	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.376644	1.787206	-2.589439	23803.682938
HLA A*6802	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.826357	1.236873	-2.589485	6704.357705
HLA A*2402	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.417995	1.827925	-2.590070	26181.534257
HLA A*3001	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.113253	1.523182	-2.590071	12979.345442
HLA A*0216	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.282809	0.692679	-2.590129	1917.822994
HLA A*2602	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.392919	0.802529	-2.590391	2471.265951
HLA A*0101	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.387534	1.797109	-2.590426	24408.102581
HLA B*4402	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.415394	1.824948	-2.590446	26025.208230
HLA A*0212	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.375258	1.784676	-2.590581	23727.826644
HLA B*1509	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.342917	1.752306	-2.590611	22025.070118
HLA A*0216	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.902269	1.311098	-2.591171	7984.891845
HLA A*2601	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.376736	1.784676	-2.592059	23808.705704
HLA B*2705	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.419995	1.827925	-2.592069	26302.347101
HLA A*0101	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.379412	1.787206	-2.592206	23955.864625
HLA A*0301	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.299090	1.706509	-2.592581	19910.859438
HLA A*0206	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.057443	1.464619	-2.592825	11414.138145
HLA A*2501	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.453975	1.861077	-2.592898	28442.980677
HLA B*1509	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.503474	1.910114	-2.593360	31876.751458

HLA A*0206	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.378709	1.784676	-2.594033	23917.145976
HLA B*3501	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.316793	1.722434	-2.594359	20739.265717
HLA A*2501	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.401344	1.806898	-2.594446	25196.736409
HLA B*0702	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.379675	1.784644	-2.595031	23970.384064
HLA A*0216	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-3.989914	1.394704	-2.595210	9770.442350
HLA B*0803	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.436800	1.841575	-2.595225	27340.117133
HLA B*4601	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.392477	1.797109	-2.595369	24687.512696
HLA B*3501	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.166520	1.571013	-2.595507	14673.047221
HLA A*3301	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.423554	1.827925	-2.595629	26518.806502
HLA A*8001	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.409394	1.813629	-2.595765	25668.094430
HLA A*2601	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.393495	1.797109	-2.596386	24745.410536
HLA B*4002	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.512212	1.914964	-2.597248	32524.587033
HLA B*3901	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.061874	1.464619	-2.597256	11531.193322
HLA A*0202	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.120461	1.523182	-2.597279	13196.568342
HLA A*0250	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.507799	1.910114	-2.597685	32195.817590
HLA B*4601	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.383122	1.784644	-2.598477	24161.377287
HLA A*0212	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.440289	1.841575	-2.598714	27560.643667
HLA B*0802	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.412629	1.813629	-2.599000	25860.020760
HLA A*1101	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.427379	1.827925	-2.599454	26753.397113
HLA A*2902	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.064553	1.465037	-2.599516	11602.529094
HLA B*3501	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.441405	1.841575	-2.599830	27631.557254
HLA B*5701	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.406873	1.806898	-2.599974	25519.527610
HLA A*0219	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.442204	1.841575	-2.600629	27682.428470
HLA B*5801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.353445	1.752306	-2.601140	22565.519798
HLA B*0801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.126321	1.525000	-2.601320	13375.826500
HLA B*0802	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.378940	1.777358	-2.601581	23929.829470
HLA A*2301	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.426651	1.824948	-2.601702	26708.567511
HLA B*1517	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.622074	1.020231	-2.601844	4188.650801
HLA B*1503	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.386646	1.784676	-2.601969	24358.240522
HLA B*0803	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.399425	1.797109	-2.602316	25085.615623
HLA B*0702	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.390067	1.787206	-2.602861	24550.863106
HLA A*2902	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.427816	1.824948	-2.602868	26780.330983
HLA A*0101	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.387762	1.784644	-2.603118	24420.914320
HLA B*4402	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.380662	1.777358	-2.603303	24024.910377
HLA A*2902	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.355800	1.752306	-2.603494	22688.173046
HLA A*2403	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.043309	1.439287	-2.604021	11048.634902
HLA B*1503	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-3.297418	0.693390	-2.604027	1983.433386
HLA B*0802	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.388829	1.784676	-2.604152	24480.967994
HLA A*3101	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.388817	1.784644	-2.604172	24480.305806
HLA B*4001	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.356608	1.752306	-2.604302	22730.435091
HLA A*2403	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.401455	1.797109	-2.604346	25203.143867
HLA B*5701	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.392423	1.787206	-2.605218	24684.441083
HLA A*0206	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.119470	1.513906	-2.605563	13166.475294
HLA B*5701	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.403301	1.797109	-2.606193	25310.540163
HLA A*0212	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.403438	1.797109	-2.606329	25318.483188
HLA A*2403	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.448040	1.841575	-2.606465	28056.940240
HLA A*2301	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.516854	1.910114	-2.606740	32874.137958
HLA B*3501	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.413677	1.806898	-2.606778	25922.491425
HLA A*3002	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.448548	1.841575	-2.606973	28089.744950
HLA A*0201	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.391862	1.784676	-2.607185	24652.545626
HLA B*1501	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.254751	1.647521	-2.607229	17978.378751
HLA B*4002	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.522362	1.914535	-2.607826	33293.661999
HLA B*0802	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.405642	1.797109	-2.608533	25447.287755
HLA B*3501	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.261970	1.653369	-2.608601	18279.760145

HLA B*1801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.385995	1.777358	-2.608637	24321.766078
HLA A*3201	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.393295	1.784644	-2.608651	24734.034208
HLA A*0203	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.406396	1.797109	-2.609287	25491.517257
HLA A*0211	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.519732	1.910114	-2.609618	33092.722116
HLA B*5801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.290162	1.680196	-2.609966	19505.718999
HLA A*6901	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.223542	1.613450	-2.610092	16731.786574
HLA B*4601	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.394911	1.784676	-2.610235	24826.265913
HLA A*6802	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.417239	1.806898	-2.610340	26135.966136
HLA B*4002	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.613663	2.003318	-2.610345	41083.038204
HLA B*4801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.397604	1.787206	-2.610398	24980.660239
HLA A*0301	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.346651	1.735543	-2.611108	22215.220659
HLA A*6801	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.472294	1.861077	-2.611217	29668.394201
HLA A*6801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.713276	1.101846	-2.611430	5167.452158
HLA B*4601	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.398830	1.787206	-2.611625	25051.304379
HLA B*1503	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.798224	1.186588	-2.611637	6283.830244
HLA A*0101	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.347682	1.735451	-2.612231	22268.043205
HLA A*6801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-3.739407	1.126836	-2.612571	5487.915765
HLA B*1517	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.419482	1.806898	-2.612584	26271.345559
HLA A*2902	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.319488	1.706509	-2.612979	20868.355921
HLA B*1517	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.454588	1.841575	-2.613013	28483.169994
HLA B*1801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.426679	1.813629	-2.613050	26710.301452
HLA B*3801	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.390640	1.777358	-2.613282	24583.291962
HLA A*0301	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.365775	1.752306	-2.613470	23215.360888
HLA B*5301	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.523962	1.910114	-2.613847	33416.546550
HLA B*2705	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.349334	1.735451	-2.613882	22352.893206
HLA B*0803	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.366389	1.752306	-2.614083	23248.163691
HLA B*5101	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.323858	1.709743	-2.614115	21079.401568
HLA A*3101	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.194277	1.580071	-2.614206	15641.454332
HLA A*0101	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.421646	1.806898	-2.614748	26402.569386
HLA B*0803	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.392280	1.777358	-2.614922	24676.296482
HLA B*5401	1:44-52	9	PPWQRAATR	0.944487	0.314914	-3.874362	1.259401	-2.614960	7487.931369
HLA B*4801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.185452	1.570424	-2.615028	15326.834410
HLA A*0201	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.402366	1.787206	-2.615161	25256.101759
HLA B*2705	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.422555	1.806898	-2.615657	26457.904426
HLA A*3001	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.021129	1.405388	-2.615742	10498.553949
HLA A*3001	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.927131	1.311098	-2.616033	8455.344137
HLA A*1101	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.351603	1.735451	-2.616152	22470.014141
HLA B*5801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.343526	1.727210	-2.616316	22055.952424
HLA B*5701	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.401133	1.784676	-2.616456	25184.471356
HLA B*5701	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.373867	1.757178	-2.616689	23651.956175
HLA A*2301	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.444897	1.827925	-2.616971	27854.585245
HLA A*3201	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.445190	1.827925	-2.617265	27873.427893
HLA B*5801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.353067	1.735543	-2.617525	22545.873965
HLA B*2705	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.442545	1.824948	-2.617597	27704.152025
HLA B*2705	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.369995	1.752306	-2.617689	23442.024437
HLA A*0216	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.459583	1.841575	-2.618008	28812.658177
HLA A*1101	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.443019	1.824948	-2.618071	27734.443604
HLA B*4402	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.353687	1.735543	-2.618145	22578.097229
HLA B*0801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.402893	1.784644	-2.618248	25286.726038
HLA A*6901	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.324831	1.706509	-2.618322	21126.665888
HLA A*6802	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.497133	0.877206	-2.619927	3141.472355
HLA B*4001	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.407211	1.787206	-2.620005	25539.415681
HLA B*1502	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.445341	1.824948	-2.620393	27883.080262
HLA A*8001	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.355872	1.735451	-2.620421	22691.978321

HLA B*0802	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.427351	1.806898	-2.620452	26751.660374
HLA B*2705	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.405136	1.784644	-2.620492	25417.706555
HLA A*2601	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.330317	1.709743	-2.620574	21395.232566
HLA A*3101	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.268716	1.647630	-2.621085	18565.893905
HLA B*1501	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.308230	0.687090	-2.621140	2033.433383
HLA B*4801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.328621	1.707126	-2.621495	21311.827066
HLA A*8001	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.331431	1.709743	-2.621688	21450.166495
HLA A*0216	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.804540	1.182783	-2.621757	6375.875966
HLA A*2902	1:285-293	9	VYNLITDLI	1.083750	0.286878	-3.992409	1.370628	-2.621782	9826.738058
HLA A*0203	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.409032	1.787206	-2.621826	25646.718657
HLA A*0101	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.136132	1.513906	-2.622226	13681.448380
HLA A*0201	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.332483	1.709743	-2.622740	21502.216819
HLA B*5101	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.436570	1.813629	-2.622941	27325.626089
HLA A*3002	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.407643	1.784676	-2.622967	25564.850773
HLA A*0206	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.200842	1.577736	-2.623106	15879.674356
HLA B*1501	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.809751	1.186588	-2.623163	6452.841795
HLA B*5401	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.533362	1.910114	-2.623248	34147.731267
HLA B*4501	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.537960	1.914535	-2.623424	34511.179068
HLA B*0803	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.430431	1.806898	-2.623532	26942.067325
HLA A*0203	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.346138	1.722434	-2.623704	22189.036452
HLA A*8001	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.408729	1.784676	-2.624052	25628.826679
HLA A*6901	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-3.786698	1.162375	-2.624323	6119.245410
HLA B*4801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.409234	1.784676	-2.624557	25658.653581
HLA A*1101	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.382149	1.757178	-2.624971	24107.323748
HLA B*1517	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.360738	1.735451	-2.625287	22947.646094
HLA B*3801	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.382765	1.757178	-2.625587	24141.517477
HLA A*3001	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.265779	1.640132	-2.625647	18440.768170
HLA A*6901	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.361584	1.735543	-2.626041	22992.381562
HLA B*1501	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.090942	1.464619	-2.626324	12329.403950
HLA A*0203	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.378721	1.752306	-2.626415	23917.792930
HLA A*8001	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.423538	1.797109	-2.626429	26517.802275
HLA A*0202	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.313977	0.687090	-2.626887	2060.519787
HLA B*4601	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.307191	1.680196	-2.626995	20285.748214
HLA A*0203	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.411673	1.784676	-2.626996	25803.144162
HLA B*4601	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.334163	1.707126	-2.627037	21585.549980
HLA B*4002	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.440686	1.813629	-2.627057	27585.853094
HLA A*6901	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.379915	1.752306	-2.627609	23983.614780
HLA B*4501	1:225-233	9	LVLGGMGVW	1.572444	0.430874	-4.631197	2.003318	-2.627879	42775.664021
HLA B*5301	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.363348	1.735451	-2.627897	23085.985644
HLA B*0702	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.434850	1.806898	-2.627952	27217.629524
HLA A*0101	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.380432	1.752306	-2.628126	24012.176487
HLA A*3101	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.199451	1.571013	-2.628437	15828.898599
HLA B*4402	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.385814	1.757178	-2.628637	24311.636677
HLA A*3101	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.093832	1.465037	-2.628795	12411.719388
HLA B*5701	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.414750	1.784644	-2.630106	25986.659391
HLA A*3001	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.277844	1.647630	-2.630213	18960.230536
HLA A*0201	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.337391	1.707126	-2.630266	21746.597230
HLA B*0803	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.415054	1.784644	-2.630409	26004.801179
HLA A*0301	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.069924	1.439287	-2.630636	11746.908579
HLA A*2403	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.311011	1.680196	-2.630816	20464.978530
HLA B*5101	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.032238	1.401173	-2.631065	10770.549211
HLA B*5801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.337643	1.706509	-2.631133	21759.189069
HLA A*0206	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-3.663867	1.032607	-2.631260	4611.761027

HLA A*3301	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.284704	1.653369	-2.631335	19262.121138
HLA A*0301	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.202453	1.571013	-2.631440	15938.716238
HLA A*0101	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.338886	1.707126	-2.631760	21821.549388
HLA A*0216	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.428901	1.797109	-2.631793	26847.348622
HLA A*0250	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.325010	0.692679	-2.632331	2113.537564
HLA A*2902	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.419562	1.787206	-2.632357	26276.178255
HLA B*4403	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.547962	1.914535	-2.633426	35315.190621
HLA B*5801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.355898	1.722434	-2.633464	22693.328733
HLA A*3201	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.098630	1.464619	-2.634011	12549.591708
HLA B*5801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.281553	1.647521	-2.634032	19122.886633
HLA A*0211	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.418719	1.784676	-2.634042	26225.195495
HLA B*0702	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.418869	1.784676	-2.634193	26234.277092
HLA A*2403	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.361488	1.727210	-2.634277	22987.282292
HLA B*5401	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.495404	1.861077	-2.634327	31289.856780
HLA A*2902	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.314888	1.680196	-2.634692	20648.473164
HLA B*4501	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.549747	1.914964	-2.634784	35460.688487
HLA A*0212	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.029541	1.394704	-2.634836	10703.865433
HLA B*0803	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.370709	1.735451	-2.635258	23480.609057
HLA A*0101	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.315513	1.680196	-2.635317	20678.208337
HLA B*1509	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.362538	1.727210	-2.635328	23042.937874
HLA A*0219	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.432454	1.797109	-2.635345	27067.853896
HLA A*2603	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.423288	1.787206	-2.636083	26502.600047
HLA B*0801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.216212	1.580071	-2.636141	16451.743243
HLA B*1501	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.343751	1.707126	-2.636626	22067.410144
HLA A*8001	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.424090	1.787206	-2.636884	26551.536431
HLA B*0803	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.422102	1.784676	-2.637426	26430.293917
HLA B*1517	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.422109	1.784644	-2.637465	26430.722875
HLA B*7301	1:183-191	9	SRGPVRASM	1.037490	0.231097	-3.906324	1.268587	-2.637737	8059.799703
HLA B*5701	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.373512	1.735451	-2.638061	23632.642941
HLA A*0206	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.345330	1.707126	-2.638205	22147.781014
HLA B*0702	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.360694	1.722434	-2.638259	22945.287475
HLA A*0216	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.029893	1.391116	-2.638778	10712.554968
HLA A*0101	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.374419	1.735543	-2.638877	23682.044595
HLA A*0201	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.391913	1.752306	-2.639608	24655.479886
HLA A*2501	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.453804	1.813629	-2.640175	28431.750138
HLA A*0301	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.367681	1.727210	-2.640471	23317.440198
HLA A*2602	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.425274	1.784644	-2.640629	26624.030214
HLA B*7301	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.454309	1.813629	-2.640680	28464.839090
HLA B*1501	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.367960	1.727210	-2.640750	23332.456258
HLA A*6802	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.011529	1.370628	-2.640902	10269.031560
HLA B*1501	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.393227	1.752306	-2.640921	24730.154069
HLA A*2601	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.393290	1.752306	-2.640984	24733.766593
HLA B*4001	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.321565	1.680196	-2.641369	20968.394555
HLA B*1509	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.351126	1.709743	-2.641384	22445.350948
HLA A*2501	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.428878	1.787206	-2.641672	26845.896250
HLA A*2402	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.552191	1.910114	-2.642076	35660.762726
HLA B*5401	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.557054	1.914964	-2.642090	36062.353129
HLA A*0206	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.012747	1.370628	-2.642119	10297.849058
HLA A*3002	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.399411	1.757178	-2.642233	25084.801374
HLA A*8001	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.427008	1.784644	-2.642363	26730.539083
HLA A*2403	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.427052	1.784676	-2.642376	26733.286800
HLA A*6901	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.369631	1.727210	-2.642421	23422.375769
HLA B*1801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.395165	1.752306	-2.642859	24840.775344
HLA B*4002	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.484434	1.841561	-2.642873	30509.411448

HLA B*5701	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.290559	1.647521	-2.643038	19523.560672
HLA A*2902	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.031260	1.388176	-2.643085	10746.337196
HLA A*0206	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.395506	1.752306	-2.643200	24860.268936
HLA A*8001	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.323428	1.680196	-2.643233	21058.543082
HLA B*4002	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.504449	1.861077	-2.643372	31948.398478
HLA A*6802	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.428213	1.784676	-2.643537	26804.826666
HLA B*5401	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.044761	1.401173	-2.643588	11085.635748
HLA B*0702	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.395969	1.752306	-2.643663	24886.777845
HLA A*3001	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.108657	1.464619	-2.644039	12842.725456
HLA A*3001	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.045390	1.401173	-2.644218	11101.719918
HLA A*2501	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.441382	1.797109	-2.644273	27630.062458
HLA A*0250	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.505401	1.861077	-2.644324	32018.474322
HLA A*3201	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.458256	1.813629	-2.644627	28724.724227
HLA A*2403	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.222405	1.577736	-2.644669	16688.033599
HLA B*5301	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.458674	1.813629	-2.645045	28752.398318
HLA B*4601	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.397421	1.752306	-2.645115	24970.121340
HLA A*0201	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.372370	1.727210	-2.645160	23570.589463
HLA B*5101	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.486830	1.841575	-2.645255	30678.230383
HLA A*2501	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.258909	1.613450	-2.645459	18151.357643
HLA B*3801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.430351	1.784644	-2.645707	26937.112158
HLA B*0802	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.430572	1.784644	-2.645928	26950.813960
HLA A*3001	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.299304	1.653369	-2.645935	19920.663966
HLA A*0219	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.430713	1.784676	-2.646036	26959.563435
HLA A*6802	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.356338	1.709743	-2.646595	22716.298039
HLA A*2501	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.431632	1.784676	-2.646955	27016.650456
HLA A*0216	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.356911	1.709743	-2.647168	22746.303646
HLA A*2603	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.557540	1.910114	-2.647426	36102.760069
HLA B*4402	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.434801	1.787206	-2.647595	27214.537568
HLA B*4402	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.400320	1.752306	-2.648014	25137.374609
HLA B*3501	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.445165	1.797109	-2.648056	27871.769229
HLA B*7301	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.288202	1.640132	-2.648070	19417.910407
HLA B*1509	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.433029	1.784676	-2.648353	27103.754034
HLA A*2902	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.433034	1.784644	-2.648390	27104.047292
HLA A*0219	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.355696	1.707126	-2.648571	22682.773107
HLA A*6802	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.039705	1.391116	-2.648589	10957.324230
HLA B*1501	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-3.422514	0.773810	-2.648703	2645.535530
HLA B*3801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.462339	1.813629	-2.648710	28996.078902
HLA A*6802	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.445919	1.797109	-2.648810	27920.212681
HLA A*0211	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.355452	1.706509	-2.648942	22670.014723
HLA A*0301	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.358976	1.709743	-2.649233	22854.726562
HLA B*0803	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.463258	1.813629	-2.649629	29057.478256
HLA A*2602	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.559845	1.910114	-2.649731	36294.870396
HLA A*2902	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.447072	1.797109	-2.649964	27994.474487
HLA A*3002	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.372650	1.722434	-2.650216	23585.768547
HLA B*4001	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.265384	1.615041	-2.650343	18424.015682
HLA A*2601	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.386037	1.735543	-2.650495	24324.134598
HLA B*1501	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.228457	1.577736	-2.650722	16922.223973
HLA B*0802	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.403048	1.752306	-2.650742	25295.756343
HLA B*3901	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.378082	1.727210	-2.650872	23882.624022
HLA B*4801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.378627	1.727210	-2.651417	23912.617786
HLA B*3501	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.436114	1.784676	-2.651438	27296.962383
HLA B*2705	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.438647	1.787206	-2.651442	27456.619556

HLA A*3002	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-3.496795	0.844974	-2.651821	3139.026025
HLA B*0801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.847131	1.195068	-2.652063	7032.849503
HLA B*1501	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.387964	1.735543	-2.652421	24432.278805
HLA A*2601	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.359841	1.707126	-2.652715	22900.271969
HLA B*3501	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.405127	1.752306	-2.652821	25417.156533
HLA B*2705	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.333096	1.680196	-2.652901	21532.598987
HLA B*2705	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.375453	1.722434	-2.653019	23738.483324
HLA A*2301	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.494720	1.841575	-2.653145	31240.636608
HLA B*3801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.478255	1.824948	-2.653307	30078.396795
HLA B*5801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.360642	1.707126	-2.653516	22942.556745
HLA B*0802	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.360889	1.707126	-2.653763	22955.592699
HLA B*4801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.390553	1.735451	-2.655102	24578.371717
HLA A*6901	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.364925	1.709743	-2.655182	23169.940882
HLA B*4801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.361777	1.706509	-2.655267	23002.583496
HLA B*4402	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.439949	1.784676	-2.655272	27539.032640
HLA B*4801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.391627	1.735543	-2.656084	24639.212479
HLA B*5701	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.408529	1.752306	-2.656223	25617.044214
HLA A*0101	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.383688	1.727210	-2.656478	24192.899032
HLA A*3002	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.408825	1.752306	-2.656519	25634.511923
HLA A*0201	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.392104	1.735543	-2.656561	24666.286310
HLA B*5101	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.463521	1.806898	-2.656623	29075.089738
HLA A*0101	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.379097	1.722434	-2.656663	23938.504710
HLA A*0203	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.384205	1.727210	-2.656995	24221.709972
HLA A*6802	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.444208	1.787206	-2.657003	27810.467986
HLA A*0211	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.364417	1.707126	-2.657292	23142.881784
HLA B*4601	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.393107	1.735543	-2.657564	24723.331854
HLA B*3501	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.384856	1.727210	-2.657645	24258.034366
HLA A*1101	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.464839	1.806898	-2.657941	29163.465157
HLA A*2301	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.455056	1.797109	-2.657947	28513.850573
HLA B*5101	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.436018	1.777358	-2.658660	27290.908439
HLA A*0101	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.368595	1.709743	-2.658852	23366.562181
HLA B*1501	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.229529	1.570424	-2.659105	16964.021101
HLA A*3301	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.255594	1.596160	-2.659433	18013.329392
HLA B*1503	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.381891	1.722434	-2.659456	24092.982041
HLA A*6901	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.896334	1.236873	-2.659462	7876.517440
HLA A*0301	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.366664	1.707126	-2.659538	23262.883438
HLA A*0211	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.386820	1.727210	-2.659610	24367.993853
HLA B*0801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.382377	1.722434	-2.659943	24119.977608
HLA B*4002	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.369821	1.709743	-2.660078	23432.641727
HLA A*8001	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.387409	1.727210	-2.660199	24401.105193
HLA B*0802	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.382647	1.722434	-2.660213	24134.988214
HLA A*3101	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.256748	1.596160	-2.660587	18061.241003
HLA B*4601	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.388065	1.727210	-2.660855	24437.963031
HLA B*1801	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.502642	1.841575	-2.661067	31815.762686
HLA B*3501	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.448327	1.787206	-2.661121	28075.464115
HLA A*0250	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.446008	1.784676	-2.661332	27925.952990
HLA A*3301	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.397735	1.735543	-2.662193	24988.229371
HLA B*2705	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.240050	1.577736	-2.662314	17380.001029
HLA A*2501	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.503951	1.841575	-2.662376	31911.777975
HLA B*4001	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.397919	1.735543	-2.662376	24998.775913
HLA A*0212	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.449817	1.787206	-2.662611	28171.924628
HLA A*6802	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.414929	1.752306	-2.662623	25997.346044
HLA B*4601	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.385170	1.722434	-2.662736	24275.626000
HLA A*2403	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.242843	1.580071	-2.662772	17492.155744
HLA B*5301	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.102549	1.439287	-2.663261	12663.347876
HLA B*0702	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.373045	1.709743	-2.663302	23607.214485

HLA B*1517	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.974793	1.311098	-2.663694	9436.108829
HLA A*2403	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.451003	1.787206	-2.663797	28248.995388
HLA A*2402	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.448785	1.784644	-2.664141	28105.097347
HLA B*4801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.386902	1.722434	-2.664468	24372.608275
HLA B*5101	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.449267	1.784644	-2.664622	28136.283956
HLA B*0803	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.400188	1.735543	-2.664646	25129.760300
HLA A*2602	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.178952	0.514013	-2.664939	1509.912868
HLA A*0216	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.371750	1.706509	-2.665241	23536.949722
HLA A*3001	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.036096	1.370628	-2.665468	10866.650613
HLA A*6901	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.066836	1.401173	-2.665664	11663.700667
HLA A*2601	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.392938	1.727210	-2.665728	24713.703694
HLA B*0802	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.401471	1.735543	-2.665929	25204.098308
HLA B*0702	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.402465	1.735543	-2.666922	25261.840985
HLA B*1517	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.464134	1.797109	-2.667026	29116.172211
HLA A*0201	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.389550	1.722434	-2.667116	24521.660649
HLA B*0803	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.374412	1.707126	-2.667287	23681.660247
HLA B*7301	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.464867	1.797109	-2.667759	29165.358472
HLA B*0802	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.403581	1.735451	-2.668130	25326.839748
HLA A*3301	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.308267	1.640132	-2.668135	20336.073125
HLA A*3201	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.578411	1.910114	-2.668297	37880.079380
HLA B*3901	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.246114	1.577736	-2.668378	17624.378804
HLA A*3101	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.348624	1.680196	-2.668428	22316.403167
HLA B*0801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.404077	1.735543	-2.668534	25355.766503
HLA B*7301	1:217-225	9	MITVAFLYL	1.461926	0.452609	-4.583093	1.914535	-2.668558	38290.708657
HLA A*0216	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.420864	1.752306	-2.668558	26355.048157
HLA A*8001	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.391150	1.722434	-2.668716	24612.168364
HLA B*3901	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.316758	1.647630	-2.669128	20737.582829
HLA B*3901	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.454424	1.784676	-2.669747	28472.385680
HLA B*0802	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.183869	1.513906	-2.669963	15271.050470
HLA B*7301	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.317905	1.647630	-2.670274	20792.402916
HLA B*1509	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.457504	1.787206	-2.670298	28675.040022
HLA B*5701	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.377170	1.706509	-2.670661	23832.546087
HLA B*1517	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.406518	1.735543	-2.670975	25498.689392
HLA B*0803	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.496057	1.824948	-2.671109	31336.950539
HLA A*6802	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.066141	1.394704	-2.671436	11645.038212
HLA A*0212	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.423768	1.752306	-2.671462	26531.864923
HLA A*3201	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.866656	1.195068	-2.671588	7356.234149
HLA A*8001	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.136813	1.465037	-2.671777	13702.929610
HLA B*5701	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.394256	1.722434	-2.671822	24788.822428
HLA B*0802	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.459123	1.787206	-2.671917	28782.123204
HLA A*0219	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.399169	1.727210	-2.671958	25070.827550
HLA B*5401	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.773992	1.101846	-2.672146	5942.810143
HLA B*4402	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.287202	1.615041	-2.672160	19373.211170
HLA A*2403	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.379377	1.707126	-2.672251	23953.920726
HLA A*3201	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.533648	1.861077	-2.672571	34170.276430
HLA A*6802	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.379835	1.707126	-2.672709	23979.203730
HLA A*0203	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-3.855571	1.182783	-2.672788	7170.850596
HLA B*4402	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.380016	1.707126	-2.672890	23989.194623
HLA B*1503	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.320889	1.647521	-2.673367	20935.750226
HLA B*4001	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.379910	1.706509	-2.673401	23983.355284
HLA A*2902	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.383258	1.709743	-2.673515	24168.959679
HLA A*2902	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.396338	1.722434	-2.673903	24907.924474
HLA A*0219	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.426293	1.752306	-2.673988	26686.614000
HLA A*2902	1:209-217	9	SVALFFVWM	1.067963	0.243135	-3.985652	1.311098	-2.674554	9675.028673
HLA A*0203	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.065727	1.391116	-2.674612	11633.955777
HLA B*1801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.459358	1.784644	-2.674713	28797.698227

HLA B*4501	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.197966	1.523182	-2.674784	15774.871218
HLA B*4001	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.397395	1.722434	-2.674960	24968.635442
HLA A*0201	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.523429	0.848433	-2.674996	3337.556899
HLA A*0212	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.382417	1.707126	-2.675291	24122.195979
HLA B*3801	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.472414	1.797109	-2.675305	29676.580970
HLA A*3002	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.076634	1.401173	-2.675461	11929.815248
HLA B*3801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.460518	1.784676	-2.675842	28874.762581
HLA B*1801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.500826	1.824948	-2.675878	31682.991927
HLA A*0301	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.312531	1.636589	-2.675943	20536.735521
HLA A*0301	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.356237	1.680196	-2.676041	22711.014269
HLA B*1801	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.460918	1.784676	-2.676241	28901.330371
HLA A*3101	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.384172	1.707126	-2.677046	24219.875526
HLA B*1509	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.474293	1.797109	-2.677185	29805.296915
HLA A*0101	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.384031	1.706509	-2.677522	24212.015192
HLA A*0301	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.331405	1.653369	-2.678036	21448.890060
HLA A*0203	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-2.659410	-0.018628	-2.678038	456.467927
HLA B*4801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.255930	1.577736	-2.678194	18027.270150
HLA B*3801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.385685	1.707126	-2.678559	24304.403974
HLA A*3001	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.274864	1.596160	-2.678704	18830.613373
HLA B*3501	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.256738	1.577736	-2.679002	18060.850170
HLA A*2602	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.259708	1.580071	-2.679637	18184.775291
HLA B*2705	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.250872	1.571013	-2.679858	17818.515770
HLA A*2402	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.521596	1.841575	-2.680021	33234.996249
HLA B*5701	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.360374	1.680196	-2.680178	22928.411805
HLA B*5701	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.415758	1.735543	-2.680216	26047.040374
HLA B*4601	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.251518	1.571013	-2.680504	17845.044452
HLA A*0216	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.468283	1.787206	-2.681078	29395.677217
HLA B*0801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.258895	1.577736	-2.681159	18150.768472
HLA B*1502	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.592360	1.910114	-2.682246	39116.480553
HLA B*5701	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.409972	1.727210	-2.682761	25702.277110
HLA B*0702	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.254128	1.571013	-2.683115	17952.623043
HLA B*0702	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.117693	1.434003	-2.683690	13112.736009
HLA A*6901	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.079176	1.394704	-2.684471	11999.851200
HLA A*0216	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-3.846990	1.162375	-2.684615	7030.567058
HLA A*2601	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.364958	1.680196	-2.684762	23171.695804
HLA A*0203	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.420323	1.735543	-2.684781	26322.275636
HLA B*1502	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.472334	1.787206	-2.685128	29671.122873
HLA A*8001	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.437517	1.752306	-2.685211	27385.266007
HLA B*1801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.365550	1.680196	-2.685354	23203.307136
HLA B*5101	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.392865	1.707126	-2.685739	24709.559391
HLA B*2705	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.392567	1.706509	-2.686057	24692.588373
HLA A*0301	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.256844	1.570424	-2.686420	18065.247529
HLA B*1501	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.302001	1.615041	-2.686960	20044.767276
HLA B*4403	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.548384	1.861077	-2.687307	35349.596599
HLA A*6901	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.334861	1.647521	-2.687340	21620.260161
HLA B*5101	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.472066	1.784676	-2.687390	29652.829521
HLA A*0201	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.393993	1.706509	-2.687483	24773.807242
HLA A*1101	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.472285	1.784644	-2.687640	29667.752197
HLA B*2705	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.201716	1.513906	-2.687810	15911.664042
HLA A*2902	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.424226	1.735543	-2.688683	26559.868908
HLA B*1801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.495801	1.806898	-2.688902	31318.477278
HLA B*1801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.476187	1.787206	-2.688982	29935.542811
HLA A*0216	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.396187	1.707126	-2.689062	24899.302024
HLA B*7301	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.604532	1.914964	-2.689569	40228.371740
HLA B*4403	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.600003	1.910114	-2.689888	39810.959754
HLA A*2902	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.397698	1.707126	-2.690572	24986.066528

HLA B*7301	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.600785	1.910114	-2.690671	39882.743562
HLA A*0211	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.532349	1.841575	-2.690774	34068.203045
HLA A*0219	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.478062	1.787206	-2.690856	30065.056649
HLA B*3901	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-3.811180	1.120296	-2.690883	6474.101509
HLA B*3501	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.205376	1.513906	-2.691470	16046.343994
HLA A*0206	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.533125	1.841575	-2.691550	34129.078084
HLA B*3901	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.478868	1.787206	-2.691662	30120.896920
HLA B*0802	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.419870	1.727210	-2.692660	26294.806664
HLA A*6802	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.428218	1.735543	-2.692675	26805.116690
HLA A*0201	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.270617	1.577736	-2.692881	18647.327473
HLA B*7301	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.534793	1.841561	-2.693232	34260.420683
HLA B*5101	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.490592	1.797109	-2.693483	30945.095692
HLA A*0211	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-3.572914	0.879222	-2.693691	3740.361098
HLA A*2501	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.429580	1.735451	-2.694129	26889.356153
HLA B*5101	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.481351	1.787206	-2.694146	30293.629216
HLA B*1501	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.308006	1.613450	-2.694556	20323.865026
HLA B*5301	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.128637	1.434003	-2.694634	13447.365805
HLA B*4601	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.342715	1.647521	-2.695194	22014.825327
HLA B*3901	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.335425	1.640132	-2.695292	21648.349563
HLA B*4601	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.401838	1.706509	-2.695328	25225.378101
HLA A*0250	1:247-255	9	ASGSSAELV	1.030749	0.206124	-3.932441	1.236873	-2.695569	8559.356681
HLA B*4801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.209549	1.513906	-2.695643	16201.259696
HLA B*1501	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.129652	1.434003	-2.695649	13478.830021
HLA B*1517	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.402451	1.706509	-2.695941	25261.021015
HLA B*4501	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.606078	1.910114	-2.695964	40371.828138
HLA A*3201	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.448414	1.752306	-2.696108	28081.084428
HLA A*3002	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.480776	1.784644	-2.696131	30253.503946
HLA A*0250	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-3.575456	0.879222	-2.696233	3762.319506
HLA B*0702	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.431704	1.735451	-2.696253	27021.181706
HLA B*3801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.423801	1.727210	-2.696590	26533.874481
HLA B*5101	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.221743	1.525000	-2.696742	16662.593933
HLA A*1101	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.432400	1.735543	-2.696857	27064.486122
HLA B*4403	1:280-288	9	TIGAFVYNL	1.455838	0.459126	-4.611865	1.914964	-2.696902	40913.364717
HLA A*6901	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.333501	1.636589	-2.696912	21552.644415
HLA A*0216	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.420507	1.722434	-2.698072	26333.385226
HLA B*3501	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.137401	1.439287	-2.698114	13721.474981
HLA B*1509	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.404892	1.706509	-2.698383	25403.409852
HLA B*4402	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.421244	1.722434	-2.698810	26378.155900
HLA B*0702	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.352315	1.653369	-2.698946	22506.877112
HLA A*0203	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.069646	1.370628	-2.699019	11739.412134
HLA B*4403	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.512757	1.813629	-2.699128	32565.434084
HLA A*0211	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.496271	1.797109	-2.699162	31352.381515
HLA B*1517	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.426484	1.727210	-2.699274	26698.310664
HLA B*5801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.352877	1.653369	-2.699508	22535.996504
HLA B*1509	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.406992	1.707126	-2.699867	25526.569530
HLA A*3301	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.139285	1.439287	-2.699998	13781.138109
HLA B*0801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.427252	1.727210	-2.700042	26745.582677
HLA A*2403	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.422732	1.722434	-2.700297	26468.641679
HLA A*2601	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.406807	1.706509	-2.700297	25515.662284
HLA A*1101	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.452981	1.752306	-2.700675	28377.966657
HLA B*5701	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.407850	1.707126	-2.700724	25577.024335
HLA A*1101	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.802594	1.101846	-2.700748	6347.379813
HLA B*3501	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.314597	1.613450	-2.701146	20634.626272
HLA B*3501	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-3.377850	0.676597	-2.701253	2386.986092
HLA B*1503	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.429327	1.727210	-2.702116	26873.650151

HLA B*5101	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.382351	1.680196	-2.702155	24118.542301
HLA A*2501	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.424604	1.722434	-2.702170	26583.012423
HLA B*5401	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.543801	1.841575	-2.702226	34978.454524
HLA A*0212	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.437862	1.735543	-2.702320	27407.052903
HLA A*0219	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.412124	1.709743	-2.702381	25829.959779
HLA A*2601	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.216602	1.513906	-2.702696	16466.524229
HLA A*0216	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.281201	1.577736	-2.703465	19107.375023
HLA B*5401	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.545081	1.841561	-2.703520	35081.736819
HLA A*0219	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.425960	1.722434	-2.703525	26666.121102
HLA A*6901	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.218049	1.513906	-2.704143	16521.490321
HLA A*2902	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.275247	1.571013	-2.704234	18847.225756
HLA B*1801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.169622	1.465037	-2.704585	14778.203255
HLA A*0211	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.397322	0.692679	-2.704643	2496.447402
HLA A*0301	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.092953	1.388176	-2.704777	12386.632162
HLA A*2403	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.440520	1.735543	-2.704977	27575.259344
HLA B*7301	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.440473	1.735451	-2.705021	27572.275923
HLA B*0802	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.411565	1.706509	-2.705055	25796.723722
HLA A*3101	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.016196	1.311098	-2.705097	10379.957272
HLA A*0301	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.352940	1.647630	-2.705310	22539.288510
HLA A*6802	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.432886	1.727210	-2.705676	27094.811183
HLA B*4402	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-3.588293	0.882547	-2.705746	3875.192316
HLA B*5401	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.230943	1.525000	-2.705943	17019.358794
HLA A*0201	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.100782	1.394704	-2.706077	12611.935031
HLA B*7301	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.568388	1.861077	-2.707311	37015.871377
HLA A*0301	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.286032	1.577736	-2.708296	19321.087566
HLA B*0803	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.430732	1.722434	-2.708297	26960.730246
HLA B*1509	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.430760	1.722434	-2.708325	26962.480558
HLA A*0206	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-3.528358	0.820012	-2.708346	3375.653784
HLA A*2301	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.493080	1.784644	-2.708436	31122.891207
HLA B*3901	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.431368	1.722434	-2.708934	27000.285821
HLA A*0301	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.349350	1.640132	-2.709218	22353.739709
HLA A*8001	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.444960	1.735543	-2.709418	27858.654178
HLA B*5401	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.537483	1.827925	-2.709557	34473.299436
HLA B*0803	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.419377	1.709743	-2.709634	26264.950709
HLA B*3801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.445313	1.735543	-2.709770	27881.270188
HLA A*0219	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.416510	1.706509	-2.710001	26092.171139
HLA A*6901	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.235029	1.525000	-2.710029	17180.229001
HLA B*5101	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.463093	1.752306	-2.710788	29046.476498
HLA B*3801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.463180	1.752306	-2.710875	29052.291194
HLA B*1501	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.417398	1.706509	-2.710889	26145.582607
HLA B*5801	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.358572	1.647630	-2.710942	22833.470108
HLA A*2902	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.358558	1.647521	-2.711037	22832.728961
HLA A*3002	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.324558	1.613450	-2.711108	21113.412069
HLA A*0202	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.289201	1.577736	-2.711465	19462.607487
HLA B*4402	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.418077	1.706509	-2.711568	26186.492098
HLA B*0702	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.325054	1.613450	-2.711604	21137.526506
HLA A*3101	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.439035	1.727210	-2.711825	27481.139147
HLA A*8001	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.418434	1.706509	-2.711925	26208.034189
HLA A*0211	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.421822	1.709743	-2.712080	26413.284182
HLA A*2501	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.283229	1.571013	-2.712215	19196.790848
HLA B*1502	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.496926	1.784676	-2.712250	31399.739247
HLA B*1517	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.464853	1.752306	-2.712547	29164.411799
HLA B*5801	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.326433	1.613450	-2.712983	21204.757633
HLA B*2705	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.147123	1.434003	-2.713120	14032.109563
HLA B*1503	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.114315	1.401173	-2.713142	13011.122281
HLA A*2402	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.227057	1.513906	-2.713151	16867.749617

HLA A*2902	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.440562	1.727210	-2.713352	27577.944698
HLA B*4002	1:76-84	9	AAADARLNR	1.236372	0.673742	-4.624078	1.910114	-2.713964	42080.202435
HLA B*4403	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.441842	1.727210	-2.714632	27659.375208
HLA A*2603	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.229334	1.513906	-2.715428	16956.405613
HLA B*5801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.355565	1.640132	-2.715432	22675.902316
HLA A*6901	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.295575	1.580071	-2.715504	19750.367310
HLA A*3101	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.154825	1.439287	-2.715537	14283.169132
HLA A*8001	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.295923	1.580071	-2.715852	19766.187043
HLA B*5301	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.396180	1.680196	-2.715984	24898.897919
HLA A*0212	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.438856	1.722434	-2.716422	27469.842556
HLA A*0212	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-3.536722	0.820012	-2.716710	3441.296276
HLA A*8001	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.423916	1.707126	-2.716790	26540.909134
HLA A*0212	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.423425	1.706509	-2.716915	26510.917167
HLA A*2603	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.330385	1.613450	-2.716935	21398.589458
HLA B*5401	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.541921	1.824948	-2.716973	34827.397991
HLA B*5101	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.294727	1.577736	-2.716991	19711.833076
HLA A*2403	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.423758	1.706509	-2.717249	26531.290791
HLA A*1101	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.397496	1.680196	-2.717300	24974.444453
HLA B*4402	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.365479	1.647630	-2.717849	23199.541622
HLA A*6901	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.371280	1.653369	-2.717911	23511.497036
HLA A*6802	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.424503	1.706509	-2.717994	26576.829263
HLA A*0211	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.008010	1.289989	-2.718021	10186.147486
HLA B*1509	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.453599	1.735543	-2.718057	28418.371589
HLA B*4801	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.289654	1.571013	-2.718641	19482.939175
HLA B*5801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.333764	1.615041	-2.718723	21565.707283
HLA B*1501	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.232642	1.513906	-2.718736	17086.057817
HLA A*2603	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.533999	1.813629	-2.720370	34197.831288
HLA A*2602	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.562174	1.841575	-2.720599	36489.976995
HLA B*5801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.357510	1.636589	-2.720921	22777.704320
HLA A*2301	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.508511	1.787206	-2.721306	32248.636136
HLA B*3801	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.508676	1.787206	-2.721470	32260.850757
HLA A*0301	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.336954	1.615041	-2.721913	21724.725953
HLA B*1502	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.336968	1.615041	-2.721927	21725.431135
HLA A*2602	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.236194	1.513906	-2.722288	17226.390701
HLA A*2603	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.583387	1.861077	-2.722310	38316.610975
HLA B*0803	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.293761	1.571013	-2.722748	19668.053206
HLA A*0219	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.458357	1.735543	-2.722814	28731.407100
HLA A*0206	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.157057	1.434003	-2.723053	14356.764933
HLA B*5101	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.338676	1.615041	-2.723635	21811.045275
HLA B*3501	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.188878	1.465037	-2.723841	15448.204663
HLA A*1101	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.433873	1.709743	-2.724130	27156.444745
HLA B*5301	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.531142	1.806898	-2.724243	33973.601760
HLA A*3201	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.521483	1.797109	-2.724374	33226.367083
HLA B*0803	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.430971	1.706509	-2.724462	26975.611517
HLA B*5701	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.295822	1.571013	-2.724809	19761.589463
HLA B*3901	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.431996	1.706509	-2.725486	27039.314305
HLA B*0702	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.452810	1.727210	-2.725600	28366.761789
HLA A*3301	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.432686	1.706509	-2.726177	27082.354754
HLA B*1517	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.190941	1.464619	-2.726322	15521.756365
HLA B*4403	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.503763	1.777358	-2.726405	31897.969829
HLA A*2403	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.373970	1.647521	-2.726449	23657.586841
HLA B*4002	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.523853	1.797109	-2.726745	33408.231713
HLA B*5401	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.540836	1.813629	-2.727207	34740.460169
HLA A*2601	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.166525	1.439287	-2.727238	14673.205981

HLA A*6901	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.368071	1.640132	-2.727939	23338.389635
HLA B*3501	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.463580	1.735543	-2.728037	29079.022329
HLA B*1517	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.133914	1.405388	-2.728526	13611.756215
HLA A*2602	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.317976	0.589436	-2.728540	2079.579908
HLA B*0801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.382302	1.653369	-2.728933	24115.802405
HLA B*1801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.235297	1.505966	-2.729331	17190.827786
HLA B*2705	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.436516	1.707126	-2.729390	27322.226242
HLA B*4601	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.342995	1.613450	-2.729544	22029.002524
HLA A*2601	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.366288	1.636589	-2.729699	23242.756211
HLA B*3801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.383662	1.653369	-2.730293	24191.459385
HLA B*0702	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.436810	1.706509	-2.730300	27340.708768
HLA B*2705	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.345551	1.615041	-2.730510	22159.046680
HLA A*6901	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.378399	1.647630	-2.730769	23900.072710
HLA B*4402	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.411177	1.680196	-2.730981	25773.707022
HLA B*5401	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.515795	1.784676	-2.731118	32794.027433
HLA B*0802	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.411424	1.680196	-2.731228	25788.351636
HLA B*4801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.311305	1.580071	-2.731234	20478.822368
HLA B*1503	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.254946	1.523182	-2.731764	17986.453230
HLA A*2402	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.529072	1.797109	-2.731963	33812.065014
HLA B*3501	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.438541	1.706509	-2.732032	27449.936193
HLA A*0202	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.573695	1.841575	-2.732121	37471.015584
HLA A*0250	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.574140	1.841575	-2.732565	37509.348131
HLA B*0801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.127307	1.394704	-2.732603	13406.252984
HLA B*1801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.197613	1.464619	-2.732995	15762.075365
HLA A*0101	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.380565	1.647521	-2.733044	24019.582112
HLA A*0203	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.439561	1.706509	-2.733052	27514.461395
HLA A*0101	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.346686	1.613450	-2.733235	22217.023460
HLA B*4001	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.381221	1.647521	-2.733700	24055.863660
HLA A*3301	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.304235	1.570424	-2.733811	20148.159425
HLA B*4001	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.387198	1.653369	-2.733829	24389.227430
HLA A*0219	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.311625	1.577736	-2.733889	20493.895102
HLA B*1517	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.349237	1.615041	-2.734196	22347.935762
HLA B*0801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.349743	1.615041	-2.734701	22373.944354
HLA B*0702	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.382229	1.647521	-2.734708	24111.758366
HLA A*0216	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.470337	1.735543	-2.734794	29534.996233
HLA A*3001	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.249091	1.513906	-2.735185	17745.597065
HLA A*2902	1:207-215	9	LLSVALFFV	1.021557	0.165031	-3.922094	1.186588	-2.735506	8357.838838
HLA A*0201	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.249645	1.513906	-2.735739	17768.267939
HLA B*5301	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.488336	1.752306	-2.736031	30784.799146
HLA B*1509	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.416651	1.680196	-2.736455	26100.641859
HLA B*5101	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.390306	1.653369	-2.736937	24564.414224
HLA B*2705	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.202491	1.465037	-2.737454	15940.095925
HLA B*4002	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.514961	1.777358	-2.737602	32731.106593
HLA A*2501	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.444478	1.706509	-2.737969	27827.775297
HLA B*3801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.318330	1.580071	-2.738259	20812.772599
HLA B*4403	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.545199	1.806898	-2.738300	35091.227518
HLA A*2501	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.490702	1.752306	-2.738396	30952.964941
HLA B*5301	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.353448	1.615041	-2.738407	22565.641876
HLA A*2601	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.351859	1.613450	-2.738409	22483.268120
HLA A*0101	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.375096	1.636589	-2.738507	23718.971118
HLA B*5301	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.580131	1.841575	-2.738556	38030.383374
HLA A*2301	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.523482	1.784676	-2.738806	33379.687811
HLA A*0211	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.491414	1.752306	-2.739108	31003.744537
HLA B*5101	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.466470	1.727210	-2.739259	29273.164111
HLA A*3001	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-3.800156	1.060834	-2.739321	6311.836215
HLA B*0801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.445966	1.706509	-2.739456	27923.233749

HLA A*0101	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.379619	1.640132	-2.739486	23967.272015
HLA A*2601	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.392870	1.653369	-2.739501	24709.826745
HLA B*2705	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.309996	1.570424	-2.739572	20417.206245
HLA A*3002	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.526941	1.787206	-2.739735	33646.563378
HLA A*6801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.475525	1.735451	-2.740073	29889.908302
HLA B*1502	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.204695	1.464619	-2.740076	16021.189138
HLA B*7301	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.450465	1.709743	-2.740722	28214.020376
HLA B*0702	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.420960	1.680196	-2.740764	26360.894499
HLA A*2602	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.602495	1.861077	-2.741418	40040.127448
HLA B*0803	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.469308	1.727210	-2.742098	29465.094980
HLA A*1101	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.469700	1.727210	-2.742490	29491.727293
HLA A*0301	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.339102	1.596160	-2.742941	21832.412891
HLA A*2902	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.396352	1.653369	-2.742983	24908.732982
HLA A*0211	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.332571	0.589436	-2.743135	2150.654334
HLA A*2601	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.390889	1.647521	-2.743368	24597.393250
HLA B*4801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.397414	1.653369	-2.744045	24969.716086
HLA A*0202	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.529114	1.784676	-2.744438	33815.357726
HLA A*3002	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.359700	1.615041	-2.744659	22892.839899
HLA A*2601	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.392322	1.647630	-2.744692	24678.699527
HLA A*2601	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.384980	1.640132	-2.744848	24264.990727
HLA B*0801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.250815	1.505966	-2.744850	17816.202411
HLA B*3901	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.325200	1.580071	-2.745129	21144.617499
HLA B*3501	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.392759	1.647521	-2.745238	24703.544704
HLA B*4801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.392759	1.647521	-2.745238	24703.544704
HLA B*4001	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.392905	1.647630	-2.745275	24711.831987
HLA A*2403	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.259795	1.513906	-2.745889	18188.415627
HLA A*2402	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.533686	1.787206	-2.746481	34173.234276
HLA B*5101	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.317517	1.571013	-2.746504	20773.851239
HLA B*1503	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.453249	1.706509	-2.746740	28395.473524
HLA B*5701	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.394481	1.647630	-2.746851	24801.699831
HLA A*0201	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.400264	1.653369	-2.746894	25134.111051
HLA A*2403	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.181444	1.434003	-2.747441	15186.029666
HLA B*2705	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.401072	1.653369	-2.747703	25180.929230
HLA A*2501	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.428004	1.680196	-2.747808	26791.923781
HLA A*3301	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.609025	1.861077	-2.747948	40646.641774
HLA A*0211	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.535514	1.787206	-2.748308	34317.368900
HLA A*6801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.458364	1.709743	-2.748621	28731.873405
HLA A*0201	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.396394	1.647521	-2.748873	24911.158662
HLA B*4801	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.396655	1.647630	-2.749024	24926.122248
HLA B*4403	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.546239	1.797109	-2.749131	35175.427338
HLA B*1502	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.137622	1.388176	-2.749446	13728.454532
HLA B*3901	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.402853	1.653369	-2.749484	25284.400572
HLA B*7301	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.577422	1.827925	-2.749496	37793.903273
HLA A*0201	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.397364	1.647630	-2.749734	24966.879496
HLA A*3101	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.263676	1.513906	-2.749770	18351.696532
HLA B*1503	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.189071	1.439287	-2.749784	15455.059175
HLA B*1509	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.397512	1.647630	-2.749882	24975.390233
HLA B*5301	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.527756	1.777358	-2.750398	33709.785090
HLA B*7301	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.508594	1.757178	-2.751416	32254.742869
HLA A*0101	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.399096	1.647630	-2.751465	25066.623361
HLA B*1501	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.388225	1.636589	-2.751636	24446.954738
HLA B*2705	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.332091	1.580071	-2.752020	21482.799382
HLA A*0216	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.902499	1.150365	-2.752134	7989.126311
HLA A*3101	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.330113	1.577736	-2.752377	21385.165047
HLA B*7301	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.537140	1.784644	-2.752495	34446.081664
HLA A*2501	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.488071	1.735543	-2.752528	30765.985612

HLA A*6802	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.400303	1.647521	-2.752782	25136.422694
HLA A*0203	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.366278	1.613450	-2.752828	23242.253253
HLA B*1801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.460117	1.707126	-2.752991	28848.063148
HLA A*0216	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.400541	1.647521	-2.753020	25150.160959
HLA B*0803	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.333136	1.580071	-2.753066	21534.579390
HLA A*0206	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.366689	1.613450	-2.753239	23264.267825
HLA B*0802	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.400809	1.647521	-2.753287	25165.676535
HLA A*2402	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.538122	1.784676	-2.753445	34524.063887
HLA B*5701	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.366983	1.613450	-2.753533	23280.005284
HLA A*2902	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.331532	1.577736	-2.753796	21455.156926
HLA A*2602	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.538627	1.784676	-2.753951	34564.243091
HLA A*2902	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.334046	1.580071	-2.753975	21579.711998
HLA A*0206	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.476899	1.722434	-2.754465	29984.653285
HLA B*4601	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.369732	1.615041	-2.754691	23427.825039
HLA B*4601	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.408139	1.653369	-2.754770	25594.049369
HLA B*4801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.391958	1.636589	-2.755369	24658.014301
HLA A*0101	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.408818	1.653369	-2.755449	25634.095887
HLA A*0201	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.395757	1.640132	-2.755625	24874.663671
HLA B*0803	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.403612	1.647630	-2.755981	25328.621011
HLA B*4801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.221202	1.465037	-2.756165	16641.873985
HLA B*5401	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.543418	1.787206	-2.756212	34947.623701
HLA A*0202	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.938240	1.181941	-2.756299	8674.404168
HLA B*5401	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.563337	1.806898	-2.756438	36587.824281
HLA B*5401	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.534057	1.777358	-2.756699	34202.456762
HLA B*4402	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.393314	1.636589	-2.756725	24735.104698
HLA B*2705	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.484039	1.727210	-2.756829	30481.695219
HLA A*0250	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.509188	1.752306	-2.756882	32298.920224
HLA B*4501	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.584816	1.827925	-2.756890	38442.849954
HLA A*2603	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.541714	1.784676	-2.757038	34810.821649
HLA B*4601	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.337394	1.580071	-2.757323	21746.714877
HLA B*1501	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.405202	1.647630	-2.757572	25421.557042
HLA B*3801	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.493235	1.735451	-2.757784	31134.005703
HLA B*4601	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.335758	1.577736	-2.758022	21664.986307
HLA A*0201	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.394770	1.636589	-2.758182	24818.208780
HLA A*6801	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.583448	1.824948	-2.758500	38322.000858
HLA B*4002	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.565604	1.806898	-2.758705	36779.332044
HLA B*5401	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.555851	1.797109	-2.758743	35962.603552
HLA A*3002	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.164176	1.405388	-2.758788	14594.039897
HLA A*1101	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.223890	1.465037	-2.758853	16745.188471
HLA B*4402	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.412293	1.653369	-2.758924	25840.022818
HLA B*1501	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.399072	1.640132	-2.758940	25065.267321
HLA B*5801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.940899	1.181941	-2.758958	8727.689163
HLA A*3201	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.600630	1.841575	-2.759055	39868.505864
HLA A*1101	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.412932	1.653369	-2.759563	25878.074138
HLA A*0211	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.150736	1.391116	-2.759621	14149.349527
HLA B*3801	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.407415	1.647630	-2.759785	25551.438900
HLA B*1502	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.566793	1.806898	-2.759894	36880.149858
HLA B*4601	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.407709	1.647630	-2.760079	25568.723550
HLA B*0801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.407643	1.647521	-2.760122	25564.850773
HLA B*3801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.396869	1.636589	-2.760280	24938.396397
HLA A*0211	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.482763	1.722434	-2.760329	30392.284501
HLA A*3301	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.574125	1.813629	-2.760496	37508.130623
HLA A*1101	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.467698	1.707126	-2.760573	29356.106064
HLA A*2603	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.557750	1.797109	-2.760641	36120.147016
HLA B*4001	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.397240	1.636589	-2.760651	24959.721915

HLA B*4001	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.338780	1.577736	-2.761044	21816.237688
HLA B*2705	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.200367	1.439287	-2.761080	15862.330564
HLA A*2501	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.488677	1.727210	-2.761467	30808.957261
HLA B*1502	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.603172	1.841575	-2.761597	40102.560516
HLA A*3301	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.398309	1.636589	-2.761720	25021.235937
HLA B*4501	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.471467	1.709743	-2.761724	29611.951002
HLA B*5701	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.415347	1.653369	-2.761978	26022.392513
HLA A*6802	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.912400	1.150365	-2.762035	8173.348507
HLA B*1501	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.201824	1.439287	-2.762537	15915.624230
HLA B*4601	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.402792	1.640132	-2.762659	25280.844391
HLA A*0211	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-3.925449	1.162375	-2.763074	8422.655875
HLA A*6802	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.343267	1.580071	-2.763197	22042.831100
HLA B*4601	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.399928	1.636589	-2.763339	25114.674467
HLA B*4403	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.591352	1.827925	-2.763426	39025.802630
HLA B*5701	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.400104	1.636589	-2.763515	25124.866605
HLA B*4403	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.499135	1.735451	-2.763683	31559.822900
HLA A*6901	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.287368	1.523182	-2.764187	19380.653891
HLA A*6801	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.577943	1.813629	-2.764314	37839.320844
HLA A*3001	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.289318	1.525000	-2.764318	19467.872726
HLA B*5101	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.499905	1.735543	-2.764363	31615.873742
HLA B*5301	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.549148	1.784644	-2.764504	35411.803424
HLA B*4501	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.578143	1.813629	-2.764514	37856.724901
HLA A*8001	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.412366	1.647521	-2.764845	25844.356723
HLA A*0212	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.412793	1.647630	-2.765163	25869.815603
HLA A*3101	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.136005	1.370628	-2.765378	13677.452147
HLA B*4801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.405573	1.640132	-2.765441	25443.295725
HLA B*4002	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.380721	1.615041	-2.765679	24028.159899
HLA B*0702	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.405938	1.640132	-2.765805	25464.639711
HLA B*4001	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.405938	1.640132	-2.765805	25464.639711
HLA A*0202	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.488531	1.722434	-2.766097	30798.625265
HLA B*0801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.406269	1.640132	-2.766137	25484.071405
HLA A*0250	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.493599	1.727210	-2.766389	31160.123538
HLA A*0212	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.414017	1.647521	-2.766496	25942.833885
HLA A*2403	1:84-92	9	RFISGASAP	0.656730	0.314634	-3.737885	0.971364	-2.766521	5468.710964
HLA B*0702	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.414196	1.647630	-2.766566	25953.502515
HLA B*3801	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.476401	1.709743	-2.766658	29950.283704
HLA A*0250	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.553941	1.787206	-2.766735	35804.778726
HLA A*2403	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-2.951517	0.184583	-2.766934	894.369621
HLA B*4501	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.573933	1.806898	-2.767034	37491.495297
HLA B*4002	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.608764	1.841575	-2.767189	40622.240886
HLA A*0203	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.172925	1.405388	-2.767537	14891.039352
HLA B*3901	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.232856	1.465037	-2.767819	17094.471352
HLA A*3002	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.475586	1.707126	-2.768460	29894.112826
HLA B*5101	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.490895	1.722434	-2.768461	30966.699060
HLA A*0250	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.159603	1.391116	-2.768488	14441.204944
HLA B*4001	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.364655	1.596160	-2.768494	23155.530482
HLA A*0203	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.005426	1.236873	-2.768553	10125.710968
HLA A*0250	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.058543	1.289989	-2.768553	11443.073395
HLA A*6901	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.364784	1.596160	-2.768623	23162.421294
HLA A*0203	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.416296	1.647630	-2.768666	26079.329127
HLA A*0212	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-3.811537	1.042623	-2.768913	6479.427372
HLA A*0206	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.556276	1.787206	-2.769071	35997.835018
HLA A*2601	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.384214	1.615041	-2.769173	24222.234124
HLA A*2402	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.476483	1.707126	-2.769358	29955.955211

HLA B*4501	1:200-208	9	STLKVSLLL	1.428092	0.413469	-4.611365	1.841561	-2.769804	40866.247138
HLA B*4801	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.383505	1.613450	-2.770054	24182.692475
HLA B*0801	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.383620	1.613450	-2.770169	24189.103783
HLA A*2301	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.450521	1.680196	-2.770326	28217.683847
HLA B*0802	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.384163	1.613450	-2.770712	24219.351425
HLA A*0203	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.418427	1.647521	-2.770906	26207.608844
HLA A*0203	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.407655	1.636589	-2.771066	25565.542297
HLA A*2301	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.478485	1.707126	-2.771359	30094.347661
HLA B*1503	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.018273	1.246696	-2.771577	10429.716666
HLA B*3801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.478257	1.706509	-2.771748	30078.559516
HLA A*0201	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.385206	1.613450	-2.771755	24277.596007
HLA B*0801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.408383	1.636589	-2.771795	25608.453362
HLA B*3901	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.018808	1.246696	-2.772112	10442.589187
HLA B*4402	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.412638	1.640132	-2.772506	25860.580365
HLA B*1509	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.143270	1.370628	-2.772642	13908.164273
HLA B*0801	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.420533	1.647630	-2.772902	26334.952340
HLA B*1801	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.509042	1.735543	-2.773500	32288.088559
HLA A*3002	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.483821	1.709743	-2.774078	30466.363135
HLA A*2403	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.387917	1.613450	-2.774467	24429.635430
HLA B*3501	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.771938	0.997451	-2.774487	5914.777416
HLA A*2403	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.427962	1.653369	-2.774593	26789.314964
HLA B*1501	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.427971	1.653369	-2.774602	26789.894679
HLA B*0702	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.411384	1.636589	-2.774795	25785.980038
HLA A*0212	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.428742	1.653369	-2.775373	26837.474039
HLA B*5401	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.560085	1.784644	-2.775441	36314.903747
HLA A*0212	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.412107	1.636589	-2.775519	25828.981637
HLA B*1502	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.346077	1.570424	-2.775653	22185.915626
HLA A*3002	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.511563	1.735543	-2.776021	32476.059853
HLA B*5701	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.356185	1.580071	-2.776114	22708.311421
HLA A*0203	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.299325	1.523182	-2.776143	19921.633907
HLA B*4801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.391197	1.615041	-2.776156	24614.831490
HLA B*7301	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.583364	1.806898	-2.776465	38314.538145
HLA A*3301	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.529147	1.752306	-2.776841	33817.918946
HLA B*0802	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.357054	1.580071	-2.776983	22753.811239
HLA A*0203	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.654568	0.877206	-2.777361	4514.062140
HLA B*5801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.373522	1.596160	-2.777361	23633.154346
HLA A*0101	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.392778	1.615041	-2.777737	24704.613875
HLA A*6802	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.303023	1.525000	-2.778023	20091.994210
HLA B*1517	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-3.919406	1.141236	-2.778170	8306.272633
HLA A*3002	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.415500	1.636589	-2.778911	26031.544709
HLA A*2601	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.375159	1.596160	-2.778999	23722.435930
HLA A*0219	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.426594	1.647521	-2.779073	26705.099967
HLA A*3001	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-3.399587	0.620011	-2.779576	2509.500716
HLA A*0101	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.359721	1.580071	-2.779650	22893.954556
HLA A*3002	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.486198	1.706509	-2.779689	30633.618045
HLA A*3301	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.604699	1.824948	-2.779751	40243.826511
HLA B*4002	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.460074	1.680196	-2.779879	28845.254118
HLA B*1801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.427511	1.647521	-2.779989	26761.503384
HLA A*0219	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.416672	1.636589	-2.780084	26101.912704
HLA A*0212	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.357884	1.577736	-2.780148	22797.305501
HLA B*5701	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.420298	1.640132	-2.780165	26320.709276
HLA A*8001	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.219811	1.439287	-2.780524	16588.661072
HLA B*0803	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.461148	1.680196	-2.780952	28916.657027
HLA B*7301	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.558323	1.777358	-2.780964	36167.857560
HLA A*2501	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.488153	1.707126	-2.781027	30771.811583
HLA A*8001	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.417915	1.636589	-2.781327	26176.718967

HLA A*2602	1:228-236	9	GGMGVWAKL	1.542096	0.271533	-4.595137	1.813629	-2.781508	39367.411890
HLA B*5301	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.352602	1.571013	-2.781589	22521.736700
HLA B*4501	1:236-244	9	LNSNVGDLL	1.466792	0.394285	-4.642735	1.861077	-2.781658	43927.357726
HLA A*0202	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.569001	1.787206	-2.781796	37068.174003
HLA B*1509	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.295758	1.513906	-2.781852	19758.703158
HLA B*1801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.504341	1.722434	-2.781907	31940.448951
HLA B*5701	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.221282	1.439287	-2.781995	16644.935310
HLA A*8001	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.397071	1.615041	-2.782029	24950.001697
HLA B*5101	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.176900	1.394704	-2.782196	15027.970710
HLA A*2403	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.422492	1.640132	-2.782360	26454.040081
HLA A*1101	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.296473	0.514013	-2.782460	1979.124550
HLA A*2601	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.353551	1.571013	-2.782538	22571.013930
HLA B*0802	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.435978	1.653369	-2.782609	27288.398661
HLA B*4001	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.396225	1.613450	-2.782774	24901.457356
HLA A*0202	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.579915	1.797109	-2.782806	38011.459989
HLA A*2902	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.430461	1.647630	-2.782831	26943.962188
HLA B*0802	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.419527	1.636589	-2.782938	26274.046074
HLA B*2705	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.430471	1.647521	-2.782950	26944.545250
HLA A*0101	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.354023	1.571013	-2.783010	22595.570723
HLA A*0203	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.248024	1.464619	-2.783405	17702.065768
HLA A*2403	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.420098	1.636589	-2.783509	26308.608728
HLA A*2902	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.420638	1.636589	-2.784050	26341.364233
HLA A*2603	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.625816	1.841575	-2.784242	42249.000516
HLA A*6802	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.307847	1.523182	-2.784665	20316.389811
HLA B*1801	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.398140	1.613450	-2.784689	25011.491763
HLA A*2902	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.398248	1.613450	-2.784797	25017.716770
HLA A*0206	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-3.966828	1.181941	-2.784887	9264.632288
HLA A*0203	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.438281	1.653369	-2.784911	27433.457517
HLA A*6802	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.399984	1.615041	-2.784943	25117.935501
HLA A*0101	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.362963	1.577736	-2.785227	23065.512338
HLA B*4001	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.299172	1.513906	-2.785266	19914.629839
HLA B*4501	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.520729	1.735451	-2.785277	33168.717095
HLA B*5801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.356039	1.570424	-2.785615	22700.696032
HLA A*0203	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.425798	1.640132	-2.785665	26656.168967
HLA A*2603	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.592569	1.806898	-2.785670	39135.318896
HLA A*0216	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.439093	1.653369	-2.785724	27484.856147
HLA B*4402	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.433377	1.647521	-2.785856	27125.463713
HLA B*1509	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.426075	1.640132	-2.785943	26673.190816
HLA B*4002	1:246-254	9	NASGSSAEL	1.312746	0.515179	-4.614295	1.827925	-2.786369	41142.868238
HLA A*0212	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.399977	1.613450	-2.786527	25117.527848
HLA A*8001	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.364408	1.577736	-2.786672	23142.380988
HLA A*2602	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.583866	1.797109	-2.786758	38358.921196
HLA B*4001	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.357992	1.571013	-2.786978	22802.979428
HLA A*0206	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-3.949400	1.162375	-2.787025	8900.198795
HLA A*2301	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.523217	1.735543	-2.787674	33359.288461
HLA B*1501	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.182534	1.394704	-2.787830	15224.197348
HLA A*2301	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.515073	1.727210	-2.787863	32739.607137
HLA A*0250	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.585133	1.797109	-2.788024	38470.936369
HLA A*3201	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.401718	1.613450	-2.788267	25218.419270
HLA A*0206	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.523926	1.735543	-2.788384	33413.834963
HLA B*1503	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-3.976062	1.187527	-2.788535	9463.715217
HLA B*0802	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.429122	1.640132	-2.788990	26861.004765
HLA B*1801	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.495723	1.706509	-2.789214	31312.886604
HLA A*2603	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.511770	1.722434	-2.789336	32491.524420
HLA B*0702	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.385509	1.596160	-2.789348	24294.544665

HLA B*4501	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.631387	1.841575	-2.789812	42794.412468
HLA B*4001	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.370103	1.580071	-2.790032	23447.858825
HLA A*2902	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.430292	1.640132	-2.790160	26933.469235
HLA B*0803	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.437862	1.647521	-2.790341	27407.052903
HLA B*5101	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.497290	1.706509	-2.790781	31426.080001
HLA A*6802	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.430917	1.640132	-2.790785	26972.255219
HLA B*0801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.059567	1.268587	-2.790980	11470.096163
HLA A*1101	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.438680	1.647630	-2.791050	27458.699157
HLA A*2602	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.526595	1.735543	-2.791053	33619.816461
HLA A*6802	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.439310	1.647630	-2.791679	27498.539034
HLA A*2603	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.428272	1.636589	-2.791683	26808.452190
HLA B*5701	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.406809	1.615041	-2.791768	25515.800321
HLA A*0212	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.431986	1.640132	-2.791854	27038.729193
HLA A*6802	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.445289	1.653369	-2.791920	27879.761883
HLA A*0216	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.789409	0.997451	-2.791958	6157.567431
HLA B*4403	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.527927	1.735543	-2.792385	33723.100452
HLA B*7301	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.617405	1.824948	-2.792457	41438.619906
HLA B*0702	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.061263	1.268587	-2.792676	11514.985279
HLA B*4402	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.372777	1.580071	-2.792706	23592.659759
HLA A*0202	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.406861	1.613450	-2.793410	25518.837330
HLA B*4403	1:187-195	9	VRASMQIRR	1.136874	0.704701	-4.635019	1.841575	-2.793444	43153.832552
HLA A*6802	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.430048	1.636589	-2.793459	26918.319960
HLA A*2601	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.181872	1.388176	-2.793696	15200.989191
HLA B*1801	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.364814	1.571013	-2.793801	23164.050331
HLA B*1509	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.373949	1.580071	-2.793878	23656.435005
HLA A*0211	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.529718	1.735543	-2.794175	33862.405320
HLA B*5401	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.516866	1.722434	-2.794432	32875.027197
HLA B*1801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.521753	1.727210	-2.794543	33247.044875
HLA B*4402	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.365035	1.570424	-2.794611	23175.832932
HLA A*8001	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.408177	1.613450	-2.794726	25596.264841
HLA A*2601	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.375030	1.580071	-2.794959	23715.378514
HLA B*0803	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.435106	1.640132	-2.794974	27233.683892
HLA A*2902	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.990657	1.195068	-2.795589	9787.159451
HLA A*3201	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-3.735319	0.939568	-2.795751	5436.499254
HLA B*1509	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.321311	1.525000	-2.796311	20956.146971
HLA B*5301	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.581141	1.784676	-2.796465	38118.954622
HLA B*5801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.155938	1.359429	-2.796509	14319.842284
HLA A*2601	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.375148	1.577736	-2.797412	23721.794260
HLA B*1509	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.450886	1.653369	-2.797516	28241.355225
HLA A*3101	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.057142	1.259401	-2.797741	11406.236980
HLA B*4001	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.320964	1.523182	-2.797782	20939.374862
HLA A*2501	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.445808	1.647521	-2.798287	27913.114456
HLA B*3501	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.434881	1.636589	-2.798292	27219.543768
HLA A*3301	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.605322	1.806898	-2.798423	40301.562266
HLA A*2403	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.446384	1.647630	-2.798754	27950.135664
HLA B*1517	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.452377	1.653369	-2.799008	28338.539007
HLA A*0101	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.187360	1.388176	-2.799184	15394.310686
HLA A*2602	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.521666	1.722434	-2.799232	33240.390616
HLA A*2602	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.158946	1.359429	-2.799516	14419.346414
HLA B*1501	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.158978	1.359429	-2.799549	14420.438554
HLA B*5301	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.313513	1.513906	-2.799607	20583.228480
HLA A*3101	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.233617	1.434003	-2.799614	17124.460887
HLA B*0803	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.436338	1.636589	-2.799749	27310.994975
HLA B*4801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.395952	1.596160	-2.799792	24885.835420
HLA A*2602	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.535277	1.735451	-2.799825	34298.623052
HLA A*2603	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.535584	1.735543	-2.800042	34322.938946

HLA B*4002	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.625537	1.824948	-2.800589	42221.810342
HLA A*3001	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.160022	1.359429	-2.800592	14455.117948
HLA A*2501	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.995666	1.195068	-2.800598	9900.696914
HLA B*3801	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.523097	1.722434	-2.800663	33350.085758
HLA A*0206	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.324079	1.523182	-2.800898	21090.123793
HLA A*2603	1:212-220	9	LFFVWMITV	1.409538	0.325913	-4.536621	1.735451	-2.801169	34404.923038
HLA B*4601	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.397345	1.596160	-2.801185	24965.798975
HLA B*0803	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.416306	1.615041	-2.801265	26079.893478
HLA A*8001	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.441405	1.640132	-2.801273	27631.557254
HLA A*0216	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.438163	1.636589	-2.801574	27426.037923
HLA A*3002	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.482150	1.680196	-2.801954	30349.401453
HLA B*0803	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.455350	1.653369	-2.801980	28533.139190
HLA A*0206	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.508709	1.706509	-2.802199	32263.294237
HLA A*2601	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-3.997273	1.195068	-2.802205	9937.400966
HLA B*3801	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.449762	1.647521	-2.802241	28168.419485
HLA A*2402	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.449824	1.647521	-2.802302	28172.381853
HLA B*5301	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.599573	1.797109	-2.802464	39771.566021
HLA A*1101	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-3.554508	0.751562	-2.802946	3585.152766
HLA B*0802	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.380765	1.577736	-2.803029	24030.629830
HLA A*6901	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.490169	0.687090	-2.803080	3091.500839
HLA B*2705	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.326285	1.523182	-2.803104	21197.531795
HLA A*8001	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.374518	1.571013	-2.803505	23687.426130
HLA B*5701	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.317566	1.513906	-2.803660	20776.211442
HLA A*0201	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.400564	1.596160	-2.804404	25151.521591
HLA B*1502	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.210066	1.405388	-2.804678	16220.553519
HLA B*0802	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.452314	1.647630	-2.804684	28334.399984
HLA B*0802	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.329720	1.525000	-2.804720	21365.853313
HLA A*2301	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.511681	1.706509	-2.805171	32484.845636
HLA A*6901	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.375791	1.570424	-2.805367	23756.983379
HLA B*4402	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.419292	1.613450	-2.805842	26259.835950
HLA A*0212	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.270506	1.464619	-2.805888	18642.586717
HLA B*1509	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.453503	1.647521	-2.805982	28412.068938
HLA A*0219	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.459529	1.653369	-2.806160	28809.073314
HLA B*3901	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.419673	1.613450	-2.806222	26282.860212
HLA A*8001	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.459614	1.653369	-2.806245	28814.684601
HLA B*3501	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.421597	1.615041	-2.806556	26399.570022
HLA A*2902	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.197698	1.391116	-2.806582	15765.145423
HLA B*0801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.330059	1.523182	-2.806877	21382.504311
HLA A*0301	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.312926	1.505966	-2.806960	20555.409051
HLA B*1502	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.443722	1.636589	-2.807133	27779.341947
HLA B*5401	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.487352	1.680196	-2.807156	30715.096930
HLA A*2301	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.387818	1.580071	-2.807747	24424.085273
HLA A*3001	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.198971	1.391116	-2.807856	15811.439188
HLA B*1501	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.331496	1.523182	-2.808315	21453.415946
HLA A*3201	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.595658	1.787206	-2.808453	39414.720373
HLA B*3901	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.456158	1.647521	-2.808637	28586.288856
HLA A*3001	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.045602	1.236873	-2.808729	11107.126550
HLA B*2705	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.422560	1.613450	-2.809110	26458.190696
HLA B*5401	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.561431	1.752306	-2.809125	36427.649759
HLA A*3201	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.594014	1.784676	-2.809337	39265.742149
HLA A*2601	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.379912	1.570424	-2.809488	23983.485032
HLA A*1101	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.380772	1.571013	-2.809759	24031.019842
HLA B*4501	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.425516	1.615041	-2.810475	26638.869752
HLA A*0101	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.406823	1.596160	-2.810663	25516.628560
HLA A*0211	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.324645	1.513906	-2.810739	21117.638677
HLA A*0219	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.458526	1.647630	-2.810896	28742.600509

HLA B*0802	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.382053	1.571013	-2.811039	24101.977205
HLA B*1502	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.518600	1.707126	-2.811474	33006.543048
HLA B*1509	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.425307	1.613450	-2.811856	26626.046753
HLA A*8001	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.459492	1.647630	-2.811861	28806.579760
HLA B*3501	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.392252	1.580071	-2.812181	24674.694581
HLA A*0202	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.246396	1.434003	-2.812393	17635.824031
HLA A*1101	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.452603	1.640132	-2.812471	28353.260432
HLA A*6802	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.246706	1.434003	-2.812703	17648.422366
HLA B*1501	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.278062	1.465037	-2.813025	18969.772201
HLA B*1502	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.540488	1.727210	-2.813278	34712.655880
HLA B*0801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.410082	1.596160	-2.813922	25708.813125
HLA A*0211	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.278605	1.464619	-2.813986	18993.493248
HLA A*2902	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.410568	1.596160	-2.814408	25737.619190
HLA A*2601	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.320583	1.505966	-2.814617	20921.031590
HLA B*1517	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.451214	1.636589	-2.814626	28262.752891
HLA B*0803	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.328750	1.513906	-2.814844	21318.169214
HLA B*5301	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.602068	1.787206	-2.814862	40000.723348
HLA A*3201	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.522352	1.707126	-2.815227	33292.941546
HLA A*0201	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-3.965785	1.150365	-2.815420	9242.405432
HLA B*5801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.338646	1.523182	-2.815464	21809.511389
HLA B*3801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.495690	1.680196	-2.815494	31310.515104
HLA B*3901	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.175735	1.360016	-2.815719	14987.700134
HLA B*1503	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.469099	1.653369	-2.815730	29450.911537
HLA B*0702	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.430903	1.615041	-2.815862	26971.379732
HLA A*0202	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.551453	1.735543	-2.815910	35600.237026
HLA A*0250	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.538773	1.722434	-2.816338	34575.838337
HLA A*6901	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.665460	0.848433	-2.817027	4628.707588
HLA B*1509	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.394921	1.577736	-2.817185	24826.803148
HLA A*2902	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.218632	1.401173	-2.817459	16543.671296
HLA A*2602	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.323494	1.505966	-2.817528	21061.733207
HLA A*2402	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.397616	1.580071	-2.817545	24981.335961
HLA A*1101	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.397879	1.580071	-2.817808	24996.476928
HLA A*0216	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.331854	1.513906	-2.817948	21471.064413
HLA A*1101	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.433004	1.615041	-2.817962	27102.141171
HLA A*2402	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.252173	1.434003	-2.818170	17871.999369
HLA A*0211	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.466308	1.647521	-2.818786	29262.238995
HLA B*0803	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.432341	1.613450	-2.818891	27060.825972
HLA A*2402	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.499118	1.680196	-2.818922	31558.627777
HLA B*0801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.207364	1.388176	-2.819188	16119.952676
HLA B*1517	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.178648	1.359429	-2.819219	15088.579546
HLA B*4501	1:258-266	9	GTIFGGAFL	1.394877	0.382481	-4.596692	1.777358	-2.819334	39508.653003
HLA B*1801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.434394	1.615041	-2.819353	27189.079103
HLA A*2501	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.434413	1.615041	-2.819372	27190.255848
HLA A*6802	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-3.415625	0.595896	-2.819729	2603.903639
HLA A*2301	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.542276	1.722434	-2.819841	34855.859881
HLA A*2403	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.284887	1.464619	-2.820269	19270.250917
HLA B*7301	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.607906	1.787206	-2.820701	40542.106965
HLA B*1501	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.416919	1.596160	-2.820759	26116.743804
HLA B*0702	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.209314	1.388176	-2.821138	16192.497364
HLA A*1101	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.024644	1.203170	-2.821475	10583.865541
HLA A*0250	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.528061	1.706509	-2.821552	33733.501035
HLA A*2402	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.557110	1.735543	-2.821568	36067.035673
HLA B*4002	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.606217	1.784644	-2.821573	40384.716215
HLA A*6901	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.213346	1.391116	-2.822230	16343.518211
HLA B*1801	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.458864	1.636589	-2.822276	28765.000409
HLA B*3501	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.419160	1.596160	-2.823000	26251.881638

HLA B*5401	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.558687	1.735543	-2.823144	36198.198215
HLA A*2501	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.403327	1.580071	-2.823256	25312.046407
HLA B*4501	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.559023	1.735543	-2.823480	36226.212488
HLA A*0201	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.394254	1.570424	-2.823830	24788.688323
HLA A*3301	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.533585	1.709743	-2.823842	34165.285644
HLA B*4501	1:176-184	9	VQLSARRSR	1.028225	0.768884	-4.621063	1.797109	-2.823955	41789.139758
HLA A*0212	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.007094	1.182783	-2.824311	10164.678829
HLA A*0219	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.437928	1.613450	-2.824478	27411.204753
HLA B*0802	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.439737	1.615041	-2.824696	27525.627424
HLA B*4801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.350224	1.525000	-2.825224	22398.771433
HLA A*0101	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.396056	1.570424	-2.825632	24891.759828
HLA A*1101	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.462323	1.636589	-2.825734	28994.980864
HLA A*3001	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.220554	1.394704	-2.825849	16617.044056
HLA A*0216	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.473673	1.647630	-2.826043	29762.759054
HLA A*0216	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.466216	1.640132	-2.826084	29256.065733
HLA A*6901	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.260152	1.434003	-2.826149	18203.378169
HLA A*3301	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.291454	1.465037	-2.826417	19563.843507
HLA B*4403	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.611661	1.784644	-2.827016	40894.112949
HLA B*1517	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.474688	1.647630	-2.827058	29832.398112
HLA B*4801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.221907	1.394704	-2.827203	16668.905123
HLA B*5701	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.423434	1.596160	-2.827274	26511.490858
HLA B*5801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.352625	1.525000	-2.827625	22522.955134
HLA A*0202	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.010773	1.182783	-2.827990	10251.158640
HLA B*7301	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.612850	1.784676	-2.828173	41006.210011
HLA A*2603	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.580485	1.752306	-2.828180	38061.462831
HLA A*3002	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.468352	1.640132	-2.828219	29400.289372
HLA B*1503	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-3.673514	0.844974	-2.828540	4715.348330
HLA A*2902	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.342762	1.513906	-2.828856	22017.207411
HLA B*3501	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.334870	1.505966	-2.828905	21620.728019
HLA B*1509	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.097821	1.268587	-2.829234	12526.258613
HLA A*2402	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.551930	1.722434	-2.829495	35639.354949
HLA B*4801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.294316	1.464619	-2.829697	19693.180112
HLA A*2501	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.483099	1.653369	-2.829730	30415.805499
HLA A*2403	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.140958	1.311098	-2.829859	13834.323227
HLA A*2602	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.354893	1.525000	-2.829892	22640.844646
HLA A*0219	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.470715	1.640132	-2.830583	29560.732189
HLA A*2301	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.408698	1.577736	-2.830962	25627.024304
HLA B*3501	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.478757	1.647630	-2.831127	30113.239210
HLA A*3201	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.013931	1.182783	-2.831148	10325.965323
HLA A*2402	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.558595	1.727210	-2.831385	36190.561719
HLA A*0216	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.445092	1.613450	-2.831641	27867.095342
HLA B*4601	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.402693	1.570424	-2.832269	25275.100848
HLA B*3501	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.472482	1.640132	-2.832350	29681.237198
HLA B*4501	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.657842	1.824948	-2.832894	45482.284386
HLA A*6801	1:121-129	9	AYASELPDL	1.278221	0.528677	-4.640017	1.806898	-2.833118	43653.264478
HLA A*2501	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.469947	1.636589	-2.833358	29508.484484
HLA A*3301	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.618033	1.784644	-2.833388	41498.518772
HLA B*5401	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.540544	1.707126	-2.833419	34717.163172
HLA A*0216	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.070304	1.236873	-2.833432	11757.208106
HLA B*0702	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.403912	1.570424	-2.833488	25346.166289
HLA B*5101	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.481523	1.647521	-2.834002	30305.595197
HLA A*3201	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.514265	1.680196	-2.834069	32678.735326
HLA B*4403	1:2-10	9	TAPNEPGAL	1.381123	0.443825	-4.659076	1.824948	-2.834128	45611.646417
HLA B*4402	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.405418	1.571013	-2.834405	25434.212750
HLA A*2602	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.481953	1.647521	-2.834432	30335.612887
HLA A*2501	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.348349	1.513906	-2.834443	22302.282312

HLA B*4801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.274279	1.439287	-2.834992	18805.264439
HLA A*0212	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.405637	1.570424	-2.835213	25447.012422
HLA B*0802	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.431601	1.596160	-2.835440	27014.750481
HLA A*8001	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.358654	1.523182	-2.835473	22837.793947
HLA A*2602	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.543039	1.707126	-2.835914	34917.197848
HLA A*2602	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.589056	1.752306	-2.836751	38820.077401
HLA B*3801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.476988	1.640132	-2.836856	29990.818037
HLA B*4403	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.594124	1.757178	-2.836947	39275.727314
HLA B*5401	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.564366	1.727210	-2.837155	36674.623077
HLA A*0250	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-3.880043	1.042623	-2.837419	7586.525290
HLA B*4601	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.351406	1.513906	-2.837500	22459.805397
HLA A*0203	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.127538	1.289989	-2.837548	13413.362450
HLA B*5301	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.490949	1.653369	-2.837580	30970.552407
HLA B*1509	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.408881	1.571013	-2.837868	25637.840456
HLA A*2603	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.418357	1.580071	-2.838286	26203.355782
HLA A*0203	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.434484	1.596160	-2.838323	27194.669094
HLA B*1801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.233723	1.394704	-2.839018	17128.630259
HLA A*2603	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.566335	1.727210	-2.839124	36841.264455
HLA A*3201	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.782953	0.943496	-2.839457	6066.703802
HLA B*0801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-3.997325	1.157848	-2.839476	9938.583761
HLA B*3901	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.454654	1.615041	-2.839613	28487.484862
HLA A*0211	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.453157	1.613450	-2.839707	28389.483117
HLA A*2402	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.546286	1.706509	-2.839777	35179.233448
HLA B*1517	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.345748	1.505966	-2.839783	22169.118719
HLA B*4402	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.436448	1.596160	-2.840287	27317.940082
HLA A*2603	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.346373	1.505966	-2.840408	22201.043723
HLA A*3201	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.228885	1.388176	-2.840709	16938.893797
HLA B*5401	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.306094	1.465037	-2.841057	20234.562615
HLA A*0301	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.364582	1.523182	-2.841400	23151.647473
HLA B*4001	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.280736	1.439287	-2.841449	19086.918962
HLA A*1101	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.419405	1.577736	-2.841669	26266.655850
HLA A*0203	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.412161	1.570424	-2.841737	25832.195671
HLA A*3002	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.568964	1.727210	-2.841753	37064.965586
HLA A*6901	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.306423	1.464619	-2.841804	20249.893764
HLA B*2705	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.438365	1.596160	-2.842205	27438.800868
HLA B*4001	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.412899	1.570424	-2.842475	25876.114247
HLA A*0250	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.578075	1.735543	-2.842532	37850.786147
HLA B*0803	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.420455	1.577736	-2.842719	26330.251277
HLA A*0202	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.549261	1.706509	-2.842751	35421.000166
HLA A*0301	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.368031	1.525000	-2.843031	23336.243346
HLA A*0201	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.366560	1.523182	-2.843379	23257.346714
HLA A*0201	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.080318	1.236873	-2.843445	12031.442794
HLA B*1517	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.483600	1.640132	-2.843467	30450.874027
HLA B*4402	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.421308	1.577736	-2.843572	26382.009159
HLA A*0219	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.238335	1.394704	-2.843630	17311.498952
HLA A*0250	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.421540	1.577736	-2.843805	26396.142594
HLA A*3301	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.046988	1.203170	-2.843818	11142.635300
HLA A*0216	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.309322	1.464619	-2.844704	20385.530308
HLA A*0201	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.245935	1.401173	-2.844763	17617.134003
HLA B*0801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.309519	1.464619	-2.844901	20394.796223
HLA B*3801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.369948	1.525000	-2.844948	23439.488199
HLA B*4601	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.350945	1.505966	-2.844980	22436.003027
HLA B*0702	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.358957	1.513906	-2.845051	22853.737451
HLA A*0301	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.359009	1.513906	-2.845103	22856.457609
HLA A*2501	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.422992	1.577736	-2.845257	26484.540810
HLA B*1801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.359399	1.513906	-2.845493	22876.992878

HLA A*6802	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.441708	1.596160	-2.845548	27650.847376
HLA A*2301	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.493212	1.647521	-2.845690	31132.321434
HLA A*8001	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.216409	1.370628	-2.845782	16459.221119
HLA A*0212	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.442251	1.596160	-2.846091	27685.423809
HLA A*2602	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.526891	1.680196	-2.846696	33642.741087
HLA A*0101	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.083983	1.236873	-2.847110	12133.410950
HLA A*0101	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.312362	1.465037	-2.847326	20528.737773
HLA B*1509	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.462459	1.615041	-2.847418	29004.080150
HLA A*2403	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.443776	1.596160	-2.847615	27782.798674
HLA A*0101	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.370937	1.523182	-2.847756	23492.933958
HLA B*4601	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.312997	1.465037	-2.847960	20558.745396
HLA A*2602	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.425896	1.577736	-2.848160	26662.226345
HLA A*2402	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.371355	1.523182	-2.848174	23515.567616
HLA B*5301	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.575747	1.727210	-2.848536	37648.403498
HLA B*1502	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.601661	1.752306	-2.849356	39963.303751
HLA A*2601	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.372908	1.523182	-2.849727	23599.808327
HLA B*1501	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.375042	1.525000	-2.850041	23716.020011
HLA A*3201	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.577518	1.727210	-2.850308	37802.287097
HLA A*0101	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.376066	1.525000	-2.851066	23772.025288
HLA A*2501	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.210771	1.359429	-2.851341	16246.900312
HLA B*5101	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.499405	1.647630	-2.851774	31579.463551
HLA B*5401	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.246718	1.394704	-2.852013	17648.899752
HLA A*2603	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.499562	1.647521	-2.852041	31590.911999
HLA B*3901	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.163156	1.311098	-2.852057	14559.814863
HLA B*5301	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.574699	1.722434	-2.852264	37557.674533
HLA A*2601	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.377701	1.525000	-2.852701	23861.702411
HLA A*6901	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.359124	1.505966	-2.853158	22862.517306
HLA A*0219	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.450037	1.596160	-2.853877	28186.254528
HLA B*1502	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.560548	1.706509	-2.854038	36353.626920
HLA A*3201	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.589890	1.735543	-2.854348	38894.703410
HLA B*1501	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.732105	0.877206	-2.854899	5396.413714
HLA B*7301	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.607683	1.752306	-2.855377	40521.276129
HLA B*1502	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.590938	1.735543	-2.855396	38988.662268
HLA B*5401	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.561908	1.706509	-2.855399	36467.676852
HLA A*3101	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.378726	1.523182	-2.855544	23918.051717
HLA A*1101	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.426604	1.570424	-2.856180	26705.677860
HLA B*4001	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.381195	1.525000	-2.856195	24054.432167
HLA B*1801	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.509844	1.653369	-2.856474	32347.707702
HLA A*0211	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.854011	0.997451	-2.856559	7145.137918
HLA B*4002	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.643987	1.787206	-2.856782	44054.203775
HLA A*0219	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.371226	1.513906	-2.857320	23508.571743
HLA A*2501	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.505079	1.647630	-2.857448	31994.752468
HLA B*3501	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.258634	1.401173	-2.857462	18139.872249
HLA B*5701	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.428681	1.570424	-2.858257	26833.699422
HLA A*2501	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.498716	1.640132	-2.858584	31529.446673
HLA A*3001	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.040766	1.181941	-2.858826	10984.150631
HLA A*0201	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.249943	1.391116	-2.858828	17780.479927
HLA B*5101	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.323536	1.464619	-2.858918	21063.784256
HLA B*1509	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.298211	1.439287	-2.858924	19870.614553
HLA B*0801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.429357	1.570424	-2.858933	26875.540202
HLA A*0206	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.506831	1.647521	-2.859310	32124.137072
HLA A*2603	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.567220	1.707126	-2.860095	36916.479929
HLA A*3201	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.507724	1.647521	-2.860203	32190.244446
HLA B*5101	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.294346	1.434003	-2.860343	19694.565153
HLA A*2603	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.055672	1.195068	-2.860604	11367.674061
HLA B*5101	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.497257	1.636589	-2.860669	31423.699929

HLA B*0803	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.385741	1.525000	-2.860741	24307.559798
HLA B*1517	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.457095	1.596160	-2.860935	28648.060313
HLA A*0250	1:191-199	9	MQIRRIDPW	1.219990	0.489753	-4.570754	1.709743	-2.861011	37218.075178
HLA B*1503	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.679707	0.818322	-2.861385	4783.073149
HLA B*5301	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.597054	1.735543	-2.861511	39541.582283
HLA B*3801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.439380	1.577736	-2.861644	27503.002317
HLA B*1801	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.509479	1.647630	-2.861849	32320.594457
HLA B*0801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-3.364951	0.502834	-2.862117	2317.134353
HLA B*0803	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.458338	1.596160	-2.862178	28730.163658
HLA A*6801	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.569605	1.707126	-2.862479	37119.747268
HLA B*5701	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.387600	1.525000	-2.862599	24411.800125
HLA B*5101	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.476126	1.613450	-2.862676	29931.332459
HLA A*3201	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.585509	1.722434	-2.863074	38504.250545
HLA A*1101	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.459435	1.596160	-2.863275	28802.839833
HLA B*3901	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.459677	1.596160	-2.863517	28818.893783
HLA B*0803	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.434148	1.570424	-2.863724	27173.639049
HLA B*2705	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-3.991122	1.126836	-2.864286	9797.648662
HLA A*2902	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.434792	1.570424	-2.864368	27213.948664
HLA B*4002	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.649363	1.784676	-2.864687	44602.887812
HLA B*5301	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-3.894967	1.030229	-2.864738	7851.756788
HLA B*4002	1:174-182	9	ARVQLSARR	0.965880	0.769663	-4.600964	1.735543	-2.865421	39899.144787
HLA B*5101	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.505582	1.640132	-2.865449	32031.814763
HLA A*3101	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.273081	1.407576	-2.865505	18753.451407
HLA A*2402	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.330348	1.464619	-2.865729	21396.737314
HLA B*4001	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.331431	1.465037	-2.866394	21450.166495
HLA B*4002	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.331558	1.465037	-2.866521	21456.433734
HLA B*4501	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.653747	1.787206	-2.866542	45055.427733
HLA B*7301	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.437012	1.570424	-2.866588	27353.432005
HLA B*4501	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.593889	1.727210	-2.866679	39254.485327
HLA B*5801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.372739	1.505966	-2.866774	23590.617708
HLA A*0250	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.380749	1.513906	-2.866843	24029.719826
HLA A*3001	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-3.135505	0.268222	-2.867283	1366.171464
HLA A*0212	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.381256	1.513906	-2.867350	24057.815832
HLA B*1517	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.392804	1.525000	-2.867804	24706.084060
HLA B*3501	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-3.009234	0.141159	-2.868076	1021.490866
HLA A*6801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-3.953041	1.084809	-2.868233	8975.143663
HLA A*0206	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.158823	1.289989	-2.868834	14415.290617
HLA B*3801	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.482735	1.613450	-2.869285	30390.311539
HLA A*0206	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.505941	1.636589	-2.869352	32058.338889
HLA B*7301	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-3.640353	0.770901	-2.869452	4368.709319
HLA B*2705	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.057227	1.187527	-2.869700	11408.458630
HLA B*4501	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.654537	1.784644	-2.869892	45137.400488
HLA A*2403	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.440456	1.570424	-2.870032	27571.231802
HLA A*8001	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.395043	1.525000	-2.870043	24833.788263
HLA A*0219	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.395278	1.525000	-2.870278	24847.226702
HLA B*1509	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.335105	1.464619	-2.870487	21632.427758
HLA A*2402	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.972335	1.101846	-2.870489	9382.863099
HLA B*4002	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.265196	1.394704	-2.870492	18416.043656
HLA B*4601	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.393976	1.523182	-2.870795	24772.869095
HLA A*8001	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.467158	1.596160	-2.870998	29319.601726
HLA A*2403	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.272400	1.401173	-2.871227	18724.052787
HLA A*0202	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.277193	1.405388	-2.871805	18931.839163
HLA B*1517	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.749012	0.877206	-2.871806	5610.636483
HLA A*0201	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.305936	1.434003	-2.871933	20227.229673
HLA A*6801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.385967	1.513906	-2.872061	24320.187192
HLA A*0203	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.397205	1.525000	-2.872204	24957.696558

HLA A*3101	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.397228	1.525000	-2.872228	24959.046778
HLA B*4402	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.386249	1.513906	-2.872343	24335.980660
HLA A*0201	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.397421	1.525000	-2.872420	24970.121340
HLA B*1509	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.396098	1.523182	-2.872916	24894.183856
HLA B*1502	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.486485	1.613450	-2.873035	30653.843105
HLA A*3001	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.541181	0.667908	-2.873273	3476.813434
HLA B*4501	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.658230	1.784676	-2.873553	45522.901441
HLA B*5801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.338883	1.464619	-2.874265	21821.431337
HLA A*0101	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.380448	1.505966	-2.874482	24013.085827
HLA B*1501	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.380479	1.505966	-2.874513	24014.774692
HLA A*2403	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.025001	1.150365	-2.874636	10592.572266
HLA A*2603	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.445891	1.571013	-2.874877	27918.400196
HLA B*4801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.380904	1.505966	-2.874938	24038.301234
HLA B*0802	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.398142	1.523182	-2.874960	25011.627073
HLA B*1801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.445533	1.570424	-2.875109	27895.452244
HLA B*1509	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.281011	1.405388	-2.875623	19099.003986
HLA A*2501	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.314911	1.439287	-2.875624	20649.590254
HLA B*1801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.315130	1.439287	-2.875843	20659.982084
HLA A*0206	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.529516	1.653369	-2.876147	33846.654485
HLA B*5701	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.399352	1.523182	-2.876170	25081.408954
HLA B*3901	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.446736	1.570424	-2.876312	27972.825940
HLA A*6802	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.446800	1.570424	-2.876376	27976.912145
HLA B*5401	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.447538	1.571013	-2.876524	28024.477059
HLA A*0206	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-3.811922	0.935291	-2.876631	6485.178612
HLA A*0250	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.524349	1.647521	-2.876828	33446.388536
HLA A*0211	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.278208	1.401173	-2.877035	18976.135979
HLA B*4002	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.027515	1.150365	-2.877150	10654.066042
HLA A*0216	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.448259	1.570424	-2.877835	28071.059791
HLA B*2705	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.266094	1.388176	-2.877918	18454.141193
HLA A*0219	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.448482	1.570424	-2.878058	28085.490324
HLA B*3501	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.312912	1.434003	-2.878909	20554.741847
HLA A*2602	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.606316	1.727210	-2.879105	40393.893284
HLA B*4601	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.404286	1.525000	-2.879285	25367.977740
HLA B*3501	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.284699	1.405388	-2.879312	19261.912728
HLA B*1503	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.404610	1.525000	-2.879610	25386.923648
HLA A*2501	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.037919	1.157848	-2.880071	10912.365507
HLA B*3801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.495335	1.615041	-2.880294	31284.948200
HLA A*0301	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.345861	1.465037	-2.880824	22174.876226
HLA A*2501	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.477120	1.596160	-2.880959	29999.905246
HLA B*4501	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.603428	1.722434	-2.880994	40126.215084
HLA A*2403	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.404319	1.523182	-2.881137	25369.899144
HLA B*1801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.406149	1.525000	-2.881149	25477.041209
HLA B*4403	1:186-194	9	PVRASMQIR	1.283702	0.503504	-4.668720	1.787206	-2.881515	46635.902421
HLA A*0202	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.529208	1.647521	-2.881687	33822.676011
HLA B*7301	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.609483	1.727210	-2.882273	40689.543695
HLA B*4601	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.277491	1.394704	-2.882787	18944.850865
HLA A*2501	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.388819	1.505966	-2.882854	24480.438242
HLA A*6801	1:103-111	9	PQPDPDASL	1.546426	0.238218	-4.667604	1.784644	-2.882960	46516.216111
HLA A*2402	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.194456	1.311098	-2.883357	15647.886663
HLA A*2301	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.523588	1.640132	-2.883456	33387.814919
HLA A*0216	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.406699	1.523182	-2.883517	25509.313376
HLA A*2301	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.537262	1.653369	-2.883893	34455.773201
HLA B*4403	1:21-29	9	LVDRGGAHR	1.168051	0.616625	-4.669007	1.784676	-2.884331	46666.692579
HLA A*0201	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-3.926995	1.042623	-2.884372	8452.691490
HLA B*4801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.318525	1.434003	-2.884522	20822.120065
HLA A*2301	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.532272	1.647630	-2.884641	34062.121516

HLA B*3501	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.455216	1.570424	-2.884792	28524.341963
HLA B*4501	1:284-292	9	FVYNLITDL	1.173320	0.583858	-4.642028	1.757178	-2.884850	43855.885651
HLA B*4002	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.637254	1.752306	-2.884948	43376.422687
HLA B*0802	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.455392	1.570424	-2.884968	28535.917826
HLA B*0802	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.391021	1.505966	-2.885055	24604.846253
HLA A*0211	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.538766	1.653369	-2.885397	34575.277187
HLA A*0219	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.408611	1.523182	-2.885430	25621.895161
HLA A*6801	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.565839	1.680196	-2.885643	36799.234638
HLA A*2902	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.280686	1.394704	-2.885982	19084.750665
HLA B*1801	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.526349	1.640132	-2.886216	33600.724538
HLA A*3301	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.501270	1.615041	-2.886229	31715.403372
HLA B*0801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.291673	1.405388	-2.886285	19573.688938
HLA A*6901	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.133031	1.246696	-2.886335	13584.096434
HLA B*5101	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.409915	1.523182	-2.886734	25698.940212
HLA A*3301	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.988852	1.101846	-2.887006	9746.580168
HLA A*0301	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.198229	1.311098	-2.887131	15784.432229
HLA B*5301	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.593730	1.706509	-2.887220	39240.047339
HLA A*8001	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.457699	1.570424	-2.887275	28687.918603
HLA A*8001	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.351946	1.464619	-2.887328	22487.768954
HLA A*6801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.457990	1.570424	-2.887566	28707.169668
HLA A*3201	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.594270	1.706509	-2.887760	39288.903118
HLA A*0211	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.524772	1.636589	-2.888183	33478.973825
HLA B*5401	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.524873	1.636589	-2.888284	33486.762785
HLA A*3002	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.402195	1.513906	-2.888289	25246.129540
HLA A*0212	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.411565	1.523182	-2.888383	25796.723722
HLA A*1101	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.276716	1.388176	-2.888540	18911.059488
HLA A*3101	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.832142	0.943496	-2.888646	6794.251356
HLA A*0216	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.414238	1.525000	-2.889238	25956.029938
HLA A*0216	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.485399	1.596160	-2.889239	30577.323511
HLA A*8001	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.277710	1.388176	-2.889534	18954.384790
HLA B*7301	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.612041	1.722434	-2.889607	40929.968343
HLA A*0206	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.295213	1.405388	-2.889826	19733.919679
HLA B*0803	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.355236	1.465037	-2.890199	22658.734441
HLA B*4001	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.285101	1.394704	-2.890397	19279.739995
HLA A*2602	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.505732	1.615041	-2.890691	32042.907151
HLA B*3501	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.413907	1.523182	-2.890725	25936.238374
HLA A*3001	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.298442	1.407576	-2.890865	19881.152133
HLA A*2902	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.250554	1.359429	-2.891125	17805.507035
HLA A*3101	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.292370	1.401173	-2.891198	19605.163989
HLA A*0211	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.018089	1.126836	-2.891253	10425.316553
HLA A*0201	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-3.976090	1.084809	-2.891281	9464.329609
HLA B*3901	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.279862	1.388176	-2.891686	19048.545569
HLA A*2601	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.710053	0.818322	-2.891731	5129.239417
HLA B*2705	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.356770	1.464619	-2.892151	22738.921545
HLA A*8001	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.406154	1.513906	-2.892248	25477.316866
HLA B*4601	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.357143	1.464619	-2.892525	22758.489352
HLA A*0211	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.540579	1.647630	-2.892949	34719.980526
HLA B*1502	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.471157	1.577736	-2.893421	29590.812497
HLA A*2603	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.600052	1.706509	-2.893543	39815.482842
HLA B*4402	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.418615	1.525000	-2.893615	26218.953720
HLA A*3301	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.541315	1.647630	-2.893684	34778.821509
HLA B*4801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.417041	1.523182	-2.893860	26124.091849
HLA A*2301	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-3.995708	1.101846	-2.893862	9901.661071
HLA A*0206	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.541825	1.647630	-2.894194	34819.673940
HLA B*7301	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.333496	1.439287	-2.894209	21552.411221
HLA A*0206	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.534656	1.640132	-2.894524	34249.672355

HLA A*3002	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.254450	1.359429	-2.895021	17965.933648
HLA B*5101	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.491522	1.596160	-2.895362	31011.460931
HLA B*5101	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.475710	1.580071	-2.895639	29902.685418
HLA A*3101	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.230974	1.334516	-2.896457	17020.555783
HLA A*2403	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.421576	1.525000	-2.896575	26398.284684
HLA B*1501	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.298002	1.401173	-2.896830	19861.049550
HLA B*2705	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.054737	1.157848	-2.896889	11343.224245
HLA A*0216	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.187741	1.289989	-2.897752	15407.808205
HLA A*2603	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.166365	1.268587	-2.897778	14667.809106
HLA B*5401	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.511599	1.613450	-2.898148	32478.695339
HLA B*0801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.144900	1.246696	-2.898204	13960.480110
HLA A*2301	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.511728	1.613450	-2.898277	32488.360614
HLA B*5401	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.513354	1.615041	-2.898313	32610.213392
HLA A*3301	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.605576	1.707126	-2.898450	40325.116061
HLA A*0201	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.404450	1.505966	-2.898485	25377.586216
HLA A*0301	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.332784	1.434003	-2.898781	21517.111526
HLA B*5101	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.413200	1.513906	-2.899294	25894.038777
HLA A*2902	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.424395	1.525000	-2.899395	26570.216312
HLA B*1801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.495702	1.596160	-2.899541	31311.362048
HLA B*4402	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.364756	1.465037	-2.899719	23160.917669
HLA B*3501	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.364887	1.464619	-2.900269	23167.935420
HLA B*0803	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.365113	1.464619	-2.900494	23179.970798
HLA A*2301	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.537182	1.636589	-2.900593	34449.436118
HLA A*3002	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.334816	1.434003	-2.900813	21618.037975
HLA B*2705	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.211912	1.311098	-2.900814	16289.672967
HLA A*0211	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.424256	1.523182	-2.901075	26561.736891
HLA A*3301	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.472092	1.571013	-2.901079	29654.594178
HLA A*3002	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.548758	1.647630	-2.901128	35380.016426
HLA A*0206	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.426164	1.525000	-2.901164	26678.674742
HLA A*0301	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.365827	1.464619	-2.901209	23218.124089
HLA B*1517	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.289483	1.388176	-2.901307	19475.246455
HLA B*4501	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.366812	1.465037	-2.901775	23270.813315
HLA B*4001	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.407819	1.505966	-2.901854	25575.225603
HLA A*0212	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.427160	1.525000	-2.902160	26739.940337
HLA A*2902	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.425356	1.523182	-2.902174	26629.071848
HLA B*1503	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.261644	1.359429	-2.902215	18266.019397
HLA B*4403	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.517651	1.615041	-2.902610	32934.482881
HLA B*0803	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.425826	1.523182	-2.902644	26657.899506
HLA B*4402	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.297351	1.394704	-2.902647	19831.309276
HLA B*2705	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.294109	1.391116	-2.902994	19683.807006
HLA B*5101	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.342537	1.439287	-2.903250	22005.775757
HLA B*5701	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.304440	1.401173	-2.903267	20157.644597
HLA A*0101	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.304482	1.401173	-2.903309	20159.607603
HLA A*3201	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.030842	1.126836	-2.904006	10735.993881
HLA B*4403	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.656689	1.752306	-2.904383	45361.632128
HLA B*5701	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.215559	1.311098	-2.904460	16427.019254
HLA B*0801	1:168-176	9	TAESRDARV	0.917270	0.090109	-3.911935	1.007379	-2.904556	8164.598246
HLA B*0801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.344059	1.439287	-2.904772	22083.054760
HLA B*4501	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.657187	1.752306	-2.904881	45413.687070
HLA B*1509	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.475492	1.570424	-2.905068	29887.644573
HLA B*0801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.306580	1.401173	-2.905408	20257.234923
HLA B*1501	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.142523	1.236873	-2.905650	13884.258006
HLA B*1517	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.476117	1.570424	-2.905693	29930.684766
HLA A*0250	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.783108	0.877206	-2.905901	6068.870322
HLA B*1801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.486097	1.580071	-2.906026	30626.492721
HLA B*1501	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-3.931713	1.025655	-2.906057	8545.014108

HLA A*8001	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.217490	1.311098	-2.906392	16500.231705
HLA A*0201	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.371024	1.464619	-2.906406	23497.636913
HLA A*2402	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.519902	1.613450	-2.906451	33105.614639
HLA B*5701	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.413571	1.505966	-2.907605	25916.181492
HLA B*4002	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.615072	1.707126	-2.907947	41216.607675
HLA B*5401	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.555781	1.647521	-2.908259	35956.767415
HLA A*2501	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.478830	1.570424	-2.908406	30118.289821
HLA B*0702	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.414476	1.505966	-2.908510	25970.216157
HLA A*2602	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.545368	1.636589	-2.908779	35104.898635
HLA B*3901	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.273889	1.365049	-2.908840	18788.384110
HLA B*3801	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.505072	1.596160	-2.908911	31994.233208
HLA A*0216	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.310140	1.401173	-2.908967	20423.945101
HLA B*1502	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.220338	1.311098	-2.909239	16608.775648
HLA B*5401	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-2.898917	-0.010665	-2.909582	792.349465
HLA A*3002	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.505814	1.596160	-2.909654	32048.974926
HLA B*0802	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.374654	1.464619	-2.910036	23694.859785
HLA B*7301	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.030715	1.120296	-2.910419	10732.857990
HLA A*2603	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.526031	1.615041	-2.910990	33576.193711
HLA A*0211	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.551244	1.640132	-2.911111	35583.100344
HLA B*4002	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.425638	1.513906	-2.911732	26646.364700
HLA B*0702	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.377128	1.464619	-2.912510	23830.225434
HLA A*6901	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.318358	1.405388	-2.912970	20814.123780
HLA A*0201	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.283839	1.370628	-2.913212	19223.811499
HLA B*1502	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.438595	1.525000	-2.913595	27453.351931
HLA B*1501	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.716721	0.802529	-2.914192	5208.597636
HLA B*4001	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.348441	1.434003	-2.914438	22306.988271
HLA A*2501	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.379128	1.464619	-2.914509	23940.188330
HLA B*5401	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.562340	1.647630	-2.914710	36503.995565
HLA A*0216	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-3.850571	0.935291	-2.915280	7088.771379
HLA A*2301	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.429442	1.513906	-2.915536	26880.774885
HLA A*0212	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.421641	1.505966	-2.915676	26402.283717
HLA B*4403	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.638118	1.722434	-2.915684	43462.864187
HLA A*0202	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.563698	1.647630	-2.916068	36618.319137
HLA B*0702	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.734483	0.818322	-2.916161	5426.039064
HLA B*1502	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.563990	1.647521	-2.916469	36642.891908
HLA B*5401	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.512712	1.596160	-2.916552	32562.086924
HLA A*3101	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.381186	1.464619	-2.916567	24053.911646
HLA B*4601	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.355957	1.439287	-2.916670	22696.398150
HLA A*6802	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.422668	1.505966	-2.916703	26464.775766
HLA A*2402	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.570183	1.653369	-2.916814	37169.180328
HLA B*1502	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.570425	1.653369	-2.917056	37189.897458
HLA A*6801	1:198-206	9	PWSTLKVSL	1.499757	0.252549	-4.670593	1.752306	-2.918287	46837.415704
HLA B*1501	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.187022	1.268587	-2.918435	15382.322818
HLA A*3301	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.598828	1.680196	-2.918632	39703.418826
HLA A*2501	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.443844	1.525000	-2.918844	27787.157770
HLA A*0212	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.310180	1.391116	-2.919064	20425.823539
HLA B*1503	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.515745	1.596160	-2.919585	32790.301991
HLA A*2601	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.384395	1.464619	-2.919777	24232.326276
HLA A*3301	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.646995	1.727210	-2.919784	44360.322735
HLA B*0702	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.442968	1.523182	-2.919786	27731.142915
HLA B*7301	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.626951	1.707126	-2.919826	42359.540516
HLA B*5801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.325754	1.405388	-2.920366	21171.630789
HLA A*1101	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.434615	1.513906	-2.920709	27202.909070
HLA A*2501	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.443910	1.523182	-2.920728	27791.367201
HLA B*4002	1:157-165	9	SAAGSSGGR	1.085856	0.636578	-4.643292	1.722434	-2.920858	43983.715034
HLA B*3801	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.491506	1.570424	-2.921082	31010.286573

HLA A*6901	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.211372	1.289989	-2.921383	16269.416747
HLA A*2602	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.309808	1.388176	-2.921633	20408.371771
HLA B*0802	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.355647	1.434003	-2.921644	22680.196316
HLA B*3801	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.493242	1.571013	-2.922229	31134.511002
HLA A*8001	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.024113	1.101846	-2.922267	10570.933244
HLA A*0101	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.387113	1.464619	-2.922495	24384.477944
HLA B*4403	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.630029	1.707126	-2.922903	42660.806934
HLA B*7301	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.629616	1.706509	-2.923106	42620.207184
HLA A*0202	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.559852	1.636589	-2.923264	36295.459454
HLA B*1509	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.519498	1.596160	-2.923337	33074.824162
HLA A*2301	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.388159	1.464619	-2.923540	24443.251870
HLA B*1501	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-3.691215	0.767455	-2.923760	4911.507373
HLA B*1801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.234991	1.311098	-2.923893	17178.741975
HLA A*0219	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.388807	1.464619	-2.924189	24479.776069
HLA B*5701	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.389059	1.464619	-2.924440	24493.950489
HLA B*4601	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.358678	1.434003	-2.924674	22839.029479
HLA B*0801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.289927	1.365049	-2.924878	19495.169475
HLA A*1101	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.448148	1.523182	-2.924967	28063.923216
HLA A*3001	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.194023	1.268587	-2.925436	15632.318200
HLA A*0219	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.514956	0.589436	-2.925520	3273.078606
HLA B*5401	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.503458	1.577736	-2.925722	31875.544333
HLA A*3101	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.316901	1.391116	-2.925786	20744.427428
HLA A*0250	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.579452	1.653369	-2.926083	37970.970925
HLA B*0702	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.286107	1.360016	-2.926091	19324.432654
HLA B*4402	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.432207	1.505966	-2.926241	27052.482683
HLA A*0211	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.331727	1.405388	-2.926339	21464.792900
HLA A*2601	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.391448	1.465037	-2.926412	24629.084110
HLA A*0101	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.366062	1.439287	-2.926775	23230.688234
HLA A*2602	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.633511	1.706509	-2.927002	43004.212845
HLA A*2402	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.574699	1.647630	-2.927068	37557.674533
HLA A*0301	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.113835	1.186588	-2.927248	12996.770901
HLA A*2402	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.567620	1.640132	-2.927487	36950.446937
HLA A*2602	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.567669	1.640132	-2.927537	36954.645030
HLA B*4501	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.634063	1.706509	-2.927554	43058.919899
HLA B*4501	1:118-126	9	PAEAYASEL	1.515766	0.191360	-4.634817	1.707126	-2.927692	43133.759881
HLA B*5401	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.568202	1.640132	-2.928070	37000.054868
HLA B*3901	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.069557	1.141236	-2.928321	11736.999043
HLA B*5101	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.498822	1.570424	-2.928398	31537.123294
HLA A*3201	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.452685	1.523182	-2.929504	28358.629520
HLA B*0702	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.112355	1.182783	-2.929573	12952.550314
HLA B*3501	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.264289	1.334516	-2.929773	18377.627082
HLA B*4402	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.335303	1.405388	-2.929915	21642.260431
HLA B*0802	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.395137	1.465037	-2.930100	24839.162767
HLA A*3201	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.290470	1.359429	-2.931041	19519.547513
HLA B*4501	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.611330	1.680196	-2.931134	40862.931044
HLA A*2402	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.568104	1.636589	-2.931515	36991.648842
HLA B*1517	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.454814	1.523182	-2.931632	28497.966552
HLA B*7301	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.611943	1.680196	-2.931747	40920.669482
HLA B*4501	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-3.793431	0.860615	-2.932817	6214.862074
HLA B*1502	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.573089	1.640132	-2.932957	37418.751844
HLA B*5301	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.334201	1.401173	-2.933028	21587.418468
HLA B*4601	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.091116	1.157848	-2.933268	12334.340790
HLA A*2301	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.458371	1.525000	-2.933371	28732.339718
HLA A*0203	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.439641	1.505966	-2.933675	27519.522766
HLA A*6802	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-2.922576	-0.011592	-2.934168	836.712164
HLA A*0211	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.504691	1.570424	-2.934267	31966.205680

HLA B*3901	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.457471	1.523182	-2.934290	28672.868301
HLA B*4601	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.339729	1.405388	-2.934341	21863.971297
HLA B*4002	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.640978	1.706509	-2.934468	43749.960578
HLA A*0211	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.305598	1.370628	-2.934971	20211.478311
HLA A*0216	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.305638	1.370628	-2.935011	20213.337208
HLA B*5301	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.330540	1.394704	-2.935836	21406.231246
HLA A*0206	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.506862	1.570424	-2.936438	32126.396395
HLA B*4001	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.341935	1.405388	-2.936547	21975.320357
HLA B*2705	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-3.781684	0.844974	-2.936711	6049.006759
HLA B*2705	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.461963	1.525000	-2.936963	28970.991270
HLA B*5801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.331879	1.394704	-2.937175	21472.342167
HLA A*6801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.272369	1.334516	-2.937853	18722.735998
HLA A*0219	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.329027	1.391116	-2.937912	21331.782373
HLA A*0202	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.402916	1.464619	-2.938298	25288.094058
HLA B*1801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.516093	1.577736	-2.938357	32816.566505
HLA B*4403	1:261-269	9	FGGAFLIGL	1.487253	0.192943	-4.619428	1.680196	-2.939232	41632.087685
HLA B*7301	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.552762	1.613450	-2.939311	35707.673302
HLA A*3001	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.299428	1.360016	-2.939413	19926.376520
HLA A*3002	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.509883	1.570424	-2.939459	32350.682797
HLA B*3801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.462884	1.523182	-2.939703	29032.494563
HLA A*6901	1:179-187	9	SARRSRGPV	0.654360	0.222846	-3.816959	0.877206	-2.939753	6560.836841
HLA B*5301	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.587682	1.647630	-2.940052	38697.414400
HLA A*0301	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.347807	1.407576	-2.940230	22274.428906
HLA A*0301	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.341780	1.401173	-2.940607	21967.475410
HLA A*6801	1:13-21	9	GDGPNADGL	1.549303	0.177907	-4.667971	1.727210	-2.940761	46555.489703
HLA B*4601	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.300509	1.359429	-2.941080	19976.026036
HLA B*5301	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.537304	1.596160	-2.941144	34459.128598
HLA A*0202	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.466291	1.525000	-2.941291	29261.130878
HLA A*0216	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.375535	1.434003	-2.941532	23742.978540
HLA B*4001	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.343429	1.401173	-2.942257	22051.060836
HLA A*2602	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.407298	1.465037	-2.942261	25544.528312
HLA B*5801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.330803	1.388176	-2.942628	21419.205374
HLA A*0250	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.579872	1.636589	-2.943284	38007.758689
HLA A*3002	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.180251	1.236873	-2.943378	15144.352355
HLA A*2603	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.045494	1.101846	-2.943647	11104.362831
HLA A*0212	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.377758	1.434003	-2.943755	23864.800752
HLA B*5801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.314425	1.370628	-2.943798	20626.478814
HLA A*2301	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.540460	1.596160	-2.944299	34710.402454
HLA A*3002	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.598161	1.653369	-2.944792	39642.464993
HLA A*0202	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.598530	1.653369	-2.945160	39676.149726
HLA B*1509	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.310217	1.365049	-2.945168	20427.591638
HLA B*5301	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.256282	1.311098	-2.945184	18041.904917
HLA A*2902	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.451626	1.505966	-2.945660	28289.522774
HLA A*0250	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.593309	1.647630	-2.945679	39202.066840
HLA B*5801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.353279	1.407576	-2.945702	22556.853999
HLA B*4403	1:40-48	9	AGDPPPWQR	1.252243	0.454266	-4.652269	1.706509	-2.945760	44902.372767
HLA B*2705	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.351502	1.405388	-2.946114	22464.787657
HLA A*0211	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.542358	1.596160	-2.946198	34862.460328
HLA B*7301	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.600028	1.653369	-2.946659	39813.328926
HLA A*2501	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.411872	1.465037	-2.946836	25815.012223
HLA B*2705	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.452923	1.505966	-2.946957	28374.128875
HLA B*7301	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.562498	1.615041	-2.947457	36517.229296
HLA A*0250	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.561102	1.613450	-2.947652	36400.070468
HLA A*2403	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.453670	1.505966	-2.947704	28422.984171
HLA A*0101	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.382006	1.434003	-2.948002	24099.369565
HLA B*5401	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.282540	1.334516	-2.948024	19166.386166

HLA B*4801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.349428	1.401173	-2.948255	22357.730796
HLA B*5401	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.519493	1.570424	-2.949069	33074.466301
HLA B*5801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.260610	1.311098	-2.949512	18222.591562
HLA B*5101	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.455765	1.505966	-2.949800	28560.474194
HLA B*7301	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.597327	1.647521	-2.949805	39566.404278
HLA B*4601	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.341282	1.391116	-2.950167	21942.295432
HLA A*0203	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.315560	1.365049	-2.950511	20680.445794
HLA B*0801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.137589	1.186588	-2.951001	13727.414799
HLA B*1501	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.342285	1.391116	-2.951170	21993.041221
HLA B*4002	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.587938	1.636589	-2.951349	38720.240140
HLA A*6901	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.311521	1.360016	-2.951505	20489.017416
HLA B*5301	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.599039	1.647521	-2.951518	39722.754732
HLA A*8001	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.457871	1.505966	-2.951905	28699.250328
HLA B*0702	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.391502	1.439287	-2.952215	24632.148835
HLA A*0219	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.263594	1.311098	-2.952496	18348.222038
HLA A*1101	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.477653	1.525000	-2.952653	30036.769105
HLA A*0219	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.323353	1.370628	-2.952726	21054.897818
HLA B*4001	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.341630	1.388176	-2.953454	21959.870864
HLA B*1502	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.601311	1.647630	-2.953681	39931.103372
HLA A*0301	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.359077	1.405388	-2.953689	22860.043766
HLA A*3002	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.756375	0.802529	-2.953847	5706.573527
HLA B*5801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.345469	1.391116	-2.954353	22154.851348
HLA B*4402	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.388432	1.434003	-2.954428	24458.595977
HLA A*3201	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.602636	1.647630	-2.955006	40053.126317
HLA A*6802	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.419898	1.464619	-2.955280	26296.513744
HLA A*0250	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.595630	1.640132	-2.955498	39412.161705
HLA B*3501	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.343812	1.388176	-2.955637	22070.514300
HLA A*2902	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.106139	1.150365	-2.955774	12768.460892
HLA A*0206	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-3.729732	0.773810	-2.955922	5367.008183
HLA A*0101	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.350896	1.394704	-2.956192	22433.454270
HLA A*0202	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.596453	1.640132	-2.956320	39486.857799
HLA B*4501	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.593072	1.636589	-2.956483	39180.652729
HLA A*2402	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.143176	1.186588	-2.956588	13905.154934
HLA A*1101	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.462631	1.505966	-2.956665	29015.536759
HLA B*0802	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.396460	1.439287	-2.957173	24914.932413
HLA A*0212	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.328437	1.370628	-2.957810	21302.835983
HLA B*0801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.349108	1.391116	-2.957993	22341.287259
HLA B*1503	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.978881	1.020231	-2.958651	9525.352251
HLA B*0803	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.464785	1.505966	-2.958819	29159.836647
HLA B*3501	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-2.716033	-0.242879	-2.958911	520.035338
HLA B*5801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.195814	1.236873	-2.958941	15696.892868
HLA A*2601	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.393001	1.434003	-2.958998	24717.313814
HLA A*3002	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.482225	1.523182	-2.959044	30354.655889
HLA A*2403	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.347882	1.388176	-2.959706	22278.285310
HLA B*4601	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.360912	1.401173	-2.959739	22956.834605
HLA A*2403	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.365183	1.405388	-2.959796	23183.733135
HLA B*1503	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.330545	1.370628	-2.959917	21406.462858
HLA A*0216	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.365355	1.405388	-2.959967	23192.890707
HLA A*3101	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.319538	1.359429	-2.960108	20870.726861
HLA A*0219	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.002874	1.042623	-2.960251	10066.395416
HLA A*6901	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.368163	1.407576	-2.960586	23343.314220
HLA A*6901	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.331271	1.370628	-2.960643	21442.277021
HLA B*1509	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.362218	1.401173	-2.961046	23025.990385
HLA A*0201	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.366443	1.405388	-2.961055	23251.056581
HLA B*5301	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.602204	1.640132	-2.962072	40013.276487

HLA A*3001	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.296773	1.334516	-2.962257	19804.934674
HLA B*5301	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.599049	1.636589	-2.962460	39723.614324
HLA A*2301	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.533651	1.570424	-2.963227	34170.461288
HLA B*0803	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.351845	1.388176	-2.963670	22482.538340
HLA B*1501	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.145629	1.181941	-2.963688	13983.912395
HLA B*5701	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.146155	1.181941	-2.964214	14000.868584
HLA B*0702	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.429251	1.465037	-2.964215	26868.998283
HLA B*1509	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.470297	1.505966	-2.964331	29532.280080
HLA A*0206	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.560520	1.596160	-2.964359	36351.266968
HLA B*4801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.329424	1.365049	-2.964375	21351.294326
HLA A*8001	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.355771	1.391116	-2.964656	22686.700208
HLA A*3002	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.122726	1.157848	-2.964878	13265.569973
HLA B*5301	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.429973	1.464619	-2.965354	26913.660359
HLA B*3801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.399930	1.434003	-2.965927	25114.810335
HLA B*5301	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.579708	1.613450	-2.966257	37993.368171
HLA A*0219	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.371720	1.405388	-2.966332	23535.294460
HLA A*0212	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.815080	0.848433	-2.966647	6532.503478
HLA A*2603	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.405970	1.439287	-2.966683	25466.568436
HLA A*0211	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.148871	1.181941	-2.966930	14088.702023
HLA B*3901	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.372340	1.405388	-2.966952	23568.931835
HLA B*0803	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.406384	1.439287	-2.967097	25490.827734
HLA B*2705	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.326607	1.359429	-2.967178	21213.248271
HLA B*1517	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.368489	1.401173	-2.967316	23360.874401
HLA A*2402	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.563525	1.596160	-2.967364	36603.662594
HLA A*0250	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.401466	1.434003	-2.967463	25203.825607
HLA B*1502	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.563705	1.596160	-2.967545	36618.913445
HLA A*0216	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-3.847169	0.879222	-2.967947	7033.458281
HLA A*0101	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.359596	1.391116	-2.968481	22887.391248
HLA A*8001	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.363311	1.394704	-2.968606	23083.987449
HLA A*3101	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.363351	1.394704	-2.968646	23086.110537
HLA A*2902	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.433288	1.464619	-2.968669	27119.887948
HLA A*1101	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.402879	1.434003	-2.968875	25285.905261
HLA A*2601	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.370120	1.401173	-2.968947	23448.746794
HLA A*0101	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.374429	1.405388	-2.969041	23682.557070
HLA A*2602	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.616891	1.647630	-2.969260	41389.553921
HLA A*0219	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.403581	1.434003	-2.969578	25326.839748
HLA A*0301	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.364789	1.394704	-2.970084	23162.671908
HLA A*2403	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.329741	1.359429	-2.970312	21366.893620
HLA A*0211	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.495420	1.525000	-2.970420	31291.041725
HLA A*8001	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.371644	1.401173	-2.970472	23531.220466
HLA B*3901	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.476843	1.505966	-2.970877	29980.760410
HLA B*4002	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.618599	1.647630	-2.970968	41552.659133
HLA B*5401	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-3.112198	0.141159	-2.971039	1294.786965
HLA A*2602	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.624689	1.653369	-2.971320	42139.432881
HLA A*3201	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.607937	1.636589	-2.971348	40544.958333
HLA A*6801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.436457	1.465037	-2.971421	27318.531237
HLA B*5101	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.376889	1.405388	-2.971501	23817.079336
HLA A*3201	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.625337	1.653369	-2.971968	42202.399504
HLA B*4601	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.360266	1.388176	-2.972090	22922.706667
HLA A*3101	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.377997	1.405388	-2.972610	23877.973191
HLA A*2601	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.380603	1.407576	-2.973027	24021.661294
HLA B*1801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.496341	1.523182	-2.973159	31357.470315
HLA A*0301	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.364582	1.391116	-2.973466	23151.647473
HLA A*3002	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.438447	1.464619	-2.973829	27443.996791
HLA B*4403	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.438910	1.465037	-2.973873	27473.260771
HLA B*4402	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.413169	1.439287	-2.973882	25892.217751

HLA A*0219	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.479953	1.505966	-2.973988	30196.274308
HLA B*7301	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.545067	1.571013	-2.974054	35080.598107
HLA B*1501	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-3.910638	0.935815	-2.974823	8140.253011
HLA A*2402	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.499868	1.525000	-2.974867	31613.137247
HLA A*3301	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.488921	1.513906	-2.975015	30826.296135
HLA B*5801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-3.995764	1.020231	-2.975534	9902.946760
HLA A*2601	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.116988	1.141236	-2.975752	13091.471734
HLA B*3901	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-3.660902	0.685107	-2.975794	4580.382480
HLA B*5101	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.346547	1.370628	-2.975920	22209.933286
HLA A*2601	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.370961	1.394704	-2.976256	23494.204934
HLA B*4601	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.158786	1.181941	-2.976845	14414.042909
HLA B*2705	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.378564	1.401173	-2.977391	23909.125196
HLA A*6801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.378890	1.401173	-2.977718	23927.111012
HLA B*4601	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.173747	1.195068	-2.978679	14919.261668
HLA A*1101	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.443391	1.464619	-2.978772	27758.160101
HLA B*0803	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.413049	1.434003	-2.979046	25885.074961
HLA A*0101	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.081253	1.101846	-2.979407	12057.376035
HLA B*1517	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-3.291929	0.312492	-2.979437	1958.525462
HLA B*5701	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.384943	1.405388	-2.979555	24262.890483
HLA B*4801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.385133	1.405388	-2.979745	24273.524836
HLA A*3201	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.620415	1.640132	-2.980283	41726.789724
HLA A*0250	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.576663	1.596160	-2.980502	37727.920092
HLA A*2902	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.388110	1.407576	-2.980533	24440.475087
HLA B*4501	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.628208	1.647630	-2.980578	42482.318932
HLA A*2402	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.368783	1.388176	-2.980607	23376.677211
HLA A*0101	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.978139	0.997451	-2.980687	9509.082334
HLA B*5301	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.561013	1.580071	-2.980942	36392.588264
HLA A*2601	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.386474	1.405388	-2.981087	24348.622819
HLA B*4501	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-2.946306	-0.034919	-2.981225	883.702089
HLA A*0216	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.487286	1.505966	-2.981320	30710.444655
HLA A*6901	1:168-176	9	TAESRDARV	0.917270	0.090109	-3.989435	1.007379	-2.982056	9759.665468
HLA A*2602	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.421348	1.439287	-2.982061	26384.435574
HLA B*3501	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.250897	1.268587	-2.982310	17819.576160
HLA A*2301	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.505687	1.523182	-2.982506	32039.613698
HLA A*2301	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.229519	1.246696	-2.982824	16963.654011
HLA B*4801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.353582	1.370628	-2.982954	22572.601373
HLA B*0801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.342633	1.359429	-2.983204	22010.657300
HLA A*0219	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.384719	1.401173	-2.983547	24250.424030
HLA B*0803	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.354265	1.370628	-2.983638	22608.164903
HLA A*0219	1:275-283	9	MTALATIGA	1.189575	-0.192124	-3.981198	0.997451	-2.983746	9576.297669
HLA A*0212	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.389139	1.405388	-2.983751	24498.456228
HLA A*3001	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.273911	1.289989	-2.983921	18789.298920
HLA B*0702	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.378672	1.394704	-2.983967	23915.075840
HLA A*0212	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.221085	1.236873	-2.984212	16637.373059
HLA A*6801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.243684	1.259401	-2.984283	17526.066335
HLA B*7301	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-3.487143	0.502834	-2.984309	3070.034330
HLA A*8001	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.418385	1.434003	-2.984382	26205.056924
HLA B*5801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.171407	1.186588	-2.984819	14839.089151
HLA A*2601	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.376137	1.391116	-2.985021	23775.883722
HLA B*1502	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.498935	1.513906	-2.985029	31545.313749
HLA B*5101	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.344604	1.359429	-2.985175	22110.788477
HLA B*4501	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.296823	1.311098	-2.985724	19807.184795
HLA B*3501	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.345490	1.359429	-2.986061	22155.930072
HLA B*5401	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.566182	1.580071	-2.986111	36828.311767
HLA A*2603	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.556739	1.570424	-2.986315	36036.220095
HLA A*1101	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.391756	1.405388	-2.986368	24646.544817

HLA B*4601	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.393986	1.407576	-2.986410	24773.405174
HLA A*6802	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.276556	1.289989	-2.986567	18904.103909
HLA B*4403	1:28-36	9	HRAATGPGR	0.868468	0.768121	-4.623474	1.636589	-2.986885	42021.737235
HLA A*0301	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.357656	1.370628	-2.987028	22785.345543
HLA B*0801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.246532	1.259401	-2.987131	17641.358555
HLA A*0101	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.394925	1.407576	-2.987349	24827.071770
HLA B*1509	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.145272	1.157848	-2.987424	13972.418106
HLA B*3801	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.501449	1.513906	-2.987543	31728.445891
HLA B*5801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.352672	1.365049	-2.987623	22525.392200
HLA A*3201	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.382346	1.394704	-2.987642	24118.281345
HLA B*1501	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-3.277438	0.289672	-2.987766	1894.251320
HLA B*3801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.256524	1.268587	-2.987937	18051.961003
HLA A*6802	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.680642	0.692679	-2.987963	4793.382851
HLA A*0212	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.389926	1.401173	-2.988753	24542.895352
HLA A*0201	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.396467	1.407576	-2.988891	24915.336778
HLA A*0301	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.348699	1.359429	-2.989270	22320.266838
HLA B*0803	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.300385	1.311098	-2.989286	19970.299249
HLA B*4403	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.637146	1.647630	-2.989515	43365.629595
HLA A*0203	1:166-174	9	SITAESRDA	0.897252	-0.111108	-3.775693	0.786144	-2.989549	5966.132346
HLA B*4501	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.637132	1.647521	-2.989610	43364.221999
HLA B*4001	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.380744	1.391116	-2.989628	24029.459831
HLA A*3002	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-3.783949	0.793787	-2.990162	6080.635537
HLA A*2603	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.630645	1.640132	-2.990512	42721.316849
HLA A*6801	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.561953	1.571013	-2.990939	36471.425480
HLA A*0101	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.302048	1.311098	-2.990950	20046.936193
HLA B*4002	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.644887	1.653369	-2.991518	44145.578167
HLA B*1509	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.426075	1.434003	-2.992072	26673.190816
HLA B*2705	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.936661	0.943496	-2.993165	8642.926097
HLA A*3002	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.304280	1.311098	-2.993182	20150.230518
HLA B*4403	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.641285	1.647521	-2.993764	43780.976967
HLA A*0202	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.589973	1.596160	-2.993812	38902.068668
HLA B*7301	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.458444	1.464619	-2.993825	28737.158724
HLA B*4501	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.647342	1.653369	-2.993973	44395.854653
HLA A*2602	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.564887	1.570424	-2.994463	36718.695590
HLA B*0702	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.681676	0.687090	-2.994586	4804.806376
HLA A*0101	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.354096	1.359429	-2.994667	22599.360466
HLA A*2603	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.591002	1.596160	-2.994841	38994.357641
HLA B*5401	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.509235	1.513906	-2.995329	32302.415085
HLA B*1503	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.056672	1.060834	-2.995838	11393.902359
HLA A*2402	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.566318	1.570424	-2.995894	36839.869331
HLA B*1517	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.390645	1.394704	-2.995940	24583.557949
HLA A*3001	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.179029	1.182783	-2.996246	15101.809004
HLA A*0250	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.081145	1.084809	-2.996336	12054.375871
HLA A*2403	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.391103	1.394704	-2.996398	24609.505526
HLA A*3301	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.183178	1.186588	-2.996590	15246.781056
HLA A*0301	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.361645	1.365049	-2.996596	22995.615831
HLA B*2705	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.367305	1.370628	-2.996677	23297.265768
HLA B*4002	1:93-101	9	VTGPAAAVR	1.119705	0.527816	-4.644208	1.647521	-2.996687	44076.612338
HLA B*3501	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.391627	1.394704	-2.996922	24639.212479
HLA B*3901	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.431143	1.434003	-2.997140	26986.266881
HLA A*1101	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.398525	1.401173	-2.997352	25033.692351
HLA B*2705	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.192557	1.195068	-2.997489	15579.636048
HLA B*4002	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.141545	1.143634	-2.997912	13853.046424
HLA B*4402	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.405573	1.407576	-2.997997	25443.295725
HLA A*0101	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.363064	1.365049	-2.998015	23070.878582
HLA B*1517	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-3.937821	0.939568	-2.998253	8666.055082

HLA B*0702	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.363348	1.365049	-2.998299	23085.985644
HLA A*2902	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.125183	1.126836	-2.998347	13340.849230
HLA A*3001	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.142020	1.143634	-2.998386	13868.193275
HLA B*0802	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.386855	1.388176	-2.998679	24369.971355
HLA B*1503	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-3.878182	0.879222	-2.998960	7554.089357
HLA A*3301	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.406614	1.407576	-2.999038	25504.345768
HLA B*5401	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.438572	1.439287	-2.999285	27451.866775
HLA B*4403	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.652760	1.653369	-2.999391	44953.171103
HLA B*1503	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.289539	1.289989	-2.999550	19477.775233
HLA A*0301	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.359798	1.360016	-2.999783	22898.042095
HLA B*5701	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.388023	1.388176	-2.999847	24435.583427
HLA A*2501	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.433939	1.434003	-2.999935	27160.558631
HLA B*0803	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.401410	1.401173	-3.000237	25200.553422
HLA A*2603	1:164-172	9	GRSITAESR	1.007055	0.640575	-4.647876	1.647630	-3.000245	44450.408244
HLA B*5801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.360459	1.360016	-3.000443	22932.877685
HLA B*4001	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.371088	1.370628	-3.000460	23501.069393
HLA A*0101	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.187243	1.186588	-3.000655	15390.147173
HLA A*3101	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.366069	1.365049	-3.001020	23231.065264
HLA A*2602	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.597237	1.596160	-3.001077	39558.271219
HLA A*0219	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.366631	1.365049	-3.001582	23261.121610
HLA B*1501	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.409203	1.407576	-3.001627	25656.849108
HLA B*5701	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.372288	1.370628	-3.001661	23566.126886
HLA B*7301	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.579658	1.577736	-3.001923	37989.052078
HLA A*2902	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.436112	1.434003	-3.002109	27296.814710
HLA B*5701	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.396826	1.394704	-3.002122	24935.968064
HLA A*3002	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.527406	1.525000	-3.002406	33682.623475
HLA A*2902	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.407951	1.405388	-3.002563	25582.974889
HLA A*0301	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.160487	1.157848	-3.002639	14470.609960
HLA A*0216	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.129793	1.126836	-3.002957	13483.205870
HLA B*4002	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.643292	1.640132	-3.003160	43983.715034
HLA B*1501	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.368468	1.365049	-3.003419	23359.737011
HLA B*1801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.363811	1.360016	-3.003795	23110.602606
HLA B*4801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.411607	1.407576	-3.004031	25799.235877
HLA B*4501	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.644354	1.640132	-3.004222	44091.398692
HLA B*4501	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.369300	1.365049	-3.004251	23404.516125
HLA A*6802	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.410418	1.405388	-3.005030	25728.709522
HLA A*2501	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.399775	1.394704	-3.005070	25105.844625
HLA A*3002	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.511046	1.505966	-3.005081	32437.430631
HLA B*4002	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.295406	1.289989	-3.005417	19742.675803
HLA B*4402	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.376369	1.370628	-3.005742	23788.620997
HLA A*0201	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-3.941726	0.935815	-3.005911	8744.324970
HLA B*1501	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.156488	1.150365	-3.006123	14337.981452
HLA B*1503	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.032181	1.025655	-3.006526	10769.150883
HLA B*4402	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.037261	1.030229	-3.007032	10895.848307
HLA A*0250	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.134041	1.126836	-3.007205	13615.733253
HLA B*5301	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.266724	1.259401	-3.007322	18480.916340
HLA B*5401	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.513412	1.505966	-3.007447	32614.624131
HLA A*0301	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.210658	1.203170	-3.007488	16242.681951
HLA B*1502	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.513553	1.505966	-3.007588	32625.212339
HLA A*6802	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.415446	1.407576	-3.007870	26028.305871
HLA A*8001	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.413383	1.405388	-3.007995	25904.967625
HLA A*6901	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.068993	1.060834	-3.008159	11721.769924
HLA B*4403	1:51-59	9	TRQSQAGHR	0.863025	0.777107	-4.648315	1.640132	-3.008183	44495.399220
HLA A*3301	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.379078	1.370628	-3.008451	23937.468695
HLA A*3001	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.255439	1.246696	-3.008743	18006.898833
HLA A*3201	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.605002	1.596160	-3.008842	40271.921502

HLA B*4601	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.379670	1.370628	-3.009043	23970.124711
HLA A*0203	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.416693	1.407576	-3.009117	26103.183611
HLA B*3901	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-3.907687	0.898490	-3.009196	8085.128942
HLA B*0702	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.268612	1.259401	-3.009211	18561.475096
HLA A*2403	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.374722	1.365049	-3.009673	23698.577487
HLA B*1509	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.397869	1.388176	-3.009694	24995.936022
HLA A*2603	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.587649	1.577736	-3.009913	38694.483629
HLA A*8001	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.369481	1.359429	-3.010051	23414.267576
HLA B*4402	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.398403	1.388176	-3.010227	25026.651008
HLA B*1503	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.417821	1.407576	-3.010245	26171.055054
HLA B*1509	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.321746	1.311098	-3.010648	20977.131000
HLA B*5401	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.533843	1.523182	-3.010662	34185.623040
HLA A*2603	1:131-139	9	GPTPRAPQR	1.211843	0.441526	-4.664350	1.653369	-3.010981	46168.986690
HLA B*4002	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.591338	1.580071	-3.011267	39024.535899
HLA A*3201	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.525237	1.513906	-3.011331	33514.854311
HLA B*5301	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.535502	1.523182	-3.012321	34316.440646
HLA B*0702	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.413644	1.401173	-3.012471	25920.528170
HLA B*1502	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.195377	1.182783	-3.012594	15681.105981
HLA B*3801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.377687	1.365049	-3.012638	23860.927889
HLA A*6901	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.377913	1.365049	-3.012864	23873.323265
HLA B*3801	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.452220	1.439287	-3.012933	28328.269209
HLA B*3801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.418423	1.405388	-3.013035	26207.325285
HLA A*0212	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.324173	1.311098	-3.013075	21094.688096
HLA A*0250	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.583737	1.570424	-3.013313	38347.509430
HLA A*0101	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.384085	1.370628	-3.013457	24215.028018
HLA A*0216	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.421268	1.407576	-3.013692	26379.582967
HLA A*3002	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.282390	1.268587	-3.013803	19159.751281
HLA B*4402	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.404970	1.391116	-3.013854	25407.945435
HLA B*4002	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.627513	1.613450	-3.014062	42414.345279
HLA A*3201	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.251017	1.236873	-3.014145	17824.493336
HLA B*1501	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.384867	1.370628	-3.014240	24258.690541
HLA B*4801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.402808	1.388176	-3.014632	25281.801775
HLA B*4001	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.422386	1.407576	-3.014810	26447.600761
HLA A*0211	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-3.950166	0.935291	-3.014875	8915.909248
HLA A*3101	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.375025	1.360016	-3.015010	23715.121921
HLA B*0801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.423054	1.407576	-3.015477	26488.266311
HLA B*5701	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.407000	1.391116	-3.015884	25526.983821
HLA A*6802	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-3.615886	0.599894	-3.015992	4129.387247
HLA A*0219	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.423624	1.407576	-3.016048	26523.110766
HLA B*4001	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.381103	1.365049	-3.016054	24049.357562
HLA A*3201	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.586512	1.570424	-3.016088	38593.299049
HLA B*1509	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.407234	1.391116	-3.016119	25540.797372
HLA B*5101	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.306305	1.289989	-3.016316	20244.417021
HLA A*3301	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.327512	1.311098	-3.016413	21257.477424
HLA A*3201	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.421893	1.405388	-3.016505	26417.571319
HLA A*0250	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.541587	1.525000	-3.016587	34800.653709
HLA B*0702	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.425330	1.407576	-3.017754	26627.487232
HLA B*5701	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.425567	1.407576	-3.017991	26642.040434
HLA B*3501	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.388800	1.370628	-3.018173	24479.378774
HLA B*1801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.168734	1.150365	-3.018368	14748.013622
HLA B*4801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.409880	1.391116	-3.018764	25696.854870
HLA B*5801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.353377	1.334516	-3.018861	22561.979844
HLA B*4801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.379137	1.360016	-3.019121	23940.706390
HLA A*3001	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.159096	1.139383	-3.019713	14424.339731
HLA B*5401	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.104621	1.084809	-3.019812	12723.915707
HLA A*0101	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.379844	1.360016	-3.019828	23979.722635

HLA B*0802	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.426148	1.405388	-3.020760	26677.664460
HLA A*2501	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.409311	1.388176	-3.021136	25663.234736
HLA B*3501	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.082832	1.060834	-3.021997	12101.289743
HLA B*5101	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.413165	1.391116	-3.022049	25891.937604
HLA A*6901	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.172718	1.150365	-3.022353	14883.951858
HLA B*0803	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.413543	1.391116	-3.022427	25914.499103
HLA B*4001	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-3.905004	0.882547	-3.022456	8035.332243
HLA B*3501	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.217767	1.195068	-3.022699	16510.768269
HLA A*0201	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.387755	1.365049	-3.022706	24420.517980
HLA A*3001	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.226352	1.203170	-3.023183	16840.396023
HLA A*0202	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.043473	1.020231	-3.023243	11052.819727
HLA B*4501	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.636702	1.613450	-3.023251	43321.312242
HLA A*0219	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.108136	1.084809	-3.023327	12827.310660
HLA A*2601	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.383399	1.360016	-3.023383	24176.806036
HLA A*6901	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.358154	1.334516	-3.023637	22811.492967
HLA A*0202	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.594261	1.570424	-3.023837	39288.052932
HLA B*5301	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.394733	1.370628	-3.024105	24816.060652
HLA A*0206	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.538667	0.514013	-3.024654	3456.745754
HLA A*2602	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.547947	1.523182	-3.024766	35314.044332
HLA A*3101	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.206819	1.181941	-3.024878	16099.733306
HLA A*0212	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.432802	1.407576	-3.025225	27089.534820
HLA B*7301	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.605632	1.580071	-3.025561	40330.352106
HLA A*2501	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.427297	1.401173	-3.026124	26748.331940
HLA B*1501	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-3.874855	0.848433	-3.026422	7496.443067
HLA A*0301	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.361448	1.334516	-3.026931	22985.168292
HLA A*0216	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.392137	1.365049	-3.027088	24668.154567
HLA B*7301	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.623798	1.596160	-3.027638	42053.120895
HLA B*1503	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.362427	1.334516	-3.027911	23037.079611
HLA A*6801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.416125	1.388176	-3.027949	26069.031862
HLA B*5701	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.393241	1.365049	-3.028192	24730.956807
HLA A*0211	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.089462	1.060834	-3.028628	12287.454031
HLA A*3001	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.170214	1.141236	-3.028977	14798.364001
HLA B*0702	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.420380	1.391116	-3.029264	26325.693472
HLA B*1801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.191787	1.162375	-3.029412	15552.015374
HLA A*2403	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.224585	1.195068	-3.029518	16772.024477
HLA A*1101	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.216508	1.186588	-3.029920	16462.961332
HLA B*3901	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.421059	1.391116	-3.029943	26366.884779
HLA B*0803	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.435781	1.405388	-3.030393	27276.000793
HLA A*3201	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.431599	1.401173	-3.030426	27014.604334
HLA A*3002	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.225516	1.195068	-3.030448	16807.993971
HLA B*4001	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.390276	1.359429	-3.030847	24562.686705
HLA B*3801	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.538030	1.505966	-3.032065	34516.780572
HLA B*3901	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.433243	1.401173	-3.032071	27117.100495
HLA B*3501	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.423538	1.391116	-3.032422	26517.802275
HLA B*5301	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.367432	1.334516	-3.032915	23304.072686
HLA B*4501	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.603407	1.570424	-3.032983	40124.261426
HLA B*5701	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.392524	1.359429	-3.033095	24690.183975
HLA B*4002	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.604227	1.571013	-3.033214	40200.089652
HLA A*0201	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.393232	1.360016	-3.033216	24730.421646
HLA B*5101	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.393401	1.360016	-3.033385	24740.056318
HLA A*6802	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.054201	1.020231	-3.033970	11329.241517
HLA A*2301	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.540084	1.505966	-3.034118	34680.370745
HLA A*0211	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.077179	1.042623	-3.034555	11944.797691
HLA A*0211	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.399655	1.365049	-3.034606	25098.918769
HLA A*0212	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.399737	1.365049	-3.034688	25103.671602

HLA A*6801	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.612537	1.577736	-3.034801	40976.716029
HLA A*3002	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.429538	1.394704	-3.034834	26886.737849
HLA B*4402	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.436244	1.401173	-3.035071	27305.085636
HLA A*3301	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.615166	1.580071	-3.035095	41225.527732
HLA A*6802	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-3.979111	0.943496	-3.035615	9530.403637
HLA B*4403	1:167-175	9	ITAESRDAR	0.938361	0.675089	-4.649255	1.613450	-3.035805	44591.789546
HLA B*4001	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.396032	1.360016	-3.036016	24890.413248
HLA B*5101	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.424583	1.388176	-3.036407	26581.718154
HLA A*2601	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.401579	1.365049	-3.036530	25210.371252
HLA B*1801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.438250	1.401173	-3.037077	27431.528230
HLA A*0250	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.560278	1.523182	-3.037096	36331.017009
HLA B*4601	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.402305	1.365049	-3.037256	25252.549558
HLA B*4001	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.348378	1.311098	-3.037279	22303.730194
HLA B*5301	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.607704	1.570424	-3.037280	40523.249118
HLA B*0702	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.397150	1.359429	-3.037721	24954.591328
HLA B*0802	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.438908	1.401173	-3.037735	27473.112144
HLA A*6802	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.403334	1.365049	-3.038285	25312.457217
HLA B*4801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.398400	1.359429	-3.038971	25026.515617
HLA A*1101	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.433814	1.394704	-3.039110	27152.772160
HLA A*2601	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.409864	1.370628	-3.039236	25695.881769
HLA B*4501	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.610293	1.571013	-3.039280	40765.558053
HLA A*3301	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.400365	1.360016	-3.040349	25139.958560
HLA B*2705	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.448412	1.407576	-3.040835	28080.932513
HLA B*1502	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.432031	1.391116	-3.040915	27041.508589
HLA A*2501	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.446335	1.405388	-3.040947	27946.960495
HLA A*2403	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.401079	1.360016	-3.041063	25181.337911
HLA B*4002	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.611499	1.570424	-3.041075	40878.850747
HLA A*2501	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.411703	1.370628	-3.041076	25804.958923
HLA A*2301	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.436088	1.394704	-3.041384	27295.338022
HLA B*5401	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-3.322660	0.281226	-3.041435	2102.134433
HLA B*4402	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.406595	1.365049	-3.041546	25503.241986
HLA A*2301	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.475670	1.434003	-3.041667	29899.935451
HLA A*3001	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.301954	1.259401	-3.042553	20042.598594
HLA B*1801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.430960	1.388176	-3.042784	26974.881851
HLA B*5401	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.413660	1.370628	-3.043033	25921.509779
HLA B*1509	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.450850	1.407576	-3.043274	28239.063579
HLA B*4403	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.438231	1.394704	-3.043527	27430.341043
HLA A*6802	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.403823	1.360016	-3.043807	25340.956266
HLA B*5401	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.230544	1.186588	-3.043956	17003.713606
HLA A*2301	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.194568	1.150365	-3.044203	15651.950551
HLA B*0803	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.403713	1.359429	-3.044283	25334.513773
HLA B*0803	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.439209	1.394704	-3.044504	27492.142924
HLA A*8001	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.231134	1.186588	-3.044546	17026.818328
HLA A*3002	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.737279	0.692679	-3.044600	5461.083328
HLA B*0801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.415577	1.370628	-3.044950	26036.192440
HLA B*5301	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.404777	1.359429	-3.045348	25396.676693
HLA B*1509	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.510520	1.465037	-3.045483	32398.146268
HLA A*0211	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.551568	1.505966	-3.045602	35609.675350
HLA A*2902	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.130644	1.084809	-3.045835	13509.636982
HLA B*1502	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.569039	1.523182	-3.045857	37071.382697
HLA B*3801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.510776	1.464619	-3.046158	32417.256374
HLA A*2301	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.228533	1.181941	-3.046592	16925.153742
HLA B*1801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.452424	1.405388	-3.047037	28341.605340
HLA B*4403	1:137-145	9	PQRNPAPAR	1.014396	0.556028	-4.617925	1.570424	-3.047501	41488.192948
HLA A*6801	1:264-272	9	AFLIGLVNI	1.253248	0.361793	-4.662548	1.615041	-3.047507	45977.810697
HLA B*0801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.407646	1.360016	-3.047630	25564.989076

HLA B*4601	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.407718	1.360016	-3.047703	25569.276852
HLA B*5101	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.234808	1.186588	-3.048220	17171.494567
HLA A*2601	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.150346	1.101846	-3.048500	14136.648526
HLA A*0212	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.409253	1.360016	-3.049237	25659.764089
HLA A*0201	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.339306	1.289989	-3.049317	21842.690960
HLA A*6802	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-3.985864	0.935815	-3.050049	9679.740495
HLA B*4501	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.628039	1.577736	-3.050303	42465.774781
HLA B*4403	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.631006	1.580071	-3.050936	42756.923788
HLA A*3301	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.628734	1.577736	-3.050999	42533.830856
HLA A*1101	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.458601	1.407576	-3.051025	28747.576756
HLA B*4801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.362127	1.311098	-3.051028	23021.132743
HLA B*3501	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.458672	1.407576	-3.051096	28752.242771
HLA A*2403	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.458709	1.407576	-3.051133	28754.731622
HLA A*8001	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.416506	1.365049	-3.051457	26091.888829
HLA B*0803	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.459271	1.407576	-3.051695	28791.934486
HLA A*8001	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.459334	1.407576	-3.051758	28796.140345
HLA B*1502	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.516810	1.465037	-3.051773	32870.759068
HLA A*1101	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.443015	1.391116	-3.051899	27734.143525
HLA A*0101	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.386486	1.334516	-3.051970	24349.281444
HLA B*4403	1:273-281	9	VLMTALATI	1.272095	0.298918	-4.623115	1.571013	-3.052101	41986.969686
HLA B*1501	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.049746	0.997451	-3.052295	11213.629727
HLA A*2603	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.575519	1.523182	-3.052337	37628.652333
HLA B*4001	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.342379	1.289989	-3.052390	21997.800933
HLA A*3101	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.289849	1.236873	-3.052977	19491.689385
HLA A*0202	1:274-282	9	LMTALATIG	0.983162	-0.546352	-3.490089	0.436810	-3.053280	3090.932252
HLA A*2501	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.460934	1.407576	-3.053358	28902.424862
HLA A*0201	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.236326	1.182783	-3.053543	17231.610292
HLA A*6801	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.633704	1.580071	-3.053633	43023.294215
HLA B*1517	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.418900	1.365049	-3.053851	26236.122176
HLA B*4002	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.650164	1.596160	-3.054004	44685.245922
HLA B*0801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.204530	1.150365	-3.054165	16015.123187
HLA B*0802	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.462055	1.407576	-3.054479	28977.104379
HLA A*3101	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.249758	1.195068	-3.054690	17772.882507
HLA A*0101	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.181618	1.126836	-3.054782	15192.110334
HLA B*0802	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.449854	1.394704	-3.055150	28174.363245
HLA B*5801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.302081	1.246696	-3.055385	20048.454574
HLA B*7301	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.578824	1.523182	-3.055643	37916.163713
HLA A*0203	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.081469	1.025655	-3.055814	12063.378602
HLA A*0219	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.292796	1.236873	-3.055923	19624.370570
HLA B*1501	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-3.995703	0.939568	-3.056135	9901.553938
HLA B*4002	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.634061	1.577736	-3.056325	43058.686955
HLA B*4501	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.652615	1.596160	-3.056454	44938.095748
HLA B*1503	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.315980	1.259401	-3.056579	20700.481821
HLA B*0802	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.427233	1.370628	-3.056606	26744.425177
HLA B*4601	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.367871	1.311098	-3.056773	23327.660163
HLA A*6901	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.238826	1.181941	-3.056885	17331.083559
HLA B*0802	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.416433	1.359429	-3.057004	26087.513415
HLA B*4402	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.416710	1.359429	-3.057281	26104.172137
HLA A*2403	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.243983	1.186588	-3.057395	17538.111860
HLA A*0206	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.563405	1.505966	-3.057439	36593.564877
HLA B*0802	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.448656	1.391116	-3.057540	28096.736090
HLA B*5301	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.463051	1.405388	-3.057663	29043.648148
HLA A*3301	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.185448	1.126836	-3.058612	15326.668578
HLA B*5801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.327307	1.268587	-3.058720	21247.474727
HLA B*1509	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.180016	1.120296	-3.059719	15136.161644
HLA B*2705	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.241784	1.181941	-3.059843	17449.529355

HLA A*3001	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.255805	1.195068	-3.060738	18022.102038
HLA B*5701	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.420918	1.360016	-3.060902	26358.327653
HLA A*0201	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.396295	1.334516	-3.061779	24905.499108
HLA A*1101	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.059388	0.997451	-3.061937	11465.381184
HLA A*2403	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.308897	1.246696	-3.062201	20365.578771
HLA A*2601	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.396760	1.334516	-3.062244	24932.191127
HLA B*4501	1:235-243	9	KLNSNVGDL	1.082316	0.497755	-4.642742	1.580071	-3.062671	43928.070658
HLA B*1501	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.422910	1.360016	-3.062894	26479.526540
HLA B*1517	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.454283	1.391116	-3.063167	28463.145233
HLA A*0203	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.423368	1.360016	-3.063353	26507.475283
HLA A*3101	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.128275	1.064763	-3.063512	13436.167162
HLA B*1502	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.423190	1.359429	-3.063761	26496.578933
HLA A*3001	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.251706	1.187527	-3.064178	17852.769301
HLA B*1517	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.071596	1.007379	-3.064218	11792.243058
HLA B*0802	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.375796	1.311098	-3.064698	23757.240425
HLA B*4402	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.424954	1.360016	-3.064938	26604.448923
HLA B*4801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.399563	1.334516	-3.065047	25093.623815
HLA A*0206	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.192172	1.126836	-3.065336	15565.819585
HLA B*0801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.399864	1.334516	-3.065348	25111.006309
HLA B*0802	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.430668	1.365049	-3.065619	26956.792460
HLA B*1801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.456837	1.391116	-3.065721	28631.017273
HLA A*2603	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.425356	1.359429	-3.065927	26629.071848
HLA B*1503	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.038069	0.971364	-3.066705	10916.144381
HLA A*1101	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.303650	1.236873	-3.066778	20121.036869
HLA A*2402	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.572819	1.505966	-3.066853	37395.479484
HLA A*0219	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.249034	1.181941	-3.067093	17743.293174
HLA A*0250	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.531748	1.464619	-3.067129	34021.053570
HLA B*4402	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.378324	1.311098	-3.067226	23895.935572
HLA A*2603	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.462797	1.394704	-3.068093	29026.683829
HLA B*5801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.358518	1.289989	-3.068529	22830.629175
HLA B*3801	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.533992	1.465037	-3.068955	34197.276273
HLA A*2501	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.460443	1.391116	-3.069328	28869.764317
HLA A*0250	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.474843	1.405388	-3.069455	29843.051751
HLA B*7301	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.465509	1.394704	-3.070804	29208.464606
HLA B*1517	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.257549	1.186588	-3.070961	18094.590630
HLA B*1517	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.442004	1.370628	-3.071377	27669.701892
HLA B*4403	1:146-154	9	PAEGGAGSR	1.143137	0.453023	-4.667828	1.596160	-3.071667	46540.128775
HLA B*5401	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.890085	0.818322	-3.071763	7763.983591
HLA A*2902	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.253881	1.181941	-3.071940	17942.428160
HLA B*1801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.506009	1.434003	-3.072006	32063.368814
HLA B*4402	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.362009	1.289989	-3.072020	23014.906497
HLA A*0101	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.362037	1.289989	-3.072048	23016.400642
HLA B*1503	1:138-146	9	QRNPAPARP	0.846785	0.035314	-3.954418	0.882099	-3.072319	9003.641767
HLA B*4001	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.406931	1.334516	-3.072415	25522.979288
HLA A*2403	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.230509	1.157848	-3.072661	17002.333839
HLA A*2902	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.437938	1.365049	-3.072889	27411.797926
HLA B*4403	1:29-37	9	RAATGPGRI	1.220311	0.357425	-4.651181	1.577736	-3.073446	44790.043001
HLA A*3002	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.017008	0.943496	-3.073513	10399.404896
HLA A*0301	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.364237	1.289989	-3.074247	23133.243359
HLA B*1509	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.469280	1.394704	-3.074575	29463.182208
HLA B*5301	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.581731	1.505966	-3.075765	38170.750829
HLA B*4601	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.410364	1.334516	-3.075847	25725.508363
HLA B*3901	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.483550	1.407576	-3.075974	30447.414771
HLA B*0803	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.234016	1.157848	-3.076168	17140.217175
HLA B*0802	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.436220	1.360016	-3.076204	27303.608501
HLA B*5801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.106482	1.030229	-3.076253	12778.549966

HLA A*3001	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.161149	1.084809	-3.076341	14492.703007
HLA A*2402	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.471213	1.394704	-3.076509	29594.654739
HLA B*4402	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.239047	1.162375	-3.076672	17339.899169
HLA A*6901	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-3.870509	0.793787	-3.076721	7421.790649
HLA A*0216	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.137556	1.060834	-3.076721	13726.375145
HLA B*7301	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.591204	1.513906	-3.077298	39012.504005
HLA A*2603	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.541977	1.464619	-3.077359	34831.920181
HLA B*1517	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.367899	1.289989	-3.077910	23329.174613
HLA A*3002	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.205212	1.126836	-3.078375	16040.268519
HLA B*4601	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.368661	1.289989	-3.078671	23370.101944
HLA B*4501	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.467073	1.388176	-3.078898	29313.892113
HLA A*8001	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.368950	1.289989	-3.078960	23385.657967
HLA A*6901	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.347724	1.268587	-3.079137	22270.211728
HLA B*5401	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.544064	1.464619	-3.079445	34999.654657
HLA B*5101	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.414079	1.334516	-3.079562	25946.483186
HLA A*0203	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.326332	1.246696	-3.079636	21199.825445
HLA B*7301	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.605357	1.525000	-3.080357	40304.832804
HLA B*5101	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.488087	1.407576	-3.080511	30767.150718
HLA A*6802	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.141531	1.060834	-3.080697	13852.596771
HLA B*4601	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.349933	1.268587	-3.081346	22383.750788
HLA A*3101	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.017798	0.935815	-3.081983	10418.325322
HLA A*3201	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.607138	1.525000	-3.082138	40470.450010
HLA B*7301	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.588540	1.505966	-3.082574	38773.902175
HLA A*0250	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.588767	1.505966	-3.082802	38794.254478
HLA B*3901	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.453747	1.370628	-3.083120	28428.058875
HLA A*1101	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.453778	1.370628	-3.083150	28430.058250
HLA A*0202	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.589611	1.505966	-3.083645	38869.671960
HLA B*5301	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.265593	1.181941	-3.083653	18432.888615
HLA A*2902	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.266681	1.182783	-3.083898	18479.116793
HLA B*4801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.330707	1.246696	-3.084011	21414.455004
HLA A*0301	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.886654	0.802529	-3.084126	7702.901789
HLA B*0801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-3.128659	0.044127	-3.084531	1344.803437
HLA A*6802	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.353194	1.268587	-3.084607	22552.461344
HLA A*2603	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.609690	1.525000	-3.084689	40708.919388
HLA B*7301	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.550212	1.465037	-3.085176	35498.692840
HLA B*3501	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.375516	1.289989	-3.085527	23741.950987
HLA A*2603	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.268840	1.182783	-3.086058	18571.217958
HLA B*4001	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.354824	1.268587	-3.086238	22637.292875
HLA A*0212	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.022920	0.935815	-3.087105	10541.921838
HLA A*2602	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.482115	1.394704	-3.087410	30346.938749
HLA A*3201	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.452603	1.365049	-3.087554	28353.260432
HLA A*2602	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.521666	1.434003	-3.087663	33240.390616
HLA A*6901	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.347113	1.259401	-3.087712	22238.909110
HLA A*0301	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.347264	1.259401	-3.087862	22246.610285
HLA B*5701	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.422574	1.334516	-3.088058	26459.049525
HLA B*3801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.495836	1.407576	-3.088260	31321.018824
HLA B*0802	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.356871	1.268587	-3.088284	22744.211808
HLA A*0101	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.283384	1.195068	-3.088316	19203.646337
HLA B*0702	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.246440	1.157848	-3.088592	17637.636874
HLA B*1501	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.190664	1.101846	-3.088817	15511.850951
HLA B*4402	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.423563	1.334516	-3.089047	26519.380364
HLA B*1509	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.348479	1.259401	-3.089077	22308.919208
HLA A*0216	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.131729	1.042623	-3.089106	13543.444778
HLA B*1501	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.424275	1.334516	-3.089759	26562.886485
HLA A*0201	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.272574	1.181941	-3.090633	18731.550121

HLA A*0203	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.272795	1.181941	-3.090854	18741.078091
HLA B*4801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.359756	1.268587	-3.091169	22895.812438
HLA B*4001	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.328076	1.236873	-3.091203	21285.095493
HLA A*8001	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.451313	1.360016	-3.091297	28269.175352
HLA B*0802	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.425936	1.334516	-3.091420	26664.678533
HLA B*1501	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.338197	1.246696	-3.091501	21786.987504
HLA B*0702	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.462142	1.370628	-3.091514	28982.905188
HLA B*5101	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.403036	1.311098	-3.091937	25295.072116
HLA B*1517	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.117595	1.025655	-3.091939	13109.756932
HLA A*3001	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.606225	0.514013	-3.092211	4038.541312
HLA A*2902	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.382762	1.289989	-3.092773	24141.386875
HLA A*3101	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.382988	1.289989	-3.092999	24153.927945
HLA B*3501	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.255756	1.162375	-3.093381	18020.054705
HLA A*2301	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.498784	1.405388	-3.093397	31534.393614
HLA A*2301	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.501110	1.407576	-3.093534	31703.738295
HLA B*4001	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.340493	1.246696	-3.093797	21902.446650
HLA B*2705	1:138-146	9	QRNPAPARP	0.846785	0.035314	-3.976156	0.882099	-3.094056	9465.763345
HLA A*1101	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.459475	1.365049	-3.094426	28805.488898
HLA A*3101	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.363250	1.268587	-3.094663	23080.740750
HLA B*5101	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.354131	1.259401	-3.094730	22601.194441
HLA A*3001	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.252714	1.157848	-3.094866	17894.250883
HLA A*6901	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.038370	0.943496	-3.094874	10923.706055
HLA A*0212	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.429686	1.334516	-3.095170	26895.903030
HLA B*1801	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.503018	1.407576	-3.095442	31843.313768
HLA A*3001	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-3.958159	0.862516	-3.095643	9081.520911
HLA B*5301	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.455812	1.360016	-3.095797	28563.564541
HLA A*3001	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.258677	1.162375	-3.096302	18141.638760
HLA B*1801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.467008	1.370628	-3.096380	29309.452072
HLA A*0203	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.431046	1.334516	-3.096530	26980.281843
HLA B*5801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.355969	1.259401	-3.096567	22697.012084
HLA A*2902	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.333468	1.236873	-3.096595	21551.012113
HLA A*0206	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.461954	1.365049	-3.096905	28970.364357
HLA B*5401	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.531031	1.434003	-3.097028	33964.964567
HLA B*5701	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.365761	1.268587	-3.097174	23214.607346
HLA B*4402	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.365914	1.268587	-3.097327	23222.772030
HLA A*1101	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.456886	1.359429	-3.097457	28634.270161
HLA A*0301	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.366490	1.268587	-3.097903	23253.572430
HLA A*0203	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-3.891692	0.793787	-3.097904	7792.766378
HLA A*2902	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.432447	1.334516	-3.097930	27067.414597
HLA A*2402	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.503389	1.405388	-3.098002	31870.543874
HLA A*0216	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.279960	1.181941	-3.098020	19052.874183
HLA A*3301	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.623056	1.525000	-3.098055	41981.291449
HLA B*3501	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.463136	1.365049	-3.098087	29049.305124
HLA B*4402	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.335218	1.236873	-3.098345	21638.045881
HLA A*2601	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.388471	1.289989	-3.098482	24460.845491
HLA A*2403	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.367185	1.268587	-3.098598	23290.838838
HLA B*3801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.490235	1.391116	-3.099119	30919.659902
HLA B*4403	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.613432	1.513906	-3.099526	41061.263018
HLA A*0250	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.261968	1.162375	-3.099593	18279.661254
HLA B*5401	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.487946	1.388176	-3.099771	30757.165526
HLA A*0219	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.389808	1.289989	-3.099819	24536.257533
HLA A*0219	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.459908	1.360016	-3.099892	28834.176722
HLA A*6802	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.262323	1.162375	-3.099948	18294.599886
HLA B*0802	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.346933	1.246696	-3.100237	22229.647167
HLA A*3001	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.071737	0.971364	-3.100373	11796.071363
HLA A*0206	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-3.979666	0.879222	-3.100443	9542.579197

HLA A*6802	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.434996	1.334516	-3.100479	27226.760206
HLA A*3001	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.220789	1.120296	-3.100492	16626.036124
HLA A*2601	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.283713	1.182783	-3.100930	19218.196390
HLA B*1517	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.347856	1.246696	-3.101160	22276.959596
HLA A*0203	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.263655	1.162375	-3.101280	18350.803028
HLA B*3901	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.259294	1.157848	-3.101446	18167.469070
HLA B*3501	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-3.792501	0.691047	-3.101454	6201.562126
HLA A*6802	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-3.780787	0.679020	-3.101767	6036.518925
HLA B*2705	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.243424	1.141236	-3.102187	17515.545132
HLA A*3001	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-3.122127	0.019638	-3.102489	1324.729605
HLA B*1517	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.510515	1.407576	-3.102939	32397.795729
HLA A*2501	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.463432	1.360016	-3.103416	29069.113218
HLA B*1509	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.463446	1.360016	-3.103430	29070.056797
HLA A*6801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.253797	1.150365	-3.103432	17938.934105
HLA B*3501	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-3.593368	0.489523	-3.103846	3920.740943
HLA A*2402	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.351211	1.246696	-3.104515	22449.722741
HLA A*0212	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.772808	0.667908	-3.104899	5926.628641
HLA A*3301	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.628485	1.523182	-3.105304	42509.446897
HLA A*2902	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.465321	1.360016	-3.105305	29195.826177
HLA A*6801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.263213	1.157848	-3.105365	18332.148663
HLA A*2402	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.255801	1.150365	-3.105436	18021.907044
HLA B*5801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.263425	1.157848	-3.105577	18341.076577
HLA B*0801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.287580	1.181941	-3.105639	19390.092435
HLA A*2902	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.374243	1.268587	-3.105656	23672.437752
HLA A*6801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.620068	0.514013	-3.106055	4169.343679
HLA B*5101	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.288043	1.181941	-3.106102	19410.768406
HLA A*3001	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.775923	0.669638	-3.106285	5969.296244
HLA A*8001	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.441130	1.334516	-3.106614	27614.073199
HLA B*1501	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.167507	1.060834	-3.106673	14706.424541
HLA B*0801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.397522	1.289989	-3.107532	24975.930696
HLA B*0803	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.472752	1.365049	-3.107703	29699.708747
HLA B*4801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.265694	1.157848	-3.107846	18437.177069
HLA B*2705	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.468340	1.360016	-3.108324	29399.494122
HLA A*0212	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.258740	1.150365	-3.108375	18144.288848
HLA A*0206	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.128792	1.020231	-3.108562	13452.168080
HLA A*6801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.468009	1.359429	-3.108579	29377.076904
HLA A*3101	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.259024	1.150365	-3.108659	18156.169926
HLA A*0101	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.377290	1.268587	-3.108703	23839.122497
HLA B*5101	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.304322	1.195068	-3.109254	20152.192803
HLA B*3901	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.468812	1.359429	-3.109383	29431.480158
HLA A*0250	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.474674	1.365049	-3.109625	29831.429788
HLA A*3201	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.615761	1.505966	-3.109795	41281.991824
HLA B*1801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.369626	1.259401	-3.110225	23422.122346
HLA B*3801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.505008	1.394704	-3.110304	31989.560247
HLA A*0212	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.107887	0.997451	-3.110435	12819.956970
HLA B*1503	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.470539	1.360016	-3.110523	29548.740601
HLA A*2501	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.379116	1.268587	-3.110529	23939.540770
HLA B*0801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.251778	1.141236	-3.110542	17855.763578
HLA A*0212	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.400541	1.289989	-3.110552	25150.160959
HLA B*5101	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.212556	1.101846	-3.110710	16313.837211
HLA A*0202	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.400703	1.289989	-3.110714	25159.550822
HLA A*2403	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.347844	1.236873	-3.110972	22276.357024
HLA B*1801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.470675	1.359429	-3.111246	29558.013670
HLA A*2501	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.476431	1.365049	-3.111383	29952.390138
HLA A*8001	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.379992	1.268587	-3.111405	23987.896869

HLA B*1503	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-3.446093	0.334139	-3.111954	2793.142095
HLA B*4002	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.546040	1.434003	-3.112036	35159.255968
HLA A*6901	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.239378	1.126836	-3.112542	17353.130992
HLA A*0203	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.173517	1.060834	-3.112683	14911.354032
HLA A*3002	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.477794	1.365049	-3.112745	30046.520423
HLA A*6802	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.359476	1.246696	-3.112781	22881.077388
HLA A*0216	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.472837	1.360016	-3.112821	29705.493507
HLA A*0206	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.520480	1.407576	-3.112903	33149.702005
HLA A*2402	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.402972	1.289989	-3.112983	25291.377610
HLA B*5701	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.403135	1.289989	-3.113145	25300.820198
HLA B*1501	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.084514	0.971364	-3.113150	12148.254754
HLA B*5801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.308300	1.195068	-3.113232	20337.613406
HLA A*6802	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-3.748312	0.634444	-3.113868	5601.598599
HLA A*0301	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.350990	1.236873	-3.114118	22438.309295
HLA A*0206	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.360975	1.246696	-3.114280	22960.188086
HLA A*3001	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.932902	0.818322	-3.114580	8568.437308
HLA B*4403	1:119-127	9	AEAYASELP	0.543268	-0.008008	-3.650000	0.535260	-3.114740	4466.837304
HLA A*3001	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.265389	1.150365	-3.115024	18424.215027
HLA A*0212	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.199939	1.084809	-3.115131	15846.720202
HLA A*0250	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.485836	1.370628	-3.115209	30608.107104
HLA B*3801	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.503664	1.388176	-3.115489	31890.722944
HLA B*4501	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.259243	1.143634	-3.115609	18165.306951
HLA B*1501	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.405658	1.289989	-3.115669	25448.251442
HLA A*2402	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.310992	1.195068	-3.115925	20464.092843
HLA A*0212	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.362639	1.246696	-3.115943	23048.298867
HLA B*3501	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.257194	1.141236	-3.115958	18079.815317
HLA A*3301	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.450855	1.334516	-3.116339	28239.369121
HLA A*2402	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.475868	1.359429	-3.116438	29913.525987
HLA A*2601	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.385227	1.268587	-3.116640	24278.778088
HLA B*0801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.060164	0.943496	-3.116668	11485.868191
HLA B*4002	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.642324	1.525000	-3.117324	43885.790032
HLA B*5401	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.477409	1.359429	-3.117980	30019.874317
HLA B*3501	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.125522	1.007379	-3.118143	13351.246122
HLA B*5101	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.483515	1.365049	-3.118466	30444.944114
HLA A*0301	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.365266	1.246696	-3.118570	23188.123301
HLA A*2602	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.453851	1.334516	-3.119334	28434.826557
HLA A*6802	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.633361	0.514013	-3.119348	4298.937009
HLA A*6801	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.644490	1.525000	-3.119490	44105.235578
HLA B*5701	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.357195	1.236873	-3.120323	22761.198173
HLA B*3901	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.308342	1.187527	-3.120815	20339.593939
HLA B*1502	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.480924	1.360016	-3.120908	30263.816793
HLA A*2402	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.303265	1.181941	-3.121324	20103.192963
HLA A*0219	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.456557	1.334516	-3.122041	28612.591220
HLA A*2301	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.510396	1.388176	-3.122220	32388.858270
HLA B*3501	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.305380	1.182783	-3.122597	20201.312076
HLA B*3801	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.433802	1.311098	-3.122704	27152.037702
HLA B*4402	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.369572	1.246696	-3.122876	23419.208172
HLA A*2601	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.207707	1.084809	-3.122898	16132.689950
HLA A*2403	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.413428	1.289989	-3.123438	25907.630479
HLA A*6801	1:78-86	9	ADARLNRFI	1.288538	0.234644	-4.646621	1.523182	-3.123440	44322.181618
HLA B*4501	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.285931	1.162375	-3.123556	19316.593517
HLA B*0801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.208435	1.084809	-3.123626	16159.768230
HLA A*2501	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.413745	1.289989	-3.123756	25926.558641
HLA B*4403	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.563196	1.439287	-3.123908	36575.950044
HLA B*4001	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.286436	1.162375	-3.124061	19339.074223
HLA A*2301	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.435252	1.311098	-3.124154	27242.819959

HLA B*4002	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.630332	1.505966	-3.124367	42690.589265
HLA A*3101	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.282324	1.157848	-3.124476	19156.849241
HLA A*2403	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.459290	1.334516	-3.124773	28793.180603
HLA A*0203	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.393612	1.268587	-3.125025	24752.104938
HLA A*0250	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.122533	0.997451	-3.125082	13259.686527
HLA B*4403	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.650188	1.525000	-3.125187	44687.663410
HLA B*5701	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.371957	1.246696	-3.125261	23548.157631
HLA B*0801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.064985	0.939568	-3.125417	11614.084229
HLA A*0201	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.394127	1.268587	-3.125540	24781.447762
HLA B*2705	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.312339	1.186588	-3.125751	20527.627221
HLA A*0250	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.527535	1.401173	-3.126362	33692.647025
HLA B*5401	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.534647	1.407576	-3.127071	34248.931215
HLA A*0206	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.396114	1.268587	-3.127527	24895.126597
HLA B*4801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.417939	1.289989	-3.127949	26178.135136
HLA B*0803	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.387753	1.259401	-3.128351	24420.385868
HLA B*4801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.388004	1.259401	-3.128603	24434.525899
HLA B*4002	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.494252	1.365049	-3.129203	31207.022038
HLA A*3301	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.517653	1.388176	-3.129477	32934.661053
HLA A*2501	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.172126	1.042623	-3.129503	14863.674510
HLA A*2601	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.376553	1.246696	-3.129857	23798.661232
HLA B*5401	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.521295	1.391116	-3.130179	33211.990117
HLA B*4501	1:74-82	9	PPAAADARL	1.380529	0.144471	-4.655389	1.525000	-3.130389	45226.127946
HLA A*2603	1:210-218	9	VALFFVWMI	1.152802	0.312235	-4.595750	1.465037	-3.130713	39423.037192
HLA B*1501	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.151192	1.020231	-3.130962	14164.207326
HLA A*8001	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.367892	1.236873	-3.131020	23328.795991
HLA A*0101	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.390661	1.259401	-3.131260	24584.488927
HLA A*2602	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.596098	1.464619	-3.131479	39454.614423
HLA A*2601	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.390938	1.259401	-3.131537	24600.187861
HLA B*4601	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.368689	1.236873	-3.131816	23371.619149
HLA B*4501	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.368752	1.236873	-3.131880	23375.033221
HLA B*1801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.313882	1.181941	-3.131942	20600.718325
HLA A*0211	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.539893	1.407576	-3.132317	34665.177100
HLA B*0702	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.466987	1.334516	-3.132470	29308.025059
HLA B*0803	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.493120	1.360016	-3.133104	31125.753653
HLA A*2402	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.498387	1.365049	-3.133338	31505.575800
HLA B*1502	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.315447	1.181941	-3.133506	20675.076304
HLA B*0803	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.402160	1.268587	-3.133573	25244.080942
HLA A*0201	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.393029	1.259401	-3.133628	24718.918482
HLA A*0206	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.493740	1.360016	-3.133724	31170.239548
HLA B*1517	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.493799	1.360016	-3.133783	31174.455522
HLA A*6801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.328983	1.195068	-3.133915	21329.589836
HLA B*0802	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.320931	1.186588	-3.134343	20937.789006
HLA B*1509	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.468887	1.334516	-3.134371	29436.575672
HLA B*3801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.505149	1.370628	-3.134522	31999.945531
HLA B*3801	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.535935	1.401173	-3.134762	34350.616911
HLA B*4601	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.285557	1.150365	-3.135192	19299.985061
HLA A*0212	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.403893	1.268587	-3.135307	25345.069353
HLA B*3901	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.297723	1.162375	-3.135348	19848.267581
HLA A*0301	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.330547	1.195068	-3.135479	21406.578665
HLA B*4501	1:199-207	9	WSTLKVSLL	1.170760	0.343146	-4.649598	1.513906	-3.135692	44627.024008
HLA A*0201	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.382572	1.246696	-3.135876	24130.810412
HLA A*2601	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.322646	1.186588	-3.136058	21020.640414
HLA A*1101	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.496266	1.360016	-3.136250	31352.042291
HLA A*3201	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.527514	1.391116	-3.136398	33691.006604
HLA A*3002	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.072268	0.935815	-3.136453	11810.502472

HLA B*2705	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.470985	1.334516	-3.136469	29579.128744
HLA A*0101	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.277799	1.141236	-3.136563	18958.281754
HLA A*0219	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.287143	1.150365	-3.136778	19370.591174
HLA A*6901	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.829458	0.692679	-3.136779	6752.405234
HLA A*0216	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.383845	1.246696	-3.137149	24201.669641
HLA A*3001	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-3.997832	0.860615	-3.137217	9950.204143
HLA A*2301	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.502624	1.365049	-3.137575	31814.385758
HLA A*1101	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.427590	1.289989	-3.137601	26766.426246
HLA B*4801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.319655	1.181941	-3.137714	20876.373041
HLA A*3301	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.497161	1.359429	-3.137732	31416.730754
HLA B*1801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.406469	1.268587	-3.137882	25495.792710
HLA A*2603	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.529481	1.391116	-3.138365	33843.907996
HLA B*0802	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.397935	1.259401	-3.138534	24999.722615
HLA B*5701	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.325172	1.186588	-3.138584	21143.244864
HLA B*1801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.428847	1.289989	-3.138858	26844.008283
HLA B*0801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.259332	1.120296	-3.139036	18169.041682
HLA A*0202	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.546900	1.407576	-3.139323	35228.940944
HLA B*1503	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.289866	1.150365	-3.139501	19492.427534
HLA B*4601	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.386239	1.246696	-3.139544	24335.454046
HLA B*4001	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.280957	1.141236	-3.139720	19096.627694
HLA A*0203	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.327408	1.187527	-3.139881	21252.418000
HLA A*2301	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.499767	1.359429	-3.140337	31605.784088
HLA A*0301	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.138162	0.997451	-3.140711	13745.547129
HLA B*5401	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.546113	1.405388	-3.140725	35165.152900
HLA A*0202	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.505948	1.365049	-3.140899	32058.859190
HLA A*2902	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.387807	1.246696	-3.141111	24423.424624
HLA B*4002	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.580485	1.439287	-3.141198	38061.462831
HLA B*0803	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.327989	1.186588	-3.141401	21280.835369
HLA A*0101	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.388187	1.246696	-3.141491	24444.838745
HLA B*2705	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.401105	1.259401	-3.141703	25182.836466
HLA B*1801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.243748	1.101846	-3.141902	17528.626502
HLA B*2705	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.432623	1.289989	-3.142634	27078.399204
HLA B*2705	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.389338	1.246696	-3.142643	24509.724203
HLA B*1503	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.207801	1.064763	-3.143037	16136.181370
HLA A*0216	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.477613	1.334516	-3.143097	30034.006807
HLA A*8001	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.390116	1.246696	-3.143420	24553.652431
HLA B*4002	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.149303	1.005856	-3.143448	14102.733175
HLA B*3501	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.228575	1.084809	-3.143766	16926.801960
HLA A*6802	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.811696	0.667908	-3.143788	6481.811414
HLA B*4001	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.339184	1.195068	-3.144116	21836.547165
HLA A*3002	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.079890	0.935291	-3.144600	12019.602468
HLA B*1501	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.177897	1.032607	-3.145290	15062.481329
HLA A*2301	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.331915	1.186588	-3.145327	21474.084683
HLA B*4501	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.651506	1.505966	-3.145540	44823.494151
HLA A*2603	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.188371	1.042623	-3.145747	15430.163422
HLA A*0216	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.414581	1.268587	-3.145994	25976.539246
HLA B*4001	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.405721	1.259401	-3.146320	25451.968864
HLA A*8001	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.304466	1.157848	-3.146618	20158.844189
HLA A*2601	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.383575	1.236873	-3.146703	24186.617564
HLA B*1502	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.548135	1.401173	-3.146963	35329.331245
HLA B*0801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.384043	1.236873	-3.147170	24212.670122
HLA B*4501	1:259-267	9	TIFGGAFLI	1.126046	0.313241	-4.586578	1.439287	-3.147291	38599.145485

HLA A*2402	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.554907	1.407576	-3.147330	35884.477949
HLA B*3901	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.482054	1.334516	-3.147537	30342.670537
HLA B*1503	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.310245	1.162375	-3.147870	20428.917813
HLA B*3801	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.507964	1.360016	-3.147948	32208.012205
HLA A*3301	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.539113	1.391116	-3.147998	34602.971438
HLA B*0702	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.289723	1.141236	-3.148486	19485.996031
HLA A*3201	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.145991	0.997451	-3.148539	13995.567567
HLA B*4402	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.408045	1.259401	-3.148644	25588.511530
HLA B*1502	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.543415	1.394704	-3.148711	34947.434639
HLA B*3801	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.508267	1.359429	-3.148838	32230.497239
HLA B*7301	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.031350	0.882099	-3.149251	10748.546610
HLA A*2603	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.290489	1.141236	-3.149252	19520.392320
HLA B*4601	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.408778	1.259401	-3.149377	25631.738476
HLA A*0219	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.842169	0.692679	-3.149490	6952.951687
HLA B*7301	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.583507	1.434003	-3.149504	38327.184153
HLA B*1502	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.418296	1.268587	-3.149709	26199.670352
HLA B*1509	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.509294	1.359429	-3.149865	32306.784192
HLA A*2501	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.484516	1.334516	-3.150000	30515.188833
HLA A*2301	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.345166	1.195068	-3.150098	22139.395409
HLA A*2902	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-3.917762	0.767455	-3.150307	8274.876907
HLA B*0702	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.148161	0.997451	-3.150710	14065.702885
HLA B*1503	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-3.653694	0.502834	-3.150860	4504.986821
HLA B*3801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.485414	1.334516	-3.150897	30578.316047
HLA B*1503	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.819351	0.667908	-3.151443	6597.068801
HLA B*1501	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.334774	1.182783	-3.151991	21615.932956
HLA A*0219	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.398783	1.246696	-3.152087	25048.594030
HLA A*2403	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.334043	1.181941	-3.152102	21579.595255
HLA A*6802	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.334177	1.181941	-3.152236	21586.250644
HLA B*5701	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.411710	1.259401	-3.152309	25805.377733
HLA B*5401	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.517747	1.365049	-3.152698	32941.788739
HLA A*0301	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.334908	1.181941	-3.152967	21622.599552
HLA B*0802	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.442965	1.289989	-3.152976	27730.992893
HLA A*3101	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.399815	1.246696	-3.153119	25108.153668
HLA B*1517	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.421862	1.268587	-3.153275	26415.713474
HLA A*2603	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.541526	1.388176	-3.153351	34795.759094
HLA B*0702	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.443541	1.289989	-3.153552	27767.772553
HLA B*1502	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.587555	1.434003	-3.153552	38686.111220
HLA B*2705	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.391183	1.236873	-3.154310	24614.032522
HLA A*0212	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.336858	1.181941	-3.154917	21719.907825
HLA A*0219	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.423697	1.268587	-3.155110	26527.559238
HLA A*0203	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.299252	1.143634	-3.155618	19918.293198
HLA B*5401	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.466895	1.311098	-3.155796	29301.842137
HLA B*5801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.359585	1.203170	-3.156415	22886.772165
HLA B*4001	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.343077	1.186588	-3.156489	22033.174025
HLA B*1503	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.959272	0.802529	-3.156743	9104.838425
HLA A*0101	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.314801	1.157848	-3.156953	20644.340458
HLA B*3901	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.339184	1.181941	-3.157243	21836.547165
HLA A*6801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.343911	1.186588	-3.157323	22075.529630
HLA A*0301	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.177605	1.020231	-3.157375	15052.380410
HLA B*4403	1:173-181	9	DARVQLSAR	0.897969	0.607997	-4.663476	1.505966	-3.157511	46076.166016
HLA B*1509	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.352670	1.195068	-3.157602	22525.270340
HLA B*0803	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.492478	1.334516	-3.157962	31079.817965
HLA A*0203	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.165421	1.007379	-3.158042	14635.944576
HLA B*4501	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.155553	0.997451	-3.158102	14307.143042

HLA B*1517	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.492995	1.334516	-3.158479	31116.830428
HLA B*1801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.523677	1.365049	-3.158628	33394.679351
HLA A*0211	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.428041	1.268587	-3.159455	26794.242943
HLA B*1501	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.418857	1.259401	-3.159456	26233.567479
HLA B*2705	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.262762	1.101846	-3.160916	18313.116970
HLA B*5101	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.323663	1.162375	-3.161288	21069.938603
HLA A*2902	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.421099	1.259401	-3.161697	26369.309803
HLA B*1801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.319773	1.157848	-3.161925	20882.020748
HLA B*3501	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.399037	1.236873	-3.162164	25063.233399
HLA B*4801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.264280	1.101846	-3.162434	18377.229403
HLA A*3201	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.304466	1.141236	-3.163229	20158.844189
HLA B*0801	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.981668	0.818322	-3.163346	9586.664618
HLA A*0212	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.422781	1.259401	-3.163380	26471.648890
HLA B*5301	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.554550	1.391116	-3.163434	35854.982159
HLA A*1101	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.432031	1.268587	-3.163444	27041.508589
HLA A*0301	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.346319	1.182783	-3.163537	22198.281475
HLA A*2902	1:85-93	9	FISGASAPV	0.612670	0.205652	-3.982640	0.818322	-3.164318	9608.159877
HLA B*3901	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.423916	1.259401	-3.164514	26540.909134
HLA A*8001	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.305760	1.141236	-3.164524	20219.024307
HLA A*2301	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.499348	1.334516	-3.164832	31575.363623
HLA A*0212	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.327270	1.162375	-3.164895	21245.635662
HLA B*4002	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.570378	1.405388	-3.164990	37185.873811
HLA B*0802	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.322933	1.157848	-3.165085	21034.518752
HLA B*5701	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.360787	1.195068	-3.165720	22950.253270
HLA A*0212	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.353734	1.187527	-3.166207	22580.540261
HLA B*4601	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.307506	1.141236	-3.166270	20300.459195
HLA B*1501	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.251400	1.084809	-3.166591	17840.218119
HLA A*0301	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.308089	1.141236	-3.166852	20327.713636
HLA A*2403	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.308293	1.141236	-3.167057	20337.283336
HLA A*0201	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.329626	1.162375	-3.167251	21361.230337
HLA A*3301	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.632480	1.464619	-3.167861	42902.201546
HLA B*7301	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.569452	1.401173	-3.168280	37106.696671
HLA B*3801	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.427802	1.259401	-3.168400	26779.461725
HLA A*0250	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.576169	1.407576	-3.168593	37685.082618
HLA B*1801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.309912	1.141236	-3.168675	20413.230258
HLA B*1801	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.503641	1.334516	-3.169124	31888.997738
HLA B*4501	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.563940	1.394704	-3.169236	36638.729231
HLA B*0803	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.296073	1.126836	-3.169237	19773.031932
HLA B*4002	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.051861	0.882547	-3.169313	11268.360903
HLA A*3002	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.576952	1.407576	-3.169376	37753.033222
HLA B*5801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.352313	1.182783	-3.169530	22506.755353
HLA A*3101	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.189869	1.020231	-3.169639	15483.512789
HLA A*0206	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.177163	1.007379	-3.169785	15037.079031
HLA B*5101	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.406953	1.236873	-3.170080	25524.222007
HLA A*0301	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.309524	1.139383	-3.170141	20395.016892
HLA A*0206	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.504790	1.334516	-3.170273	31973.469718
HLA A*0211	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.357987	1.187527	-3.170460	22802.732707
HLA B*3501	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.840200	0.669638	-3.170563	6921.501913
HLA B*5801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.358158	1.187527	-3.170631	22811.739784
HLA A*0101	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.352583	1.181941	-3.170642	22520.762000

HLA B*4801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.358389	1.187527	-3.170861	22823.837071
HLA B*7301	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.562498	1.391116	-3.171382	36517.229296
HLA A*0202	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.440092	1.268587	-3.171505	27548.122110
HLA A*0206	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.197280	1.025655	-3.171624	15749.971522
HLA B*7301	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.579268	1.407576	-3.171692	37954.951643
HLA A*1101	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.506315	1.334516	-3.171798	32085.926450
HLA A*3002	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.143477	0.971364	-3.172113	13914.787113
HLA B*4501	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.577734	1.405388	-3.172346	37821.106348
HLA A*0301	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.322871	1.150365	-3.172506	21031.560305
HLA A*3301	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.573703	1.401173	-3.172530	37471.623731
HLA B*4801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.367930	1.195068	-3.172862	23330.815378
HLA B*5801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.323330	1.150365	-3.172965	21053.758802
HLA B*4403	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.203633	1.030229	-3.173404	15982.060866
HLA A*0206	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.113084	0.939568	-3.173516	12974.290816
HLA B*5401	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.331405	1.157848	-3.173557	21448.890060
HLA A*0212	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.377544	1.203170	-3.174374	23853.055004
HLA A*0211	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.421103	1.246696	-3.174408	26369.595115
HLA B*4001	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.377741	1.203170	-3.174572	23863.897028
HLA B*3801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.421710	1.246696	-3.175014	26406.426212
HLA B*4501	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.609227	1.434003	-3.175223	40665.557043
HLA A*2601	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.379386	1.203170	-3.176216	23954.439084
HLA A*3001	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.021364	0.844974	-3.176391	10504.235087
HLA B*1509	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.317801	1.141236	-3.176565	20787.454183
HLA A*2602	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.584625	1.407576	-3.177049	38426.007948
HLA A*3001	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.220361	1.042623	-3.177738	16609.674188
HLA B*4001	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.360022	1.181941	-3.178081	22909.813327
HLA A*3301	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.612307	1.434003	-3.178304	40954.997197
HLA A*0211	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.263235	1.084809	-3.178426	18333.041259
HLA B*0801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.366156	1.187527	-3.178629	23235.715796
HLA A*8001	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.373712	1.195068	-3.178644	23643.512688
HLA A*3001	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-3.166626	-0.012369	-3.178996	1467.663481
HLA A*3101	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.264005	1.084809	-3.179196	18365.601087
HLA A*0301	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.367784	1.187527	-3.180257	23322.991228
HLA B*1503	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-3.662302	0.481784	-3.180518	4595.174814
HLA B*5801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.307435	1.126836	-3.180599	20297.164765
HLA A*2403	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.368611	1.187527	-3.181084	23367.447072
HLA B*4601	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.367751	1.186588	-3.181163	23321.224848
HLA B*0803	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.376390	1.195068	-3.181323	23789.779269
HLA B*4801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.418378	1.236873	-3.181505	26204.631628
HLA A*2902	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.384677	1.203170	-3.181507	24248.062687
HLA A*0216	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.369452	1.187527	-3.181925	23412.747602
HLA A*6801	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.552644	1.370628	-3.182017	35698.015880
HLA B*4001	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.340030	1.157848	-3.182182	21879.116592
HLA A*6802	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.441861	1.259401	-3.182460	27660.572307
HLA A*2301	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.309557	1.126836	-3.182721	20396.561637
HLA B*7301	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.588117	1.405388	-3.182729	38736.163301
HLA A*2902	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.003128	0.820012	-3.183116	10072.278608
HLA A*0211	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.122749	0.939568	-3.183181	13266.287645
HLA A*0101	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.370867	1.187527	-3.183340	23489.121442
HLA A*0250	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.244349	1.060834	-3.183515	17552.919269
HLA A*2301	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.543537	1.360016	-3.183522	34957.267233
HLA A*3201	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.473673	1.289989	-3.183684	29762.759054
HLA A*0301	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.285580	1.101846	-3.183734	19301.029197
HLA B*0801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-3.752832	0.568895	-3.183937	5660.208041

HLA B*1517	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.214403	1.030229	-3.184174	16383.354161
HLA A*0203	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.063477	0.879222	-3.184254	11573.816754
HLA B*1517	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.379454	1.195068	-3.184386	23958.197513
HLA B*1517	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.002710	0.818322	-3.184388	10062.584072
HLA B*5401	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.367420	1.182783	-3.184637	23303.442332
HLA A*3301	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.342560	1.157848	-3.184712	22006.966278
HLA A*0203	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.444143	1.259401	-3.184741	27806.255661
HLA B*1801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.372039	1.186588	-3.185451	23552.616805
HLA B*5301	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.287744	1.101846	-3.185898	19397.436703
HLA B*5301	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.593847	1.407576	-3.186271	39250.662990
HLA A*2501	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.373031	1.186588	-3.186443	23606.448223
HLA B*1502	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.594702	1.407576	-3.187126	39328.031533
HLA A*0203	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.879813	0.692679	-3.187133	7582.504215
HLA B*3901	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.424132	1.236873	-3.187259	26554.122092
HLA A*3101	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-3.989914	0.802529	-3.187385	9770.442350
HLA B*1501	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.390591	1.203170	-3.187421	24580.499270
HLA B*4403	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.575721	1.388176	-3.187545	37646.163155
HLA A*2603	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.593203	1.405388	-3.187815	39192.524454
HLA B*3901	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.289906	1.101846	-3.188060	19494.220298
HLA A*6901	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.123506	0.935291	-3.188215	13289.417450
HLA A*0101	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.371283	1.182783	-3.188500	23511.624231
HLA A*2603	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.622633	1.434003	-3.188630	41940.430803
HLA B*5801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.351075	1.162375	-3.188700	22442.679716
HLA A*2301	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.478842	1.289989	-3.188853	30119.104515
HLA A*0201	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.315922	1.126836	-3.189086	20697.682327
HLA A*3002	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.330780	1.141236	-3.189544	21418.046650
HLA A*0101	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.392722	1.203170	-3.189552	24701.406502
HLA B*0802	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.426728	1.236873	-3.189856	26713.336120
HLA A*2602	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.595466	1.405388	-3.190078	39397.239451
HLA A*0211	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.550095	1.360016	-3.190079	35489.091939
HLA B*5301	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.578401	1.388176	-3.190226	37879.259681
HLA A*1101	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.329753	1.139383	-3.190370	21367.471591
HLA A*0219	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.449781	1.259401	-3.190380	28169.638616
HLA B*1509	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.427339	1.236873	-3.190466	26750.936766
HLA B*4601	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.373259	1.182783	-3.190476	23618.839176
HLA B*5801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.331926	1.141236	-3.190690	21474.665553
HLA A*2902	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.330235	1.139383	-3.190851	21391.181845
HLA A*6901	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.394333	1.203170	-3.191164	24793.248281
HLA A*2601	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.341536	1.150365	-3.191171	21955.119360
HLA B*3501	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.378554	1.186588	-3.191966	23908.607819
HLA B*0702	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.253216	1.060834	-3.192382	17914.979345
HLA A*3001	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.225084	1.032607	-3.192477	16791.271288
HLA A*0203	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.319437	1.126836	-3.192600	20865.872368
HLA B*3901	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.482794	1.289989	-3.192805	30394.422022
HLA B*7301	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.581155	1.388176	-3.192979	38120.191958
HLA A*2602	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.558114	1.365049	-3.193065	36150.447647
HLA B*1517	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.880635	0.687090	-3.193545	7596.874993
HLA B*1509	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.440369	1.246696	-3.193673	27565.713534
HLA B*1502	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.381230	1.186588	-3.194642	24056.384224
HLA B*5301	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.390212	1.195068	-3.195145	24559.099169
HLA B*1509	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.085468	0.890279	-3.195189	12174.966688
HLA A*6802	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.228326	1.032607	-3.195719	16917.098098

HLA B*0803	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.443111	1.246696	-3.196415	27740.295792
HLA B*4601	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.399789	1.203170	-3.196619	25106.659557
HLA A*2501	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.379736	1.182783	-3.196953	23973.755906
HLA B*2705	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.400372	1.203170	-3.197202	25140.366576
HLA B*0802	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.392353	1.195068	-3.197285	24680.435205
HLA B*2705	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.348114	1.150365	-3.197749	22290.220288
HLA B*1517	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.324608	1.126836	-3.197772	21115.810851
HLA A*0201	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.385429	1.187527	-3.197902	24290.076429
HLA B*4801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.381007	1.182783	-3.198224	24044.023875
HLA A*2501	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.445045	1.246696	-3.198349	27864.080347
HLA B*1517	1:165-173	9	RSITAESRD	1.002229	-0.648282	-3.552332	0.353947	-3.198385	3567.237648
HLA A*0201	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.401560	1.203170	-3.198391	25209.280193
HLA B*4001	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.348770	1.150365	-3.198405	22323.889637
HLA A*8001	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.457920	1.259401	-3.198519	28702.510968
HLA A*1101	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.445367	1.246696	-3.198671	27884.739599
HLA A*2501	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.458082	1.259401	-3.198681	28713.227109
HLA A*2403	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.458261	1.259401	-3.198859	28725.035024
HLA A*0250	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.467468	1.268587	-3.198881	29340.546488
HLA A*3201	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.866994	0.667908	-3.199086	7361.967065
HLA A*6801	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.633234	1.434003	-3.199231	42976.769139
HLA A*2601	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.381571	1.181941	-3.199630	24075.262271
HLA B*1502	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.570258	1.370628	-3.199631	37175.615482
HLA A*0219	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.387482	1.187527	-3.199955	24405.197761
HLA A*2602	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.197454	0.997451	-3.200002	15756.277998
HLA B*4403	1:188-196	9	RASMQIRRI	1.055395	0.378608	-4.634157	1.434003	-3.200154	43068.238666
HLA B*1801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.395236	1.195068	-3.200168	24844.807247
HLA A*1101	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.382198	1.181941	-3.200258	24110.062680
HLA A*6901	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-3.969680	0.768800	-3.200880	9325.678984
HLA B*1517	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-3.627243	0.426351	-3.200892	4238.800947
HLA B*7301	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.571947	1.370628	-3.201320	37320.499452
HLA B*4601	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.363708	1.162375	-3.201333	23105.102126
HLA B*1501	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.388880	1.187527	-3.201353	24483.881832
HLA A*3101	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.384289	1.182783	-3.201507	24226.427755
HLA A*0101	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.363889	1.162375	-3.201514	23114.728826
HLA A*2602	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.572204	1.370628	-3.201576	37342.513016
HLA B*4001	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.384776	1.182783	-3.201993	24253.572845
HLA B*4501	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.352531	1.150365	-3.202166	22518.081794
HLA A*2902	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.364598	1.162375	-3.202223	23152.524225
HLA B*4002	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.398057	1.195068	-3.202990	25006.756382
HLA A*2602	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.594249	1.391116	-3.203133	39286.990227
HLA B*7301	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.462743	1.259401	-3.203342	29023.072338
HLA B*4402	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.390934	1.187527	-3.203407	24599.921694
HLA B*0702	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.398680	1.195068	-3.203612	25042.632294
HLA A*3301	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.354089	1.150365	-3.203724	22598.993689
HLA A*0206	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.066315	0.862516	-3.203799	11649.701025
HLA B*0801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.386839	1.182783	-3.204056	24369.048501
HLA A*2601	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.201951	0.997451	-3.204499	15920.274404
HLA B*0801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.083729	0.879222	-3.204507	12126.323856
HLA A*3001	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-3.522996	0.318175	-3.204821	3334.236283
HLA A*0301	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.367216	1.162375	-3.204841	23292.476906
HLA B*0801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.408118	1.203170	-3.204948	25592.803251
HLA A*6901	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.392736	1.187527	-3.205209	24702.208306
HLA A*3201	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.612892	1.407576	-3.205316	41010.203308
HLA A*2603	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.606602	1.401173	-3.205430	40420.562315
HLA B*3801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.332284	1.126836	-3.205447	21492.331501
HLA A*2402	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.442667	1.236873	-3.205794	27711.946694

HLA A*2603	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.613371	1.407576	-3.205795	41055.487866
HLA A*3101	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.347471	1.141236	-3.206234	22257.203756
HLA A*0219	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.368999	1.162375	-3.206624	23388.314908
HLA B*4801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.409828	1.203170	-3.206659	25693.796675
HLA A*3101	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.394550	1.187527	-3.207022	24805.591195
HLA A*0301	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.239674	1.032607	-3.207067	17364.963718
HLA A*6901	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.146639	0.939568	-3.207071	14016.480369
HLA A*2602	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.475861	1.268587	-3.207274	29913.040505
HLA B*0801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.268399	1.060834	-3.207564	18552.339532
HLA A*0202	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.370543	1.162375	-3.208168	23471.591837
HLA B*4002	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.579019	1.370628	-3.208392	37933.192682
HLA A*2601	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.396124	1.187527	-3.208597	24895.665323
HLA B*0801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.310595	1.101846	-3.208749	20445.391661
HLA B*5801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.206349	0.997451	-3.208898	16082.323172
HLA A*2301	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.446238	1.236873	-3.209366	27940.762394
HLA B*5701	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.412584	1.203170	-3.209415	25857.362799
HLA B*3901	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.100180	0.890279	-3.209901	12594.480452
HLA A*0211	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.544545	1.334516	-3.210029	35038.491761
HLA B*4403	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.615610	1.405388	-3.210222	41267.701114
HLA B*1517	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.354176	1.143634	-3.210542	22603.517689
HLA B*1517	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.393389	1.182783	-3.210606	24739.387123
HLA A*0216	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.470062	1.259401	-3.210661	29516.307765
HLA B*1517	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.470083	1.259401	-3.210682	29517.744919
HLA B*3901	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.397456	1.186588	-3.210868	24972.147706
HLA A*2603	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.500939	1.289989	-3.210950	31691.220266
HLA A*2602	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.571026	1.360016	-3.211011	37241.438605
HLA B*4601	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.029611	0.818322	-3.211289	10705.602776
HLA A*3101	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.373956	1.162375	-3.211581	23656.818944
HLA B*3901	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.338672	1.126836	-3.211836	21810.809286
HLA A*6801	1:252-260	9	AELVSSGTI	1.198347	0.266272	-4.676737	1.464619	-3.212118	47504.727123
HLA A*3002	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.899224	0.687090	-3.212135	7929.103841
HLA A*3002	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.394136	1.181941	-3.212195	24781.984027
HLA B*5701	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.370134	1.157848	-3.212286	23449.507937
HLA A*3001	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.219844	1.007379	-3.212465	16589.917519
HLA A*0301	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.297300	1.084809	-3.212491	19828.949142
HLA B*0702	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.415911	1.203170	-3.212742	26056.201238
HLA B*1517	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.882397	0.669638	-3.212759	7627.761299
HLA A*2501	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.314641	1.101846	-3.212795	20636.747370
HLA B*4001	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.400550	1.187527	-3.213023	25150.705203
HLA B*5801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.352762	1.139383	-3.213378	22530.023351
HLA B*0802	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.395529	1.181941	-3.213589	24861.613885
HLA B*5101	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.482390	1.268587	-3.213803	30366.153138
HLA B*0702	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.450691	1.236873	-3.213818	28228.677115
HLA A*3301	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.608606	1.394704	-3.213902	40607.519513
HLA A*8001	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.395851	1.181941	-3.213910	24880.047020
HLA A*2902	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.211541	0.997451	-3.214090	16275.755114
HLA A*2402	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.341179	1.126836	-3.214343	21937.073017
HLA A*0211	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.150544	0.935815	-3.214729	14143.074113
HLA A*3002	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.505213	1.289989	-3.215223	32004.620009
HLA A*2402	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.575307	1.360016	-3.215291	37610.335777
HLA B*5301	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.580645	1.365049	-3.215596	38075.467170
HLA B*1801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.462520	1.246696	-3.215824	29008.160068
HLA A*0206	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.009626	0.793787	-3.215839	10224.131008
HLA B*4601	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.403372	1.187527	-3.215845	25314.648313

HLA B*4002	1:277-285	9	ALATIGAFV	1.170021	0.218155	-4.604023	1.388176	-3.215847	40181.173515
HLA A*6901	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.359827	1.143634	-3.216193	22899.528653
HLA B*3801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.506538	1.289989	-3.216549	32102.420912
HLA A*0101	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.366967	1.150365	-3.216602	23279.123705
HLA A*0101	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.360360	1.143634	-3.216726	22927.667576
HLA A*2501	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.357973	1.141236	-3.216737	22801.992557
HLA B*1509	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.115903	0.898490	-3.217413	13058.792175
HLA A*0206	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.405202	1.187527	-3.217675	25421.557042
HLA B*1501	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-3.486232	0.268222	-3.218009	3063.596973
HLA B*4402	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.404789	1.186588	-3.218201	25397.363668
HLA A*0206	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.063195	0.844974	-3.218221	11566.305624
HLA B*4002	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.609530	1.391116	-3.218414	40693.946452
HLA A*2603	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.589103	1.370628	-3.218476	38824.277874
HLA A*0202	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.578768	1.360016	-3.218752	37911.241099
HLA B*5801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.362597	1.143634	-3.218963	23046.054578
HLA B*5301	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.509120	1.289989	-3.219131	32293.853348
HLA A*0216	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.155388	0.935815	-3.219573	14301.726063
HLA A*0211	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.889680	0.669638	-3.220043	7756.762557
HLA A*2601	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.382675	1.162375	-3.220300	24136.555076
HLA A*0301	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.364105	1.143634	-3.220471	23126.236117
HLA B*3901	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.403269	1.182783	-3.220486	25308.623255
HLA A*8001	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.347715	1.126836	-3.220879	22269.729816
HLA B*4402	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.416534	1.195068	-3.221466	26093.582735
HLA B*1501	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.384061	1.162375	-3.221687	24213.718048
HLA B*0801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.365714	1.143634	-3.222081	23212.095712
HLA B*5101	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.379973	1.157848	-3.222125	23986.858717
HLA B*4001	1:124-132	9	SELPDLSGP	0.499243	0.082735	-3.804202	0.581978	-3.222223	6370.910940
HLA B*0702	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.409981	1.187527	-3.222454	25702.833302
HLA B*4801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.363828	1.141236	-3.222591	23111.477804
HLA A*2602	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.623869	1.401173	-3.222696	42059.946530
HLA A*2403	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.385227	1.162375	-3.222852	24278.778088
HLA A*0216	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.307748	1.084809	-3.222939	20311.774140
HLA B*1502	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.588063	1.365049	-3.223014	38731.343758
HLA A*3101	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.100899	0.877206	-3.223693	12615.346950
HLA A*0203	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.426982	1.203170	-3.223812	26728.948429
HLA A*2602	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.266869	1.042623	-3.224246	18487.116122
HLA A*3201	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.382713	1.157848	-3.224865	24138.644384
HLA B*1502	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.472217	1.246696	-3.225521	29663.098084
HLA A*2402	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.560198	1.334516	-3.225681	36324.335033
HLA A*3001	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.290550	1.064763	-3.225786	19523.138196
HLA B*0803	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.515823	1.289989	-3.225834	32796.156447
HLA B*1509	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.407829	1.181941	-3.225888	25575.779046
HLA B*0702	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.408231	1.181941	-3.226290	25599.449917
HLA B*5701	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.409133	1.182783	-3.226350	25652.685425
HLA B*4601	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.328249	1.101846	-3.226403	21293.618299
HLA B*4002	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.627600	1.401173	-3.226427	42422.836034
HLA A*1101	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.486633	1.259401	-3.227232	30664.292420
HLA B*1503	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.088019	0.860615	-3.227404	12246.706852
HLA B*5401	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-3.772610	0.545171	-3.227439	5923.936011
HLA A*3101	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.199986	0.971364	-3.228622	15848.434875
HLA B*1501	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.355821	1.126836	-3.228985	22689.277738
HLA B*4801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.415723	1.186588	-3.229135	26044.926785
HLA B*4402	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.411311	1.181941	-3.229370	25781.655923
HLA B*4501	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.630565	1.401173	-3.229392	42713.459573
HLA B*1501	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.373085	1.143634	-3.229451	23609.385696

HLA A*3101	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.368867	1.139383	-3.229484	23381.230403
HLA B*4403	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.600113	1.370628	-3.229486	39821.083567
HLA B*4001	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.356603	1.126836	-3.229767	22730.189154
HLA B*1509	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.418145	1.187527	-3.230618	26190.600735
HLA B*0803	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.433833	1.203170	-3.230663	27153.947333
HLA A*2403	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.291748	1.060834	-3.230913	19577.077759
HLA B*5301	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.418456	1.186588	-3.231868	26209.310263
HLA B*1509	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.522004	1.289989	-3.232015	33266.295769
HLA B*5401	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.522402	1.289989	-3.232412	33296.724095
HLA B*1501	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-3.213785	-0.018628	-3.232414	1636.007728
HLA B*4801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.359437	1.126836	-3.232600	22878.973155
HLA A*0202	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.240414	1.007379	-3.233035	17394.580842
HLA A*0219	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.377215	1.143634	-3.233581	23834.995910
HLA B*4501	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.173160	0.939568	-3.233592	14899.097419
HLA B*1801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.377474	1.143634	-3.233840	23849.184047
HLA A*3001	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.027919	0.793787	-3.234132	10663.984274
HLA B*4001	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.373679	1.139383	-3.234296	23641.722033
HLA A*3002	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.097041	0.862516	-3.234526	12503.780602
HLA B*4402	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.438003	1.203170	-3.234834	27415.950494
HLA A*2602	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.472017	1.236873	-3.235144	29649.460924
HLA B*4403	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.472193	1.236873	-3.235320	29661.493387
HLA A*8001	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.418214	1.182783	-3.235431	26194.710016
HLA B*1503	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.418470	1.182783	-3.235687	26210.161013
HLA B*4402	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.386103	1.150365	-3.235738	24327.819422
HLA B*1501	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.356081	1.120296	-3.235785	22702.906688
HLA A*3301	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.641377	1.405388	-3.235989	43790.215100
HLA B*1517	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.398386	1.162375	-3.236011	25025.703286
HLA B*4402	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.419229	1.182783	-3.236446	26256.000535
HLA B*5701	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.424597	1.187527	-3.237070	26582.580993
HLA B*4601	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.380742	1.143634	-3.237108	24029.329835
HLA B*4001	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.339020	1.101846	-3.237173	21828.279399
HLA B*4002	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.645157	1.407576	-3.237581	44173.051321
HLA A*6801	1:202-210	9	LKVSLLLSV	1.198288	0.196416	-4.632374	1.394704	-3.237669	42891.758490
HLA B*0702	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.381390	1.143634	-3.237756	24065.235533
HLA B*0702	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.173578	0.935815	-3.237763	14913.451568
HLA A*6802	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.177525	0.939568	-3.237957	15049.611986
HLA B*5101	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.389129	1.150365	-3.238764	24497.926098
HLA A*3002	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.599093	1.360016	-3.239078	39727.697640
HLA A*3201	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.507689	1.268587	-3.239102	32187.632368
HLA B*0803	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.476150	1.236873	-3.239277	29932.951755
HLA A*0216	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.442681	1.203170	-3.239512	27712.846220
HLA A*2301	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.508215	1.268587	-3.239628	32226.661472
HLA A*3002	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.422591	1.182783	-3.239808	26460.051528
HLA A*0212	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.366659	1.126836	-3.239823	23262.631740
HLA B*5401	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.381738	1.141236	-3.240502	24084.511407
HLA A*2501	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.477721	1.236873	-3.240849	30041.481847
HLA A*2603	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.600971	1.360016	-3.240955	39899.792342
HLA A*0250	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.601102	1.360016	-3.241086	39911.881966
HLA B*4403	1:281-289	9	IGAFVYNLI	1.264501	0.136672	-4.642322	1.401173	-3.241149	43885.552616
HLA A*0301	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.361720	1.120296	-3.241424	22999.597095
HLA B*4501	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.649020	1.407576	-3.241444	44567.672406
HLA B*7301	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.531489	1.289989	-3.241500	34000.814079
HLA A*6802	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.444720	1.203170	-3.241551	27843.285772
HLA B*4403	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.552881	1.311098	-3.241783	35717.526563
HLA B*0702	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.362214	1.120296	-3.241917	23025.741250
HLA B*4501	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.633713	1.391116	-3.242598	43024.225230

HLA A*2601	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.369438	1.126836	-3.242602	23411.987652
HLA A*0211	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.250261	1.007379	-3.242882	17793.470377
HLA A*6901	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.382302	1.139383	-3.242918	24115.802405
HLA B*5801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.363452	1.120296	-3.243155	23091.481574
HLA B*1502	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.405557	1.162375	-3.243182	25442.332225
HLA B*0802	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.446457	1.203170	-3.243287	27954.823479
HLA A*2403	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.426246	1.182783	-3.243464	26683.726723
HLA A*2501	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.393859	1.150365	-3.243494	24766.169077
HLA B*5101	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.426590	1.182783	-3.243807	26704.811025
HLA B*7301	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.604152	1.360016	-3.244136	40193.130957
HLA B*4403	1:16-24	9	PNADGLVDR	1.043984	0.363592	-4.651795	1.407576	-3.244218	44853.330363
HLA B*4402	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.364904	1.120296	-3.244607	23168.812789
HLA A*3002	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.270344	1.025655	-3.244689	18635.629067
HLA B*0702	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.371612	1.126836	-3.244775	23529.438316
HLA B*1509	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.407448	1.162375	-3.245073	25553.374200
HLA B*3901	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.395795	1.150365	-3.245430	24876.816871
HLA B*4501	1:285-293	9	VYNLITDLI	1.083750	0.286878	-4.616597	1.370628	-3.245970	41361.574270
HLA A*0250	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.266216	1.020231	-3.245985	18459.333336
HLA A*2501	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.064393	0.818322	-3.246071	11598.261628
HLA A*0101	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.330949	1.084809	-3.246140	21426.390862
HLA A*6801	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.637409	1.391116	-3.246293	43391.913121
HLA A*2902	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.434279	1.187527	-3.246752	27181.872653
HLA B*5701	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.397310	1.150365	-3.246945	24963.773124
HLA B*0802	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.388185	1.141236	-3.246949	24444.706502
HLA B*1502	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.536997	1.289989	-3.247007	34434.716221
HLA A*0219	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.095462	0.848433	-3.247030	12458.406317
HLA B*1509	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.430053	1.182783	-3.247270	26918.611212
HLA B*0801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.410110	1.162375	-3.247735	25710.482161
HLA A*2601	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.387219	1.139383	-3.247836	24390.414946
HLA A*0201	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.391648	1.143634	-3.248014	24640.412167
HLA A*6802	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.435581	1.187527	-3.248054	27263.461064
HLA B*5701	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.410470	1.162375	-3.248095	25731.771872
HLA B*3501	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.278546	1.030229	-3.248317	18990.924604
HLA B*4403	1:232-240	9	VWAKLNSNV	1.127893	0.263223	-4.640071	1.391116	-3.248955	43658.696480
HLA B*4801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.411666	1.162375	-3.249291	25802.725389
HLA A*0301	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.185241	0.935815	-3.249426	15319.373744
HLA A*0101	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.389400	1.139383	-3.250016	24513.171913
HLA A*3201	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.496752	1.246696	-3.250056	31387.171449
HLA B*5101	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.391359	1.141236	-3.250123	24624.021487
HLA A*2301	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.509660	1.259401	-3.250259	32334.060776
HLA A*2403	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.352247	1.101846	-3.250401	22503.346358
HLA B*0702	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.437028	1.186588	-3.250440	27354.467878
HLA A*8001	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.413052	1.162375	-3.250677	25885.214997
HLA B*0702	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.390330	1.139383	-3.250947	24565.743167
HLA B*1502	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.128205	0.877206	-3.250998	13433.986693
HLA B*7301	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.610672	1.359429	-3.251242	40801.080002
HLA B*5701	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.379170	1.126836	-3.252334	23942.519691
HLA A*3101	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.373277	1.120296	-3.252981	23619.861401
HLA A*3101	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.396955	1.143634	-3.253322	24943.388713
HLA A*8001	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.456583	1.203170	-3.253413	28614.293971
HLA A*0219	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.456637	1.203170	-3.253467	28617.854597
HLA A*2403	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.456985	1.203170	-3.253815	28640.777046
HLA A*2601	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.397658	1.143634	-3.254024	24983.768712
HLA B*2705	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.437411	1.182783	-3.254628	27378.600012

HLA B*5701	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.395929	1.141236	-3.254692	24884.489160
HLA A*3201	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.190579	0.935815	-3.254764	15508.830219
HLA B*3501	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.442352	1.187527	-3.254825	27691.864886
HLA A*3101	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.103333	0.848433	-3.254900	12686.250001
HLA B*4801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.394989	1.139383	-3.255606	24830.698451
HLA A*0250	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.399632	1.143634	-3.255998	25097.560982
HLA A*1101	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.451280	1.195068	-3.256212	28267.034369
HLA B*1517	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.459607	1.203170	-3.256437	28814.216952
HLA B*1503	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.383300	1.126836	-3.256464	24171.313318
HLA A*2402	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.515959	1.259401	-3.256558	32806.448628
HLA B*7301	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.568198	1.311098	-3.257099	36999.654537
HLA A*0201	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.192764	0.935291	-3.257474	15587.054815
HLA B*4402	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.401194	1.143634	-3.257560	25188.013980
HLA A*2501	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.419940	1.162375	-3.257566	26299.074570
HLA A*6901	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-3.943249	0.685107	-3.258141	8775.032941
HLA B*1502	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.592928	1.334516	-3.258412	39167.725120
HLA B*1503	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-3.945504	0.687090	-3.258415	8820.724565
HLA A*6901	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.378794	1.120296	-3.258498	23921.804437
HLA A*2402	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.527145	1.268587	-3.258558	33662.403209
HLA A*0201	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.398276	1.139383	-3.258893	25019.340939
HLA B*4001	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.402627	1.143634	-3.258993	25271.272544
HLA B*0803	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.398433	1.139383	-3.259050	25028.411158
HLA A*3201	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.619113	1.360016	-3.259098	41601.918474
HLA B*0802	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.421686	1.162375	-3.259311	26404.997692
HLA A*0202	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.593859	1.334516	-3.259342	39251.724713
HLA A*0250	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.195320	0.935815	-3.259505	15679.070120
HLA A*0202	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.506662	1.246696	-3.259966	32111.626771
HLA A*0202	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.952806	0.692679	-3.260127	8970.289523
HLA A*0216	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.404096	1.143634	-3.260462	25356.863902
HLA B*5701	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.404248	1.143634	-3.260615	25365.782028
HLA A*0203	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-3.895357	0.634444	-3.260913	7858.811159
HLA B*1501	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-3.657960	0.397004	-3.260957	4549.463547
HLA B*5701	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.281932	1.020231	-3.261701	19139.549773
HLA B*0803	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.403008	1.141236	-3.261771	25293.430047
HLA A*6901	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.287632	1.025655	-3.261976	19392.400334
HLA B*7301	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-3.743787	0.481784	-3.262003	5543.536057
HLA B*3801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.443992	1.181941	-3.262051	27796.629887
HLA A*3201	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.448719	1.186588	-3.262131	28100.840396
HLA B*3801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.401579	1.139383	-3.262196	25210.371252
HLA A*8001	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.449833	1.187527	-3.262306	28172.991497
HLA A*2902	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.233723	0.971364	-3.262359	17128.630259
HLA B*4801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.412732	1.150365	-3.262367	25866.177085
HLA A*0202	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.389378	1.126836	-3.262542	24511.978420
HLA B*0803	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.444805	1.181941	-3.262864	27848.708947
HLA B*4402	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.421646	1.157848	-3.263798	26402.569386
HLA A*3101	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.272433	1.007379	-3.265054	18725.470972
HLA A*0216	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.204657	0.939568	-3.265089	16019.802433
HLA A*2602	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.406344	1.141236	-3.265108	25488.483499
HLA A*0250	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.600054	1.334516	-3.265538	39815.698239
HLA A*0101	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.386000	1.120296	-3.265703	24322.029235
HLA A*1101	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.428340	1.162375	-3.265965	26812.658412
HLA A*1101	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.448752	1.182783	-3.265969	28102.968791
HLA B*5301	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-3.957148	0.691047	-3.266101	9060.419555

HLA A*6801	1:159-167	9	AGSSGGRSI	1.162126	0.243262	-4.671758	1.405388	-3.266370	46963.263545
HLA A*0219	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.393229	1.126836	-3.266393	24730.287857
HLA B*3901	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.469693	1.203170	-3.266524	29491.248656
HLA B*3501	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.286772	1.020231	-3.266541	19354.040993
HLA A*2902	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.410268	1.143634	-3.266634	25719.802938
HLA B*4002	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.626138	1.359429	-3.266709	42280.325173
HLA A*3002	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.287091	1.020231	-3.266861	19368.285870
HLA A*2403	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.393958	1.126836	-3.267121	24771.796970
HLA B*5801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.352275	1.084809	-3.267467	22504.807292
HLA A*6901	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.287925	1.020231	-3.267695	19405.518611
HLA B*4403	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.558807	1.289989	-3.268818	36208.186833
HLA B*1503	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.472153	1.203170	-3.268983	29658.765601
HLA B*1801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.353958	1.084809	-3.269149	22592.148275
HLA B*1801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.452011	1.182783	-3.269228	28314.632993
HLA B*0803	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.452107	1.182783	-3.269325	28320.914030
HLA B*0702	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.355095	1.084809	-3.270286	22651.380760
HLA A*3002	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.473539	1.203170	-3.270370	29753.582715
HLA A*3201	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.940227	0.669638	-3.270589	8714.195877
HLA A*2601	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.391096	1.120296	-3.270799	24609.106125
HLA B*1517	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.133430	0.862516	-3.270915	13596.595218
HLA A*1101	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.458559	1.187527	-3.271032	28744.777511
HLA A*3301	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.636342	1.365049	-3.271293	43285.469462
HLA A*0250	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.057523	0.786144	-3.271379	11416.237812
HLA B*3801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.474944	1.203170	-3.271775	29849.994806
HLA B*2705	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-3.753749	0.481784	-3.271964	5672.162876
HLA B*1501	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.314700	1.042623	-3.272077	20639.538622
HLA B*0802	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.398974	1.126836	-3.272138	25059.572754
HLA A*6901	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.304825	1.032607	-3.272218	20175.536835
HLA B*5301	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.422612	1.150365	-3.272247	26461.339873
HLA A*2403	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.416381	1.143634	-3.272747	26084.408727
HLA A*3001	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.303338	1.030229	-3.273109	20106.564683
HLA A*0203	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.212805	0.939568	-3.273237	16323.195035
HLA B*3501	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.476448	1.203170	-3.273278	29953.524433
HLA B*0802	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.456092	1.182783	-3.273309	28581.959022
HLA B*1503	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-3.563032	0.289672	-3.273360	3656.213918
HLA B*0702	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.424047	1.150365	-3.273682	26548.951021
HLA A*3301	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.468824	1.195068	-3.273756	29432.276274
HLA B*7301	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.418030	1.143634	-3.274397	26183.658931
HLA B*2705	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.436880	1.162375	-3.274505	27345.146434
HLA B*4601	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.414111	1.139383	-3.274728	25948.448406
HLA B*1501	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.414469	1.139383	-3.275085	25969.794673
HLA A*3002	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.609833	1.334516	-3.275316	40722.355680
HLA A*6901	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.154585	0.879222	-3.275363	14275.289729
HLA A*2902	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.308032	1.032607	-3.275425	20325.074511
HLA A*2501	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.478612	1.203170	-3.275442	30103.140528
HLA A*8001	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.425856	1.150365	-3.275491	26659.774384
HLA A*0211	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.419438	1.143634	-3.275804	26268.645321
HLA B*4403	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.641610	1.365049	-3.276561	43813.674502
HLA A*0202	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.480320	1.203170	-3.277150	30221.768990
HLA A*0250	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.523966	1.246696	-3.277270	33416.908112
HLA B*0801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.416703	1.139383	-3.277320	26103.748479
HLA B*5401	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.459508	1.181941	-3.277567	28807.670664
HLA A*0203	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.397933	1.120296	-3.277636	24999.587370

HLA A*0202	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.867421	0.589436	-3.277985	7369.219226
HLA A*0211	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.537396	1.259401	-3.277995	34466.399748
HLA A*0201	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.285768	1.007379	-3.278390	19309.384319
HLA A*2603	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.643837	1.365049	-3.278788	44038.953400
HLA B*0801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.169081	0.890279	-3.278802	14759.826548
HLA A*0301	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.946900	0.667908	-3.278992	8849.115327
HLA A*1101	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.437867	1.157848	-3.280019	27407.349443
HLA B*3501	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.381914	1.101846	-3.280068	24094.285480
HLA A*0201	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.400388	1.120296	-3.280092	25141.318641
HLA A*6802	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.424019	1.143634	-3.280386	26547.227554
HLA A*0212	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.424170	1.143634	-3.280536	26556.420670
HLA B*1503	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.278960	0.997451	-3.281508	19009.015244
HLA B*4402	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.420941	1.139383	-3.281558	26359.753647
HLA A*8001	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.402439	1.120296	-3.282143	25260.337728
HLA A*8001	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.425786	1.143634	-3.282152	26655.447942
HLA A*0101	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.289657	1.007379	-3.282278	19483.044576
HLA B*4601	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.402613	1.120296	-3.282317	25270.452269
HLA A*0212	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.343166	1.060834	-3.282332	22037.703978
HLA A*3002	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.426021	1.143634	-3.282387	26669.872145
HLA B*1509	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.432884	1.150365	-3.282519	27094.664604
HLA B*5401	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.308227	1.025655	-3.282572	20334.202941
HLA B*2705	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.421992	1.139383	-3.282608	26423.574478
HLA A*3201	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.101040	0.818322	-3.282718	12619.442473
HLA A*3101	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.034752	0.751562	-3.283190	10833.076209
HLA A*0219	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.103258	0.820012	-3.283246	12684.053993
HLA B*4601	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.410218	1.126836	-3.283382	25716.881137
HLA B*5701	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.403879	1.120296	-3.283583	25344.246682
HLA B*1503	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.219840	0.935815	-3.284024	16589.738020
HLA A*3301	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.349087	1.064763	-3.284324	22340.199511
HLA B*5701	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.423787	1.139383	-3.284403	26533.013223
HLA A*0203	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.954099	0.669638	-3.284461	8997.019820
HLA A*2501	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.472029	1.187527	-3.284501	29650.262936
HLA B*4002	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.644530	1.360016	-3.284514	44109.292040
HLA B*1801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.521509	1.236873	-3.284636	33228.344402
HLA B*4402	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.386651	1.101846	-3.284804	24358.504075
HLA B*4402	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.426122	1.141236	-3.284886	26676.076952
HLA A*0201	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.345857	1.060834	-3.285022	22174.636300
HLA A*3001	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-3.978618	0.693390	-3.285228	9519.582516
HLA B*1501	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.036274	0.750956	-3.285318	10871.119372
HLA A*3201	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.620290	1.334516	-3.285774	41714.827362
HLA A*2603	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.620429	1.334516	-3.285913	41728.144170
HLA A*0201	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.306244	1.020231	-3.286014	20241.569700
HLA B*5801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.350929	1.064763	-3.286166	22435.153409
HLA A*0206	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.545574	1.259401	-3.286173	35121.615011
HLA A*0206	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.163720	0.877206	-3.286513	14578.731217
HLA A*0250	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.468652	1.181941	-3.286712	29420.655118
HLA B*3801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.524034	1.236873	-3.287162	33422.151194
HLA B*4801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.407693	1.120296	-3.287396	25567.755301
HLA B*0802	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.427010	1.139383	-3.287627	26730.683693
HLA B*4403	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.647575	1.359429	-3.288146	44419.638510
HLA A*0301	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.353241	1.064763	-3.288478	22554.901602
HLA A*0219	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.224421	0.935815	-3.288606	16765.674244
HLA A*3001	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.294483	1.005856	-3.288627	19700.745757
HLA A*2601	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.056156	0.767455	-3.288701	11380.349681

HLA B*5301	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.557540	1.268587	-3.288953	36102.760069
HLA B*0801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.137391	0.848433	-3.288958	13721.178058
HLA B*4001	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.410087	1.120296	-3.289790	25709.091290
HLA A*1101	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.233640	0.943496	-3.290145	17125.387326
HLA A*0203	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.429646	1.139383	-3.290263	26893.429578
HLA B*4501	1:288-296	9	LITDLIGGI	1.024772	0.334657	-4.649699	1.359429	-3.290270	44637.406587
HLA B*0801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.417196	1.126836	-3.290360	26133.421192
HLA A*0206	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.434120	1.143634	-3.290486	27171.875030
HLA B*2705	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.310887	1.020231	-3.290656	20459.111568
HLA B*4002	1:209-217	9	SVALFFVWM	1.067963	0.243135	-4.601838	1.311098	-3.290739	39979.521820
HLA B*1517	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.441328	1.150365	-3.290963	27626.624733
HLA A*0216	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.153744	0.862516	-3.291228	14247.668956
HLA B*5401	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.478807	1.187527	-3.291280	30116.660499
HLA A*0212	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.298679	1.007379	-3.291300	19892.018139
HLA A*1101	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.433006	1.141236	-3.291770	27102.287791
HLA B*5101	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.479582	1.187527	-3.292055	30170.474693
HLA B*0802	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.299532	1.007379	-3.292153	19931.120262
HLA B*4001	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.263780	0.971364	-3.292416	18356.065400
HLA A*0216	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.300039	1.007379	-3.292660	19954.424108
HLA A*2301	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.495904	1.203170	-3.292734	31325.933063
HLA B*4501	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.653059	1.360016	-3.293043	44984.067058
HLA B*3501	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.419889	1.126836	-3.293053	26295.944705
HLA B*0702	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.456463	1.162375	-3.294088	28606.400252
HLA A*3001	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-3.986775	0.692679	-3.294096	9700.079967
HLA A*2902	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.414725	1.120296	-3.294428	25985.113003
HLA A*8001	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.433882	1.139383	-3.294499	27157.032405
HLA B*5401	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.563247	1.268587	-3.294660	36580.303483
HLA B*7301	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.629179	1.334516	-3.294662	42577.342622
HLA B*1509	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.434091	1.139383	-3.294708	27170.111125
HLA A*3002	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.355778	1.060834	-3.294944	22687.068409
HLA B*0803	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.415326	1.120296	-3.295030	26021.125539
HLA A*0211	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.315391	1.020231	-3.295160	20672.392081
HLA B*4801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.438851	1.143634	-3.295218	27469.545340
HLA B*4601	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.172676	0.877206	-3.295470	14882.502559
HLA A*2501	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.477555	1.181941	-3.295614	30029.945065
HLA B*1509	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.482355	1.186588	-3.295767	30363.689075
HLA A*6802	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.416381	1.120296	-3.296085	26084.408727
HLA A*3001	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.231498	0.935291	-3.296207	17041.101862
HLA B*5301	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.533148	1.236873	-3.296275	34130.924479
HLA B*3901	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.268206	0.971364	-3.296842	18544.111337
HLA B*1502	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.556711	1.259401	-3.297310	36033.880748
HLA A*0203	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.188507	0.890279	-3.298228	15435.005759
HLA B*1509	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.501681	1.203170	-3.298512	31745.443533
HLA A*0301	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.066085	0.767455	-3.298630	11643.526350
HLA A*2402	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.456623	1.157848	-3.298775	28616.925695
HLA A*2603	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.480724	1.181941	-3.298783	30249.903462
HLA B*0801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.234951	0.935815	-3.299136	17177.162151
HLA A*2501	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.426364	1.126836	-3.299528	26690.945500
HLA A*3101	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.360362	1.060834	-3.299528	22927.791612
HLA B*4001	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.144745	0.844974	-3.299772	13955.496373
HLA B*4403	1:73-81	9	NPPAAADAR	0.833991	0.526025	-4.660293	1.360016	-3.300277	45739.644225
HLA A*0301	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.361203	1.060834	-3.300369	22972.239819
HLA B*1801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.298035	0.997451	-3.300584	19862.553852
HLA B*1502	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.537473	1.236873	-3.300601	34472.553457
HLA B*5101	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.444342	1.143634	-3.300709	27819.045046
HLA B*1501	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-3.517536	0.216823	-3.300713	3292.578742

HLA A*6802	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.440106	1.139383	-3.300723	27549.016318
HLA A*0212	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.440289	1.139383	-3.300906	27560.643667
HLA B*3501	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.444899	1.143634	-3.301265	27854.735936
HLA A*6802	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.191566	0.890279	-3.301287	15544.108725
HLA A*2501	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.298841	0.997451	-3.301390	19899.444864
HLA B*3801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.421717	1.120296	-3.301420	26406.854783
HLA A*8001	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.386357	1.084809	-3.301548	24342.037542
HLA B*4601	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.362695	1.060834	-3.301861	23051.291591
HLA B*5801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.237682	0.935815	-3.301866	17285.482905
HLA B*0801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.335570	1.032607	-3.302964	21655.611922
HLA A*6801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.055286	0.751562	-3.303725	11357.592885
HLA B*4801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.324161	1.020231	-3.303931	21094.117504
HLA A*3301	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.388784	1.084809	-3.303975	24478.451776
HLA A*0101	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.364906	1.060834	-3.304072	23168.938130
HLA A*3002	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.454699	1.150365	-3.304334	28490.413182
HLA A*0301	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.152818	0.848433	-3.304385	14217.332445
HLA B*0802	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.492126	1.187527	-3.304599	31054.607440
HLA B*3501	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-3.822072	0.517364	-3.304707	6638.526863
HLA A*6801	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.541653	1.236873	-3.304781	34805.925603
HLA A*2902	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.347428	1.042623	-3.304805	22255.036500
HLA A*6901	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.369575	1.064763	-3.304811	23419.334868
HLA B*5101	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.508121	1.203170	-3.304952	32219.688520
HLA A*2603	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.302525	0.997451	-3.305074	20068.963982
HLA A*3002	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.425441	1.120296	-3.305144	26634.258525
HLA A*2501	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.390008	1.084809	-3.305199	24547.542894
HLA B*4501	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.492037	1.186588	-3.305449	31048.224021
HLA A*2501	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.449156	1.143634	-3.305523	28129.130799
HLA B*5701	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.335949	1.030229	-3.305720	21674.482006
HLA B*2705	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.449365	1.143634	-3.305732	28142.677678
HLA B*3501	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.445437	1.139383	-3.306054	27889.265567
HLA A*1101	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.450152	1.143634	-3.306519	28193.727260
HLA A*0101	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.349287	1.042623	-3.306663	22350.474803
HLA A*0216	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.327018	1.020231	-3.306788	21233.341012
HLA A*6802	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.433676	1.126836	-3.306839	27144.106827
HLA B*5801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.349970	1.042623	-3.307347	22385.688369
HLA A*2601	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.350189	1.042623	-3.307566	22396.953883
HLA A*0201	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.188201	0.879222	-3.308979	15424.154358
HLA A*3001	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.060653	0.751562	-3.309091	11498.800019
HLA B*5801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.370023	1.060834	-3.309189	23443.546311
HLA A*0206	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.512494	1.203170	-3.309324	32545.708417
HLA B*4403	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-3.527724	0.218302	-3.309421	3370.726667
HLA B*4402	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.374527	1.064763	-3.309764	23687.938721
HLA A*3101	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-3.977763	0.667908	-3.309854	9500.855002
HLA A*0212	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.002601	0.692679	-3.309922	10060.080260
HLA B*3801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.497485	1.187527	-3.309958	31440.194133
HLA A*6801	1:181-189	9	RRSRGPVRA	1.335614	0.029435	-4.675090	1.365049	-3.310041	47324.914583
HLA A*0250	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.513328	1.203170	-3.310158	32608.272855
HLA A*2902	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.245653	0.935291	-3.310363	17605.700905
HLA A*2403	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.450007	1.139383	-3.310623	28184.272299

HLA B*1509	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.437496	1.126836	-3.310660	27383.932678
HLA B*4001	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.395687	1.084809	-3.310878	24870.626923
HLA A*3001	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.097041	0.786144	-3.310897	12503.780602
HLA A*2601	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.372105	1.060834	-3.311271	23556.184753
HLA A*0219	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.331926	1.020231	-3.311696	21474.665553
HLA A*0219	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.451205	1.139383	-3.311822	28262.141304
HLA A*0101	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.344849	1.032607	-3.312242	22123.232136
HLA B*5401	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.549174	1.236873	-3.312301	35413.910799
HLA A*2403	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.433170	1.120296	-3.312874	27112.553160
HLA B*1801	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.516213	1.203170	-3.313043	32825.621988
HLA B*4601	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.398039	1.084809	-3.313230	25005.674136
HLA A*2301	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.471749	1.157848	-3.313901	29631.180928
HLA A*3002	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.573707	1.259401	-3.314306	37472.029168
HLA B*2705	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.399133	1.084809	-3.314325	25068.793177
HLA A*3002	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.501916	1.187527	-3.314389	31762.622112
HLA A*3001	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.246010	0.931448	-3.314562	17620.184082
HLA A*3001	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.307595	0.992668	-3.314927	20304.632907
HLA A*3201	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.163560	0.848433	-3.315127	14573.369089
HLA A*0250	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.250956	0.935291	-3.315666	17821.986371
HLA B*4002	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.650338	1.334516	-3.315822	44703.138428
HLA B*5801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.348476	1.032607	-3.315869	22308.798519
HLA A*0212	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.436265	1.120296	-3.315968	27306.415126
HLA A*0301	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.358694	1.042623	-3.316071	22839.894392
HLA B*1801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.346557	1.030229	-3.316328	22210.413904
HLA A*1101	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.466698	1.150365	-3.316333	29288.529506
HLA A*0101	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.381336	1.064763	-3.316573	24062.241343
HLA B*0801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.359693	1.042623	-3.317069	22892.468359
HLA A*2602	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.564051	1.246696	-3.317355	36648.046354
HLA A*0206	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.324154	1.005856	-3.318299	21093.775157
HLA B*5801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.344043	1.025655	-3.318387	22082.218508
HLA A*2501	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.457821	1.139383	-3.318438	28695.990058
HLA B*1502	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.217124	0.898490	-3.318633	16486.312329
HLA B*1517	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.506871	1.187527	-3.319344	32127.091604
HLA B*5301	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.477259	1.157848	-3.319410	30009.482247
HLA B*5701	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.404338	1.084809	-3.319529	25370.997155
HLA B*1503	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-3.996436	0.676597	-3.319839	9918.280739
HLA A*0250	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.507541	1.187527	-3.320014	32176.663951
HLA B*7301	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.567657	1.246696	-3.320961	36953.645441
HLA B*5401	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.483619	1.162375	-3.321244	30452.191943
HLA A*0211	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.524652	1.203170	-3.321483	33469.738105
HLA B*4002	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.509284	1.187527	-3.321757	32306.085095
HLA B*0803	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.484387	1.162375	-3.322012	30506.110576
HLA B*4601	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.387024	1.064763	-3.322261	24379.465601
HLA B*1517	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.383380	1.060834	-3.322546	24175.759707
HLA A*2602	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.612612	1.289989	-3.322623	40983.810387
HLA B*4403	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.485557	1.162375	-3.323182	30588.408655
HLA B*3901	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.463270	1.139383	-3.323886	29058.264256
HLA B*4501	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.658777	1.334516	-3.324261	45580.319428
HLA A*0201	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.389059	1.064763	-3.324295	24493.950489
HLA A*3201	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.583801	1.259401	-3.324399	38353.111145
HLA A*0219	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.385875	1.060834	-3.325041	24315.056523
HLA B*1503	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.464484	1.139383	-3.325101	29139.651447

HLA A*3001	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.215498	0.890279	-3.325219	16424.708839
HLA B*5101	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.386402	1.060834	-3.325567	24344.539737
HLA B*4403	1:62-70	9	PPVSHPEGR	1.060579	0.273937	-4.660086	1.334516	-3.325570	45717.874124
HLA B*4402	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.331525	1.005856	-3.325669	21454.808718
HLA A*2602	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.512531	1.186588	-3.325943	32548.525638
HLA B*3901	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.411050	1.084809	-3.326241	25766.178745
HLA A*2301	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.467792	1.141236	-3.326556	29362.459283
HLA B*3901	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.470436	1.143634	-3.326802	29541.707800
HLA A*3101	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.324370	0.997451	-3.326919	21104.276348
HLA B*3501	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.175448	0.848433	-3.327015	14977.811419
HLA A*8001	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.324798	0.997451	-3.327347	21125.065848
HLA B*1517	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.263338	0.935815	-3.327523	18337.405686
HLA B*4001	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.388509	1.060834	-3.327675	24462.962870
HLA A*6901	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-3.997498	0.669638	-3.327861	9942.563289
HLA A*2603	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.564763	1.236873	-3.327890	36708.168963
HLA B*0803	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.471631	1.143634	-3.327998	29623.166941
HLA B*4402	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.454856	1.126836	-3.328020	28500.741762
HLA B*4801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.412904	1.084809	-3.328095	25876.394223
HLA B*5401	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.471765	1.143634	-3.328132	29632.303059
HLA A*0203	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.021566	0.693390	-3.328176	10509.123325
HLA B*4002	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.597019	1.268587	-3.328432	39538.373680
HLA B*0802	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.472381	1.143634	-3.328747	29674.333397
HLA B*4402	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.413569	1.084809	-3.328760	25916.041289
HLA B*0803	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.516298	1.187527	-3.328770	32832.015598
HLA B*3801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.511577	1.182783	-3.328795	32477.114022
HLA A*0301	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.354940	1.025655	-3.329284	22643.294468
HLA B*3501	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.449706	1.120296	-3.329410	28164.762410
HLA B*0801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.327187	0.997451	-3.329736	21241.613265
HLA A*0219	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.355562	1.025655	-3.329907	22675.779642
HLA A*2403	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.355579	1.025655	-3.329923	22676.638372
HLA B*4801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.394747	1.064763	-3.329984	24816.866178
HLA B*4402	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.391505	1.060834	-3.330670	24632.282092
HLA A*2402	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.472132	1.141236	-3.330896	29657.321580
HLA A*2601	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.396018	1.064763	-3.331255	24889.605335
HLA B*4402	1:119-127	9	AEAYASELP	0.543268	-0.008008	-3.866651	0.535260	-3.331391	7356.154557
HLA A*2501	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.451713	1.120296	-3.331416	28295.185938
HLA B*3801	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.526703	1.195068	-3.331636	33628.183958
HLA A*2301	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.494229	1.162375	-3.331854	31205.333818
HLA B*4501	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.621888	1.289989	-3.331899	41868.567334
HLA B*5801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.180627	0.848433	-3.332194	15157.466713
HLA B*5301	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.339715	1.007379	-3.332336	21863.261618
HLA B*4501	1:124-132	9	SELPDLSGP	0.499243	0.082735	-3.914458	0.581978	-3.332480	8212.174446
HLA A*0216	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.472557	1.139383	-3.333174	29686.375954
HLA B*0802	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.483741	1.150365	-3.333376	30460.759783
HLA A*3201	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.153401	0.820012	-3.333389	14236.419966
HLA A*2603	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.592811	1.259401	-3.333410	39157.131900
HLA A*6801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.473250	1.139383	-3.333867	29733.790779
HLA A*0250	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.594230	1.259401	-3.334829	39285.289957
HLA B*1801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.455335	1.120296	-3.335039	28532.213039
HLA B*3801	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.492920	1.157848	-3.335072	31111.444059
HLA A*3301	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.603762	1.268587	-3.335175	40157.052056
HLA A*2602	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.594655	1.259401	-3.335254	39323.776558
HLA A*3001	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-3.705415	0.369909	-3.335506	5074.755088
HLA B*1517	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.420349	1.084809	-3.335541	26323.842089

HLA A*2403	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.109635	0.773810	-3.335824	12871.660735
HLA B*0802	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.456668	1.120296	-3.336371	28619.867320
HLA B*0702	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.369194	1.032607	-3.336587	23398.819106
HLA A*1101	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.272851	0.935815	-3.337036	18743.511541
HLA B*4801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.110950	0.773810	-3.337140	12910.715048
HLA A*2403	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.357529	1.020231	-3.337298	22778.690140
HLA A*2403	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.380016	1.042623	-3.337392	23989.194623
HLA B*4501	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.606029	1.268587	-3.337442	40367.241849
HLA B*0802	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.439448	1.101846	-3.337602	27507.317513
HLA B*0702	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-3.997691	0.659875	-3.337816	9946.974897
HLA A*3101	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.370580	1.032607	-3.337973	23473.623585
HLA B*1501	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.217471	0.879222	-3.338249	16499.517605
HLA B*4601	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.380944	1.042623	-3.338320	24040.512093
HLA A*0219	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.458754	1.120296	-3.338458	28757.687412
HLA A*0202	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.228744	0.890279	-3.338465	16933.396437
HLA B*5701	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.364204	1.025655	-3.338548	23131.491349
HLA A*0301	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.368778	1.030229	-3.338549	23376.424282
HLA A*0201	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.278220	0.939568	-3.338651	18976.649280
HLA B*1502	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.489283	1.150365	-3.338918	30851.988930
HLA B*0702	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.440924	1.101846	-3.339078	27600.930090
HLA A*3001	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.076497	0.737162	-3.339336	11926.072575
HLA A*3002	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.586127	1.246696	-3.339431	38559.073417
HLA A*0202	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-3.861759	0.522301	-3.339458	7273.764193
HLA A*2501	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.400611	1.060834	-3.339777	25154.243077
HLA B*5701	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.337351	0.997451	-3.339900	21744.597329
HLA A*3301	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.630144	1.289989	-3.340155	42672.117154
HLA A*6901	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.276023	0.935815	-3.340208	18880.903071
HLA B*1801	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.479855	1.139383	-3.340471	30189.414030
HLA A*0101	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.360766	1.020231	-3.340536	22949.135873
HLA A*2603	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.460890	1.120296	-3.340593	28899.454196
HLA A*1101	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.425849	1.084809	-3.341041	26659.341708
HLA A*2902	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.406299	1.064763	-3.341536	25485.863726
HLA A*6901	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.371875	1.030229	-3.341646	23543.699301
HLA B*0803	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.492523	1.150365	-3.342158	31083.012758
HLA A*2902	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.372551	1.030229	-3.342323	23580.410107
HLA B*1501	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-3.358161	0.015810	-3.342351	2281.188662
HLA A*0202	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.601892	1.259401	-3.342490	39984.496679
HLA B*5401	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.002827	0.659875	-3.342952	10065.306313
HLA B*4002	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.590071	1.246696	-3.343375	38910.908819
HLA B*1501	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.374135	1.030229	-3.343906	23666.547482
HLA B*4001	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.408764	1.064763	-3.344001	25630.906500
HLA A*6802	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.369763	1.025655	-3.344107	23429.472742
HLA B*5801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.349968	1.005856	-3.344112	22385.567265
HLA A*2403	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.429179	1.084809	-3.344370	26864.492553
HLA B*4403	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.613040	1.268587	-3.344453	41024.182912
HLA A*3101	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.370244	1.025655	-3.344589	23455.471080
HLA B*0702	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.014358	0.669638	-3.344720	10336.137274
HLA B*1801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.532594	1.187527	-3.345066	34087.376179
HLA B*0803	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.446934	1.101846	-3.345088	27985.540539
HLA A*0201	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.371238	1.025655	-3.345583	23509.207645
HLA A*3201	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.527857	1.181941	-3.345916	33717.627749
HLA B*1501	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.410792	1.064763	-3.346028	25750.850168

HLA A*0202	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-3.980606	0.634444	-3.346162	9563.251274
HLA B*1517	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.466648	1.120296	-3.346352	29285.202293
HLA B*7301	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.504381	1.157848	-3.346533	31943.386589
HLA A*2301	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.534121	1.187527	-3.346594	34207.452978
HLA A*1101	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.286384	0.939568	-3.346816	19336.772671
HLA B*1517	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.486720	1.139383	-3.347337	30670.430980
HLA B*1801	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.475139	1.126836	-3.348303	29863.401084
HLA A*0211	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.211132	0.862516	-3.348617	16260.441617
HLA A*0202	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.536179	1.187527	-3.348652	34369.948984
HLA A*0216	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.413449	1.064763	-3.348685	25908.891927
HLA B*3801	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.535420	1.186588	-3.348832	34309.943577
HLA B*2705	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.414027	1.064763	-3.349263	25943.395282
HLA A*2601	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.379515	1.030229	-3.349287	23961.567641
HLA B*4601	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.375300	1.025655	-3.349645	23730.137325
HLA B*7301	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.586632	1.236873	-3.349759	38603.948577
HLA A*2902	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.019433	0.669638	-3.349795	10457.627209
HLA B*5101	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.489344	1.139383	-3.349961	30856.328787
HLA B*1509	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.493940	1.143634	-3.350306	31184.576185
HLA B*4002	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.452551	1.101846	-3.350705	28349.886097
HLA A*2602	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.435576	1.084809	-3.350768	27263.166081
HLA A*6801	1:196-204	9	IDPWSTLKV	1.227329	0.062660	-4.640785	1.289989	-3.350796	43730.556922
HLA B*4601	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.384026	1.032607	-3.351419	24211.753224
HLA A*0101	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.377593	1.025655	-3.351938	23855.765048
HLA B*1503	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.495768	1.143634	-3.352134	31316.105355
HLA A*0219	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.359516	1.007379	-3.352138	22883.181815
HLA B*3501	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.323522	0.971364	-3.352158	21063.100551
HLA B*4403	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.598999	1.246696	-3.352304	39719.101673
HLA A*2301	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.535089	1.182783	-3.352306	34283.782124
HLA B*3801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.493590	1.141236	-3.352353	31159.449254
HLA A*3101	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.395017	1.042623	-3.352394	24832.310479
HLA A*2402	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.535270	1.182783	-3.352487	34298.066401
HLA B*5101	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.359923	1.007379	-3.352544	22904.608457
HLA A*0202	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.292157	0.939568	-3.352589	19595.514744
HLA B*4801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.413491	1.060834	-3.352657	25911.415006
HLA B*7301	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.515170	1.162375	-3.352795	32746.869765
HLA B*5801	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.360254	1.007379	-3.352875	22922.086629
HLA B*5301	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.535984	1.182783	-3.353201	34354.519626
HLA A*0301	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.292960	0.939568	-3.353392	19631.803574
HLA A*0216	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.473812	1.120296	-3.353515	29772.260350
HLA A*0212	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.418963	1.064763	-3.354200	26239.954688
HLA A*6801	1:183-191	9	SRGPVRASM	1.037490	0.231097	-4.622800	1.268587	-3.354213	41956.543306
HLA B*0702	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.419541	1.064763	-3.354778	26274.898926
HLA B*1503	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.237331	0.882547	-3.354784	17271.555150
HLA B*5801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.298319	0.943496	-3.354824	19875.560068
HLA B*5701	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.415676	1.060834	-3.354842	26042.108934
HLA A*0301	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.363170	1.007379	-3.355791	23076.495756
HLA B*4601	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.386178	1.030229	-3.355950	24332.031332
HLA A*0202	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.381691	1.025655	-3.356035	24081.905657
HLA B*1509	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.386531	1.030229	-3.356302	24351.784384
HLA A*3201	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.327681	0.971364	-3.356317	21265.759080
HLA A*0202	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.142809	0.786144	-3.356665	13893.424730
HLA B*5401	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.376914	1.020231	-3.356684	23818.496704
HLA A*0216	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.382600	1.025655	-3.356945	24132.377003
HLA B*4001	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.389832	1.032607	-3.357225	

									24537.584953
HLA B*0801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.422039	1.064763	-3.357275	26426.433605
HLA A*0211	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.234622	0.877206	-3.357416	17164.157360
HLA A*3001	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.255965	0.898490	-3.357475	18028.733093
HLA B*4601	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.365275	1.007379	-3.357896	23188.625087
HLA B*3501	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-3.347255	-0.010665	-3.357920	2224.615173
HLA B*4601	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.378383	1.020231	-3.358152	23899.167650
HLA B*5801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.350863	0.992668	-3.358195	22431.755259
HLA A*3101	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.203294	0.844974	-3.358321	15969.615305
HLA B*3901	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.378775	1.020231	-3.358545	23920.769145
HLA B*3901	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.365949	1.007379	-3.358570	23224.656596
HLA B*0802	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.235936	0.877206	-3.358729	17216.142535
HLA A*0203	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.423582	1.064763	-3.358819	26520.528124
HLA B*0801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.384503	1.025655	-3.358848	24238.357359
HLA A*0212	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.298458	0.939568	-3.358890	19881.905031
HLA B*1502	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.479314	1.120296	-3.359018	30151.873473
HLA A*0216	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.364876	1.005856	-3.359020	23167.308749
HLA B*3801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.521417	1.162375	-3.359042	33221.334437
HLA B*0702	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.401763	1.042623	-3.359139	25221.011551
HLA A*3101	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.294445	0.935291	-3.359155	19699.040569
HLA B*4601	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.126617	0.767455	-3.359162	13384.947187
HLA A*2403	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.391977	1.032607	-3.359370	24659.081502
HLA A*0201	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.389801	1.030229	-3.359573	24535.859321
HLA A*8001	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.402580	1.042623	-3.359957	25268.538396
HLA A*0202	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.154510	0.793787	-3.360722	14272.818656
HLA B*2705	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.393375	1.032607	-3.360768	24738.584112
HLA A*2602	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.511552	1.150365	-3.361187	32475.181406
HLA B*1501	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.368670	1.007379	-3.361291	23370.607668
HLA B*3501	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.426192	1.064763	-3.361429	26680.406742
HLA A*3201	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.394362	1.032607	-3.361755	24794.857878
HLA B*1509	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.422729	1.060834	-3.361895	26468.498487
HLA A*2402	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.565174	1.203170	-3.362004	36742.938166
HLA B*5401	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.565583	1.203170	-3.362413	36777.541339
HLA B*4001	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.405233	1.042623	-3.362609	25423.344967
HLA A*0301	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.368564	1.005856	-3.362709	23364.918902
HLA A*0212	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.388474	1.025655	-3.362818	24460.977822
HLA B*1503	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.393619	1.030229	-3.363391	24752.506660
HLA B*1509	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-3.774687	0.411293	-3.363394	5952.334149
HLA A*2902	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.031524	0.667908	-3.363615	10752.850456
HLA A*2603	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.526257	1.162375	-3.363882	33593.636014
HLA A*1101	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.484415	1.120296	-3.364119	30508.091056
HLA B*5701	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.428908	1.064763	-3.364145	26847.784349
HLA A*3002	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.241429	0.877206	-3.364222	17435.280773
HLA A*2601	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.371640	1.007379	-3.364261	23530.965865
HLA A*0101	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.300368	0.935291	-3.365078	19969.543003
HLA A*0206	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-3.548018	0.182878	-3.365141	3531.981242
HLA B*5401	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-3.887627	0.522301	-3.365326	7720.173267
HLA A*2601	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.391049	1.025655	-3.365393	24606.443618
HLA A*2601	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.398097	1.032607	-3.365490	25009.056312
HLA B*1502	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.509345	1.143634	-3.365712	32310.629496

HLA A*2601	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.386171	1.020231	-3.365941	24331.636435
HLA B*1801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.430873	1.064763	-3.366109	26969.482940
HLA B*5701	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.398884	1.032607	-3.366277	25054.421643
HLA A*8001	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.427464	1.060834	-3.366629	26758.608005
HLA A*0203	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.372493	1.005856	-3.366637	23577.221138
HLA B*1503	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.215239	0.848433	-3.366806	16414.937603
HLA A*0206	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.487112	1.120296	-3.366816	30698.152748
HLA B*1502	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.399723	1.032607	-3.367116	25102.856766
HLA A*8001	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.399728	1.032607	-3.367121	25103.128375
HLA B*3501	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.400245	1.032607	-3.367638	25133.023293
HLA B*5301	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.530533	1.162375	-3.368158	33926.032598
HLA A*2902	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.429059	1.060834	-3.368224	26857.081545
HLA B*4001	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.375655	1.007379	-3.368276	23749.530234
HLA B*3901	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.429282	1.060834	-3.368448	26870.888007
HLA A*0212	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.388678	1.020231	-3.368448	24472.493345
HLA A*1101	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.389026	1.020231	-3.368795	24492.095425
HLA B*3501	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.411649	1.042623	-3.369026	25801.748278
HLA A*0219	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.433854	1.064763	-3.369091	27155.269464
HLA B*1502	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.572359	1.203170	-3.369189	37355.848641
HLA B*4801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.399500	1.030229	-3.369271	25089.958732
HLA A*0203	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.143195	0.773810	-3.369384	13905.756750
HLA B*4002	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.607138	1.236873	-3.370265	40470.450010
HLA B*2705	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.231037	0.860615	-3.370422	17023.042106
HLA B*3501	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-3.223724	-0.146721	-3.370444	1673.877503
HLA B*1517	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.314897	0.943496	-3.371402	20648.919993
HLA A*0301	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.123022	0.751562	-3.371460	13274.615479
HLA B*2705	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.432968	1.060834	-3.372134	27099.941966
HLA B*4001	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.392412	1.020231	-3.372181	24683.773392
HLA A*2403	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.369692	0.997451	-3.372241	23425.670525
HLA B*4001	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.369903	0.997451	-3.372452	23437.079027
HLA B*4402	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.392919	1.020231	-3.372688	24712.634130
HLA B*0801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.233410	0.860615	-3.372795	17116.310381
HLA A*8001	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.437975	1.064763	-3.373212	27414.170745
HLA A*0202	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.517174	1.143634	-3.373540	32898.333838
HLA A*2301	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.513147	1.139383	-3.373764	32594.692334
HLA B*1501	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.194108	0.820012	-3.374096	15635.362984
HLA B*4501	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.476002	1.101846	-3.374155	29922.751655
HLA B*1501	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.309728	0.935291	-3.374438	20404.618277
HLA A*2602	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.577746	1.203170	-3.374576	37822.129402
HLA A*3001	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.046955	0.672009	-3.374946	11141.791406
HLA A*0202	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.436016	1.060834	-3.375181	27290.760799
HLA B*7301	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.570512	1.195068	-3.375444	37197.342352
HLA B*3801	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.477376	1.101846	-3.375530	30017.600744
HLA B*4001	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.401753	1.025655	-3.376098	25220.465786
HLA A*0203	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.347485	0.971364	-3.376121	22257.926222
HLA A*0101	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.406537	1.030229	-3.376308	25499.792977
HLA B*5801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.348002	0.971364	-3.376638	22284.432833
HLA B*0802	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.441445	1.064763	-3.376682	27634.098593
HLA A*0301	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.369368	0.992668	-3.376700	23408.188273
HLA B*7301	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.527068	1.150365	-3.376703	33656.394119
HLA B*1503	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.046368	0.669638	-3.376730	11126.732628

HLA A*0211	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.382621	1.005856	-3.376766	24133.552013
HLA A*3301	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.559636	1.182783	-3.376853	36277.399343
HLA A*0203	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.159035	0.782174	-3.376861	14422.310987
HLA A*0212	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.256395	0.879222	-3.377173	18046.590551
HLA A*0301	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.348568	0.971364	-3.377204	22313.505853
HLA A*0101	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.383082	1.005856	-3.377226	24159.155313
HLA A*0101	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.317169	0.939568	-3.377601	20757.225029
HLA B*4402	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.403367	1.025655	-3.377712	25314.374416
HLA A*0101	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.370427	0.992668	-3.377760	23465.370705
HLA A*0250	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.403433	1.025655	-3.377778	25318.209249
HLA B*4402	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.420674	1.042623	-3.378050	26343.501878
HLA A*6801	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.560266	1.181941	-3.378325	36330.034288
HLA B*4801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.349766	0.971364	-3.378402	22375.154792
HLA A*1101	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.439331	1.060834	-3.378496	27499.877943
HLA A*8001	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.408745	1.030229	-3.378517	25629.797241
HLA A*3002	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.463399	1.084809	-3.378590	29066.911651
HLA B*4002	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.565359	1.186588	-3.378772	36758.644765
HLA A*0219	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.409027	1.030229	-3.378798	25646.441167
HLA A*0203	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.968689	0.589436	-3.379253	9304.412992
HLA B*1501	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-3.996850	0.617415	-3.379435	9927.728833
HLA B*5701	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.386824	1.007379	-3.379446	24368.257510
HLA A*3002	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.541860	1.162375	-3.379485	34822.499614
HLA B*0702	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.387280	1.007379	-3.379901	24393.845873
HLA A*6802	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.444699	1.064763	-3.379936	27841.930143
HLA A*0216	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.969530	0.589436	-3.380094	9322.450686
HLA B*1501	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-3.860171	0.480013	-3.380158	7247.212000
HLA B*2705	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.315614	0.935291	-3.380323	20683.019170
HLA A*0212	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.315790	0.935291	-3.380500	20691.412835
HLA A*3002	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.387940	1.007379	-3.380562	24430.957082
HLA B*5101	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.507489	1.126836	-3.380653	32172.834591
HLA A*6802	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-3.970367	0.589436	-3.380930	9340.422285
HLA B*5701	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.423556	1.042623	-3.380933	26518.949967
HLA A*2402	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.568505	1.187527	-3.380978	37025.885319
HLA B*3501	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-3.998621	0.617415	-3.381206	9968.307304
HLA B*5101	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.501508	1.120296	-3.381211	31732.737366
HLA A*2403	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.446118	1.064763	-3.381355	27933.054480
HLA B*5401	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.424299	1.042623	-3.381675	26564.323546
HLA A*2602	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.564171	1.181941	-3.382230	36658.159105
HLA B*3801	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.532838	1.150365	-3.382473	34106.560103
HLA A*2601	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.375155	0.992668	-3.382487	23722.179260
HLA B*0801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-3.900014	0.517364	-3.382649	7943.529861
HLA A*0206	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.273128	0.890279	-3.382849	18755.480599
HLA A*3201	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.586037	1.203170	-3.382868	38551.147420
HLA B*0702	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.413125	1.030229	-3.382896	25889.556481
HLA B*7301	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-3.754844	0.371790	-3.383054	5686.480486
HLA B*1801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.265723	0.882547	-3.383175	18438.374025
HLA A*2403	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.389038	1.005856	-3.383182	24492.757932
HLA B*0802	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.468164	1.084809	-3.383355	29387.567941
HLA B*1517	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.416031	1.032607	-3.383424	26063.391249
HLA A*2902	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.409194	1.025655	-3.383539	25656.293912
HLA B*4402	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.376459	0.992668	-3.383791	23793.511864
HLA A*6901	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.389649	1.005856	-3.383793	24527.232979

HLA A*3001	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.266134	0.882099	-3.384035	18455.838464
HLA B*4001	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.414469	1.030229	-3.384240	25969.794673
HLA A*2403	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.376933	0.992668	-3.384265	23819.527569
HLA A*3201	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.534713	1.150365	-3.384348	34254.119530
HLA A*6802	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.390422	1.005856	-3.384566	24570.926734
HLA B*4402	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.382243	0.997451	-3.384792	24112.541030
HLA A*0203	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.245510	0.860615	-3.384895	17599.891925
HLA B*4002	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.542760	1.157848	-3.384912	34894.726200
HLA B*1501	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.178822	0.793787	-3.385035	15094.621194
HLA B*4801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.230680	0.844974	-3.385707	17009.049759
HLA B*1502	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.487711	1.101846	-3.385865	30740.530740
HLA A*6801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.154717	0.768800	-3.385916	14279.615138
HLA B*1501	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.391956	1.005856	-3.386100	24657.880905
HLA A*3301	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.633004	1.246696	-3.386308	42953.990221
HLA B*5801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.326170	0.939568	-3.386602	21191.913401
HLA B*1503	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-3.402515	0.015810	-3.386705	2526.473703
HLA A*0212	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.417011	1.030229	-3.386782	26122.254644
HLA A*0212	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.138059	0.750956	-3.387102	13742.275596
HLA A*2902	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.407476	1.020231	-3.387246	25555.033145
HLA B*3901	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.452013	1.064763	-3.387250	28314.786173
HLA A*0216	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.417673	1.030229	-3.387445	26162.136876
HLA A*6801	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.528900	1.141236	-3.387664	33798.714526
HLA A*0206	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-3.910088	0.522301	-3.387787	8129.954670
HLA B*5101	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.430459	1.042623	-3.387836	26943.816424
HLA B*1509	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.452666	1.064763	-3.387903	28357.402210
HLA B*5101	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.472888	1.084809	-3.388080	29709.029193
HLA A*0201	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.394061	1.005856	-3.388205	24777.694230
HLA A*0212	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.359801	0.971364	-3.388437	22898.165971
HLA A*6801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.431512	1.042623	-3.388888	27009.197473
HLA A*0211	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.414593	1.025655	-3.388938	25977.241907
HLA A*2402	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.419259	1.030229	-3.389030	26257.847146
HLA A*6901	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.382057	0.992668	-3.389390	24102.237984
HLA B*4002	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.531369	1.141236	-3.390133	33991.434400
HLA A*2301	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.533780	1.143634	-3.390146	34180.630013
HLA A*2902	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.397590	1.007379	-3.390211	24979.849396
HLA A*3301	1:247-255	9	ASGSSAELV	1.030749	0.206124	-4.627438	1.236873	-3.390565	42407.003293
HLA A*2601	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.396948	1.005856	-3.391093	24942.983893
HLA A*3201	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.253632	0.862516	-3.391117	17932.142056
HLA B*3901	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.236284	0.844974	-3.391310	17229.932393
HLA A*2602	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.160299	0.768800	-3.391499	14464.348563
HLA B*4002	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.651038	1.259401	-3.391637	44775.264580
HLA A*3301	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.573867	1.181941	-3.391926	37485.816632
HLA B*4501	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.638666	1.246696	-3.391970	43517.683852
HLA B*4601	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.398041	1.005856	-3.392185	25005.809414
HLA B*2705	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.417925	1.025655	-3.392269	26177.285425
HLA A*2403	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.422647	1.030229	-3.392418	26463.487254
HLA B*1502	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.336019	0.943496	-3.392523	21677.999988
HLA B*0802	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.390196	0.997451	-3.392745	24558.169152
HLA B*1502	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.364227	0.971364	-3.392863	23132.742771
HLA B*1501	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.255432	0.862516	-3.392916	18006.606589
HLA B*4601	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.391112	0.997451	-3.393661	24610.038070
HLA A*0203	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.423956	1.030229	-3.393727	26543.350164

HLA A*3301	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.535678	1.141236	-3.394442	34330.367082
HLA B*7301	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.581061	1.186588	-3.394473	38111.943810
HLA B*1509	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.479357	1.084809	-3.394548	30154.809745
HLA B*1503	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.479568	1.084809	-3.394759	30169.495396
HLA B*0702	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.420502	1.025655	-3.394847	26333.100306
HLA B*7301	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.577638	1.182783	-3.394855	37812.718351
HLA A*8001	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.338528	0.943496	-3.395033	21803.612835
HLA B*1509	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.415319	1.020231	-3.395088	26020.703228
HLA B*1502	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.583063	1.187527	-3.395536	38288.015821
HLA B*3501	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.421202	1.025655	-3.395547	26375.587372
HLA B*4801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.438194	1.042623	-3.395570	27427.966824
HLA A*2402	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.557977	1.162375	-3.395602	36139.106371
HLA B*3501	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.294459	0.898490	-3.395969	19699.679997
HLA B*4801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.421982	1.025655	-3.396327	26423.002690
HLA B*4002	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.578594	1.181941	-3.396653	37896.067061
HLA B*0801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.368214	0.971364	-3.396850	23346.092650
HLA A*3001	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.279657	0.882547	-3.397110	19039.582283
HLA B*4501	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.656954	1.259401	-3.397553	45389.370964
HLA B*1517	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.911578	0.514013	-3.397565	8157.887231
HLA B*7301	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.579814	1.181941	-3.397873	38002.618593
HLA B*4402	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.430572	1.032607	-3.397965	26950.813960
HLA A*2402	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.369382	0.971364	-3.398018	23408.948099
HLA B*4403	1:44-52	9	PPWQRAATR	0.944487	0.314914	-4.657542	1.259401	-3.398140	45450.800362
HLA A*6801	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.644854	1.246696	-3.398158	44142.234776
HLA B*4501	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.085472	0.687090	-3.398383	12175.098419
HLA A*0201	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.391103	0.992668	-3.398435	24609.505526
HLA A*6901	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.369821	0.971364	-3.398457	23432.641727
HLA A*2601	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.334022	0.935291	-3.398732	21578.544591
HLA A*2403	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.261275	0.862516	-3.398759	18250.511692
HLA A*2602	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.586399	1.187527	-3.398872	38583.278648
HLA A*0202	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-3.581752	0.182878	-3.398875	3817.264857
HLA B*4402	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.406525	1.007379	-3.399146	25499.103231
HLA A*2501	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.429641	1.030229	-3.399413	26893.138599
HLA B*7301	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.298169	0.898490	-3.399679	19868.679686
HLA A*2501	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.425457	1.025655	-3.399802	26635.267163
HLA B*4601	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.371379	0.971364	-3.400015	23516.839816
HLA B*4403	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.550494	1.150365	-3.400129	35521.745601
HLA A*0203	1:274-282	9	LMTALATIG	0.983162	-0.546352	-3.837188	0.436810	-3.400379	6873.664070
HLA A*3101	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.406497	1.005856	-3.400641	25497.447916
HLA A*6802	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.280003	0.879222	-3.400780	19054.729604
HLA A*2501	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.433950	1.032607	-3.401344	27161.293319
HLA A*8001	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.427325	1.025655	-3.401669	26750.068463
HLA B*5301	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.605026	1.203170	-3.401856	40274.100227
HLA A*3002	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.400007	0.997451	-3.402556	25119.294390
HLA A*2402	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.542039	1.139383	-3.402655	34836.819883
HLA B*2705	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.338559	0.935815	-3.402744	21805.146306
HLA B*1801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.445385	1.042623	-3.402762	27885.946452
HLA A*3101	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.433328	1.030229	-3.403099	27122.382227
HLA A*8001	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.423375	1.020231	-3.403145	26507.905494
HLA A*0101	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.346930	0.943496	-3.403434	22229.526907
HLA A*0101	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.374962	0.971364	-3.403598	23711.658177

HLA B*4501	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.598821	1.195068	-3.403753	39702.774458
HLA A*6801	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.586564	1.182783	-3.403781	38597.892603
HLA B*1502	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.464679	1.060834	-3.403845	29152.738695
HLA A*6801	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.222255	0.818322	-3.403933	16682.256652
HLA B*3501	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.283417	0.879222	-3.404194	19205.100847
HLA A*0250	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.343798	0.939568	-3.404230	22069.797918
HLA A*2603	1:185-193	9	GPVRASMQI	1.134441	0.112255	-4.651003	1.246696	-3.404307	44771.631289
HLA B*1501	1:274-282	9	LMTALATIG	0.983162	-0.546352	-3.841511	0.436810	-3.404702	6942.427545
HLA B*3801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.549033	1.143634	-3.405399	35402.417545
HLA A*0202	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.525836	1.120296	-3.405540	33561.120686
HLA A*3201	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.567996	1.162375	-3.405621	36982.444435
HLA B*1501	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.266303	0.860615	-3.405688	18463.028635
HLA A*1101	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.470678	1.064763	-3.405914	29558.173576
HLA A*3002	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.438720	1.032607	-3.406113	27461.224598
HLA B*0801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.436683	1.030229	-3.406454	27332.722783
HLA A*0101	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.342311	0.935815	-3.406496	21994.350039
HLA A*0206	1:124-132	9	SELPDLSGP	0.499243	0.082735	-3.988650	0.581978	-3.406672	9742.046622
HLA B*4801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.439286	1.032607	-3.406679	27497.051433
HLA A*0201	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.099475	0.692679	-3.406796	12574.056608
HLA A*2501	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.209342	0.802529	-3.406813	16193.548594
HLA A*6802	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.437167	1.030229	-3.406938	27363.200365
HLA B*1503	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.439700	1.032607	-3.407093	27523.244957
HLA A*0203	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-3.420343	0.013159	-3.407184	2632.344190
HLA A*3201	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.594789	1.187527	-3.407262	39335.904452
HLA A*0211	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.546716	1.139383	-3.407333	35214.078476
HLA A*6901	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.269869	0.862516	-3.407354	18615.275220
HLA B*4403	1:265-273	9	FLIGLVNIV	0.994940	0.200128	-4.602566	1.195068	-3.407498	40046.626355
HLA B*3501	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.347320	0.939568	-3.407752	22249.498914
HLA B*4801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.405209	0.997451	-3.407758	25421.969629
HLA B*0702	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.351838	0.943496	-3.408342	22482.173458
HLA B*5701	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.414635	1.005856	-3.408780	25979.771642
HLA B*1509	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.510746	1.101846	-3.408900	32414.976595
HLA A*0202	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-3.727355	0.318175	-3.409180	5337.705132
HLA A*1101	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.441967	1.032607	-3.409360	27667.306955
HLA A*2601	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.381127	0.971364	-3.409763	24050.658641
HLA B*3901	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.086370	0.676597	-3.409773	12200.285221
HLA B*7301	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.551617	1.141236	-3.410381	35613.721112
HLA B*2705	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.407869	0.997451	-3.410418	25578.131310
HLA B*5701	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.353979	0.943496	-3.410483	22593.248291
HLA A*2301	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.530839	1.120296	-3.410542	33949.900680
HLA B*5801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.346145	0.935291	-3.410855	22189.396576
HLA B*5301	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.552278	1.141236	-3.411041	35667.901509
HLA A*1101	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.454104	1.042623	-3.411481	28451.444971
HLA B*5101	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.409060	0.997451	-3.411609	25648.383662
HLA B*0803	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.496874	1.084809	-3.412066	31396.002349
HLA A*6802	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.275121	0.862516	-3.412605	18841.720644
HLA B*0702	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.352184	0.939568	-3.412616	22500.059601
HLA A*2403	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.257624	0.844974	-3.412650	18097.723373
HLA B*2705	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.384155	0.971364	-3.412791	24218.958356
HLA B*2705	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.456003	1.042623	-3.413379	28576.083867
HLA A*2501	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.478208	1.064763	-3.413444	30075.142555

HLA A*2403	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.349461	0.935815	-3.413646	22359.424200
HLA A*0216	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.200038	0.786144	-3.413894	15850.321230
HLA B*5301	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.601441	1.187527	-3.413913	39942.986396
HLA B*5101	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.439594	1.025655	-3.413939	27516.545376
HLA A*0206	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.553344	1.139383	-3.413961	35755.612743
HLA A*2403	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.357766	0.943496	-3.414270	22791.139790
HLA A*0211	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.534943	1.120296	-3.414647	34272.284822
HLA B*4402	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.386463	0.971364	-3.415099	24347.964211
HLA B*0702	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.346930	0.931448	-3.415482	22229.526907
HLA A*0219	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.408238	0.992668	-3.415570	25599.865391
HLA B*4501	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.603163	1.187527	-3.415636	40101.692724
HLA A*0203	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.183173	0.767455	-3.415719	15246.616090
HLA A*6801	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.536179	1.120296	-3.415883	34369.948984
HLA B*0802	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.436159	1.020231	-3.415928	27299.768324
HLA B*4002	1:124-132	9	SELPDLSGP	0.499243	0.082735	-3.998194	0.581978	-3.416216	9958.497340
HLA B*3801	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.424026	1.007379	-3.416647	26547.658411
HLA A*3201	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.501482	1.084809	-3.416673	31730.849046
HLA B*1501	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.348389	0.931448	-3.416941	22304.333505
HLA B*0803	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.481957	1.064763	-3.417194	30335.941113
HLA A*0212	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.051945	0.634444	-3.417502	11270.555698
HLA B*1801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.478532	1.060834	-3.417698	30097.603979
HLA B*3901	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.415241	0.997451	-3.417790	26016.058262
HLA B*4403	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.519742	1.101846	-3.417896	33093.438235
HLA B*5101	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.482843	1.064763	-3.418080	30397.875258
HLA A*0301	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.353384	0.935291	-3.418094	22562.346021
HLA B*4801	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.425908	1.007379	-3.418529	26662.947554
HLA B*4001	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.350083	0.931448	-3.418635	22391.502120
HLA A*0201	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.390017	0.971364	-3.418653	24548.074098
HLA A*1101	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.444389	1.025655	-3.418734	27822.055168
HLA B*3501	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.034108	0.615291	-3.418817	10817.030131
HLA A*2301	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.503758	1.084809	-3.418950	31897.624702
HLA A*3101	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.358699	0.939568	-3.419131	22840.141516
HLA B*0802	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.479998	1.060834	-3.419164	30199.378279
HLA B*0801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.201570	0.782174	-3.419396	15906.327956
HLA A*0219	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.088099	0.667908	-3.420191	12248.959672
HLA B*4801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.426246	1.005856	-3.420391	26683.726723
HLA A*3001	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.012939	0.592259	-3.420681	10302.418310
HLA A*2601	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.223500	0.802529	-3.420971	16730.157345
HLA B*1501	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.203196	0.782174	-3.421021	15965.987175
HLA A*2301	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.392421	0.971364	-3.421057	24684.307543
HLA B*1517	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.485940	1.064763	-3.421176	30615.393775
HLA B*5801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.352639	0.931448	-3.421192	22523.686226
HLA B*1501	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.311676	0.890279	-3.421397	20496.334381
HLA B*1501	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.414203	0.992668	-3.421535	25953.923735
HLA B*5401	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.560973	1.139383	-3.421590	36389.241460
HLA B*1501	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.304287	0.882547	-3.421740	20150.557552
HLA B*5301	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.565571	1.143634	-3.421937	36776.546540
HLA A*2602	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.542241	1.120296	-3.421944	34853.031501
HLA A*8001	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.429392	1.007379	-3.422014	26877.721196
HLA A*0206	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.208590	0.786144	-3.422446	16165.539148
HLA A*0203	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.415209	0.992668	-3.422541	26014.087921
HLA B*5301	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.107999	0.685107	-3.422892	12823.286421
HLA A*1101	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.271566	0.848433	-3.423133	18688.127553
HLA A*2603	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.508596	1.084809	-3.423787	32254.917364
HLA B*5101	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.454100	1.030229	-3.423871	28451.137135
HLA A*0211	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.174875	0.750956	-3.423919	14958.053557

HLA A*2403	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.431340	1.007379	-3.423961	26998.533055
HLA B*5701	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.301834	0.877206	-3.424628	20037.069517
HLA B*1501	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.120485	0.695802	-3.424683	13197.282281
HLA A*0206	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.213811	0.789030	-3.424781	16361.034082
HLA A*2403	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.360167	0.935291	-3.424877	22917.498868
HLA A*6901	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.101496	0.676597	-3.424899	12632.693764
HLA B*0802	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.455716	1.030229	-3.425487	28557.229689
HLA B*4402	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.286142	0.860615	-3.425527	19326.000863
HLA B*4801	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.243854	0.818322	-3.425532	17532.894278
HLA A*3101	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.418373	0.992668	-3.425706	26204.348101
HLA A*2603	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.629367	1.203170	-3.426197	42595.773707
HLA B*5801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.122120	0.695802	-3.426318	13247.067451
HLA B*5101	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.446835	1.020231	-3.426604	27979.182517
HLA A*6901	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.316984	0.890279	-3.426705	20748.355676
HLA B*4601	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.419581	0.992668	-3.426913	26277.315490
HLA B*1801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.459663	1.032607	-3.427056	28817.958356
HLA B*4001	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.433074	1.005856	-3.427218	27106.540115
HLA A*6802	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.248217	0.820012	-3.428205	17709.920339
HLA A*6801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.493075	1.064763	-3.428312	31122.554466
HLA A*0212	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.434171	1.005856	-3.428316	27175.109153
HLA A*0250	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.291149	0.862516	-3.428633	19550.089375
HLA B*5301	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.568130	1.139383	-3.428746	36993.850236
HLA B*1503	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.113901	0.685107	-3.428794	12998.739760
HLA A*2603	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.615507	1.186588	-3.428919	41257.879121
HLA A*0206	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.400308	0.971364	-3.428944	25136.694666
HLA A*2902	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.368651	0.939568	-3.429083	23369.596231
HLA B*3901	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.459562	1.030229	-3.429334	28811.255352
HLA B*4501	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.223227	0.793787	-3.429440	16719.661677
HLA B*4601	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.364864	0.935291	-3.429573	23166.682094
HLA A*0301	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.361076	0.931448	-3.429629	22965.529826
HLA B*1801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.320069	0.890279	-3.429790	20896.259747
HLA B*5401	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.550382	1.120296	-3.430085	35512.522701
HLA A*3101	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-3.944137	0.514013	-3.430124	8792.995700
HLA A*1101	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.437996	1.007379	-3.430617	27415.505546
HLA B*7301	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.634042	1.203170	-3.430872	43056.823454
HLA B*1517	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-3.800842	0.369909	-3.430933	6321.814824
HLA A*2402	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.515823	1.084809	-3.431014	32796.156447
HLA A*0219	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.370686	0.939568	-3.431118	23479.338817
HLA A*2301	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.461728	1.030229	-3.431500	28955.322524
HLA A*3001	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.117726	0.686161	-3.431565	13113.729185
HLA A*0216	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.308944	0.877206	-3.431737	20367.782401
HLA B*0803	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.452168	1.020231	-3.431938	28324.897848
HLA A*0212	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.424858	0.992668	-3.432190	26598.548566
HLA B*2705	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.439754	1.007379	-3.432375	27526.669818
HLA B*5701	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.372373	0.939568	-3.432805	23570.716977
HLA B*7301	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.458594	1.025655	-3.432939	28747.110197
HLA A*2902	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.438826	1.005856	-3.432970	27467.910710
HLA B*5401	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.465666	1.032607	-3.433059	29219.053500
HLA B*0803	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.458801	1.025655	-3.433146	28760.799099
HLA B*5401	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.310525	0.877206	-3.433319	20442.073711
HLA B*4403	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.615530	1.181941	-3.433590	41260.111187
HLA B*3501	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.033619	0.599894	-3.433726	10804.865039
HLA A*2601	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.377894	0.943496	-3.434398	23872.290071
HLA B*0801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.440367	1.005856	-3.434511	27565.564407

HLA A*2603	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.578343	1.143634	-3.434709	37874.136962
HLA B*3901	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.477653	1.042623	-3.435030	30036.769105
HLA B*0803	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.443224	1.007379	-3.435845	27747.500180
HLA B*4402	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.017882	0.581978	-3.435904	10420.354551
HLA A*3301	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.478682	1.042623	-3.436059	30108.026564
HLA B*0702	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.296726	0.860615	-3.436111	19802.791940
HLA B*4601	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.123468	0.687090	-3.436379	13288.267191
HLA B*5701	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.372232	0.935815	-3.436417	23563.067321
HLA B*4403	1:207-215	9	LLSVALFFV	1.021557	0.165031	-4.623014	1.186588	-3.436426	41977.203594
HLA B*5401	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.563264	1.126836	-3.436428	36581.688777
HLA A*2402	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.580265	1.143634	-3.436631	38042.112372
HLA A*2403	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.376320	0.939568	-3.436752	23785.918581
HLA B*5401	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.372791	0.935815	-3.436976	23593.425573
HLA A*3002	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.576599	1.139383	-3.437216	37722.409690
HLA A*6801	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.444746	1.007379	-3.437368	27844.942741
HLA B*5701	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.430090	0.992668	-3.437422	26920.941340
HLA A*3002	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.480080	1.042623	-3.437457	30205.096955
HLA B*1503	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.133374	0.695802	-3.437572	13594.829987
HLA B*0702	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-3.747927	0.310085	-3.437842	5596.630943
HLA A*3001	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.134187	0.695802	-3.438385	13620.300915
HLA B*0702	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.444272	1.005856	-3.438416	27814.530474
HLA A*0250	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.558753	1.120296	-3.438456	36203.681821
HLA B*1503	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.445851	1.007379	-3.438472	27915.832712
HLA B*1801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.209586	0.770901	-3.438685	16202.662109
HLA A*3002	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.075515	0.636799	-3.438717	11899.134215
HLA A*1101	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.444960	1.005856	-3.439105	27858.654178
HLA A*0216	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.431937	0.992668	-3.439269	27035.657560
HLA A*1101	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.469804	1.030229	-3.439575	29498.748195
HLA A*0219	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.318805	0.879222	-3.439582	20835.529179
HLA A*6802	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.432278	0.992668	-3.439610	27056.873567
HLA A*2501	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.375476	0.935815	-3.439661	23739.767585
HLA B*4001	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.432708	0.992668	-3.440040	27083.673399
HLA B*0802	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.482745	1.042623	-3.440121	30390.969178
HLA A*3101	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.260208	0.820012	-3.440196	18205.741801
HLA A*0203	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.285261	0.844974	-3.440287	19286.833785
HLA A*2602	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.583942	1.143634	-3.440308	38365.562331
HLA B*2705	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.260500	0.820012	-3.440488	18217.958788
HLA B*1502	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.579971	1.139383	-3.440588	38016.395616
HLA A*0203	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.303298	0.862516	-3.440782	20104.715605
HLA B*4501	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.384677	0.943496	-3.441181	24248.062687
HLA B*4601	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.377163	0.935815	-3.441348	23832.159296
HLA B*4403	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.585034	1.143634	-3.441400	38462.196175
HLA B*4001	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.376773	0.935291	-3.441483	23810.766633
HLA A*0301	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.261522	0.820012	-3.441510	18260.881628
HLA A*0201	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.111829	0.669638	-3.442191	12936.863723
HLA B*4601	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.321716	0.879222	-3.442493	20975.655760
HLA A*0101	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.236300	0.793787	-3.442513	17230.584890
HLA B*1509	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.449946	1.007379	-3.442567	28180.308259
HLA A*3001	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.262725	0.820012	-3.442713	18311.531888
HLA B*0801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-3.922733	0.480013	-3.442720	8370.146366
HLA B*0802	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.475407	1.032607	-3.442800	29881.824341

HLA B*5101	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.475506	1.032607	-3.442899	29888.614721
HLA B*4801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.435644	0.992668	-3.442977	27267.443647
HLA A*2501	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.435689	0.992668	-3.443021	27270.246554
HLA B*7301	1:218-226	9	ITVAFLYLV	0.916657	0.185189	-4.545025	1.101846	-3.443179	35077.182195
HLA A*0250	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.582746	1.139383	-3.443362	38260.062950
HLA B*4001	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.383108	0.939568	-3.443540	24160.593038
HLA A*3101	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.217434	0.773810	-3.443623	16498.089498
HLA B*3501	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.449664	1.005856	-3.443808	28162.019915
HLA A*6801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.464127	1.020231	-3.443897	29115.699669
HLA B*4801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.387605	0.943496	-3.444109	24412.064257
HLA A*0219	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.450070	1.005856	-3.444215	28188.389392
HLA A*1101	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.379581	0.935291	-3.444290	23965.197540
HLA B*4402	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.384003	0.939568	-3.444435	24210.443431
HLA A*0101	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.292897	0.848433	-3.444464	19628.936225
HLA A*2501	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.464792	1.020231	-3.444562	29160.309906
HLA B*0802	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.470668	1.025655	-3.445013	29557.533957
HLA B*4002	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.648184	1.203170	-3.445014	44481.921212
HLA B*1503	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.060634	0.615291	-3.445343	11498.302372
HLA A*0201	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.322839	0.877206	-3.445632	21029.967468
HLA B*3501	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.381597	0.935815	-3.445782	24076.695003
HLA B*2705	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.476023	1.030229	-3.445794	29924.208599
HLA A*3201	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.566149	1.120296	-3.445853	36825.522554
HLA A*3001	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.063458	0.617415	-3.446042	11573.315860
HLA A*8001	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.381905	0.935291	-3.446614	24093.764096
HLA A*2402	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.567063	1.120296	-3.446766	36903.101512
HLA B*0803	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.489504	1.042623	-3.446881	30867.682069
HLA A*2601	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.386601	0.939568	-3.447033	24355.736919
HLA B*4601	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.386940	0.939568	-3.447372	24374.718016
HLA A*8001	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.453477	1.005856	-3.447621	28410.378221
HLA A*0202	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.587090	1.139383	-3.447707	38644.694466
HLA B*3501	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.338063	0.890279	-3.447784	21780.270224
HLA B*5801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.346801	0.898490	-3.448311	22222.913631
HLA B*5801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.308932	0.860615	-3.448317	20367.231471
HLA A*3002	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.327697	0.879222	-3.448475	21266.564413
HLA B*4501	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.631349	1.182783	-3.448567	42790.708420
HLA B*5701	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.419987	0.971364	-3.448623	26301.920226
HLA A*2601	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.384468	0.935815	-3.448653	24236.390536
HLA A*0219	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.383949	0.935291	-3.448658	24207.431175
HLA A*0201	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.234904	0.786144	-3.448760	17175.303721
HLA B*4501	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.651969	1.203170	-3.448799	44871.290172
HLA A*0219	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.420328	0.971364	-3.448964	26322.560439
HLA A*0101	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.267466	0.818322	-3.449144	18512.536949
HLA B*1503	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.388725	0.939568	-3.449157	24475.141357
HLA B*1801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.385093	0.935815	-3.449278	24271.292548
HLA A*2603	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.637096	1.187527	-3.449569	43360.703207
HLA B*1503	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.269590	0.820012	-3.449578	18603.294994
HLA A*0203	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-3.632525	0.182878	-3.449647	4290.665566
HLA B*2705	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.268373	0.818322	-3.450051	18551.235538
HLA B*0801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.236225	0.786144	-3.450081	17227.602250
HLA B*4002	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.514918	1.064763	-3.450155	32727.919459
HLA B*0803	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.511011	1.060834	-3.450177	32434.798495
HLA B*4001	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.386016	0.935815	-3.450201	24322.950309
HLA B*3801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.511058	1.060834	-3.450224	32438.308058
HLA A*8001	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.442895	0.992668	-3.450227	27726.492610

HLA A*3101	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.381811	0.931448	-3.450363	24088.550876
HLA B*4801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.385894	0.935291	-3.450604	24316.108879
HLA A*8001	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.422062	0.971364	-3.450698	26427.863284
HLA A*0212	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.341334	0.890279	-3.451055	21944.907106
HLA B*1509	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.493764	1.042623	-3.451140	31171.925869
HLA A*2603	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.577997	1.126836	-3.451161	37844.029388
HLA A*2301	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.516180	1.064763	-3.451417	32823.135920
HLA B*0702	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.423030	0.971364	-3.451666	26486.833364
HLA B*0801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.387273	0.935291	-3.451983	24393.449972
HLA B*2705	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.225835	0.773810	-3.452025	16820.364917
HLA A*2902	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.350786	0.898490	-3.452295	22427.750957
HLA A*0301	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.329685	0.877206	-3.452479	21364.119580
HLA B*5101	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.458366	1.005856	-3.452511	28732.028842
HLA A*3101	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.351129	0.898490	-3.452638	22445.472376
HLA A*0202	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.424130	0.971364	-3.452766	26553.978438
HLA B*4601	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.396676	0.943496	-3.453180	24927.335906
HLA B*1503	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.495855	1.042623	-3.453231	31322.374399
HLA A*2501	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.460713	1.007379	-3.453335	28887.730861
HLA B*4402	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.343629	0.890279	-3.453350	22061.203140
HLA B*1509	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.332643	0.879222	-3.453421	21510.128348
HLA B*5101	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.302001	0.848433	-3.453568	20044.767276
HLA A*2603	1:213-221	9	FFVWMITVA	1.295131	-0.144766	-4.603990	1.150365	-3.453625	40178.130371
HLA B*2705	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.333317	0.879222	-3.454095	21543.551735
HLA A*0101	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.386552	0.931448	-3.455104	24352.970077
HLA A*2602	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.617614	1.162375	-3.455239	41458.576582
HLA B*3501	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.447911	0.992668	-3.455243	28048.593311
HLA B*5801	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.273671	0.818322	-3.455349	18778.933681
HLA A*2301	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.498160	1.042623	-3.455536	31489.047295
HLA B*0702	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-3.638248	0.182632	-3.455616	4347.584286
HLA B*1502	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.582581	1.126836	-3.455745	38245.576904
HLA B*1517	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.498561	1.042623	-3.455938	31518.191009
HLA A*0301	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.354810	0.898490	-3.456320	22636.558096
HLA A*0216	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.427729	0.971364	-3.456365	26774.971011
HLA A*8001	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.396063	0.939568	-3.456495	24892.163816
HLA B*3901	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.489537	1.032607	-3.456930	30870.020028
HLA B*4601	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.355659	0.898490	-3.457168	22680.809811
HLA B*4501	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.518135	1.060834	-3.457300	32971.206752
HLA A*3301	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.644885	1.187527	-3.457358	44145.339345
HLA A*3001	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.239545	0.782174	-3.457370	17359.797647
HLA A*0202	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.150845	0.693390	-3.457454	14152.871100
HLA B*5301	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.584292	1.126836	-3.457455	38396.500261
HLA B*4501	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.578063	1.120296	-3.457767	37849.762318
HLA B*1501	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.356406	0.898490	-3.457915	22719.862206
HLA A*3301	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.620307	1.162375	-3.457932	41716.407100
HLA B*2705	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.335373	0.877206	-3.458167	21645.773183
HLA A*3001	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.231993	0.773810	-3.458183	17060.565158
HLA B*0702	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.337633	0.879222	-3.458411	21758.718215
HLA A*6901	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.357012	0.898490	-3.458521	22751.595626
HLA A*2902	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.394425	0.935815	-3.458610	24798.479853
HLA B*4403	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.646468	1.187527	-3.458941	44306.598782
HLA A*6901	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.390523	0.931448	-3.459075	24576.643217
HLA B*2705	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.230154	0.770901	-3.459253	16988.450418

HLA B*3501	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.146399	0.687090	-3.459310	14008.748087
HLA A*2601	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.390927	0.931448	-3.459479	24599.522449
HLA B*1501	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.127425	0.667908	-3.459517	13409.879791
HLA A*2402	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.479906	1.020231	-3.459676	30193.007315
HLA A*0206	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.524478	1.064763	-3.459715	33456.341786
HLA B*1503	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.391359	0.931448	-3.459911	24624.021487
HLA B*3801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.480188	1.020231	-3.459958	30212.614577
HLA A*1101	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.262527	0.802529	-3.459998	18303.212456
HLA A*8001	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.396133	0.935815	-3.460318	24896.204060
HLA B*1801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.486027	1.025655	-3.460371	30621.522546
HLA A*3001	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-3.772869	0.312492	-3.460377	5927.462322
HLA B*4001	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.403877	0.943496	-3.460381	25344.109573
HLA A*2902	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.453129	0.992668	-3.460462	28387.640170
HLA B*1801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.308993	0.848433	-3.460560	20370.096469
HLA A*3301	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.599949	1.139383	-3.460565	39806.006486
HLA B*5801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.339861	0.879222	-3.460638	21870.596073
HLA A*0301	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.305732	0.844974	-3.460758	20217.711758
HLA A*2603	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.600329	1.139383	-3.460946	39840.907843
HLA B*0801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.453641	0.992668	-3.460974	28421.139048
HLA B*3801	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.545918	1.084809	-3.461109	35149.366560
HLA B*7301	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.545948	1.084809	-3.461139	35151.838651
HLA A*0211	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.148655	0.687090	-3.461565	14081.691683
HLA A*6802	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-3.678739	0.216823	-3.461916	4772.424152
HLA B*3801	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.526788	1.064763	-3.462025	33634.733886
HLA B*7301	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.523127	1.060834	-3.462293	33352.431304
HLA A*2601	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.339715	0.877206	-3.462509	21863.261618
HLA B*4002	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.645576	1.182783	-3.462793	44215.608701
HLA B*0801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.156474	0.693390	-3.463084	14337.516059
HLA B*4601	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.394557	0.931448	-3.463109	24805.993785
HLA A*3101	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.342480	0.879222	-3.463258	22002.918772
HLA B*3901	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.342781	0.879222	-3.463559	22018.160317
HLA A*2403	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.362211	0.898490	-3.463721	23025.616684
HLA B*0702	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.354181	0.890279	-3.463902	22603.762256
HLA B*1517	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.079566	0.615291	-3.464275	12010.632406
HLA A*3201	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.607920	1.143634	-3.464287	40543.422956
HLA A*6802	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.435656	0.971364	-3.464292	27268.181226
HLA B*1502	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.354712	0.890279	-3.464433	22631.415307
HLA A*2501	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.404232	0.939568	-3.464664	25364.821464
HLA B*1502	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.549496	1.084809	-3.464687	35440.167719
HLA B*1517	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.396157	0.931448	-3.464709	24897.550953
HLA B*4501	1:267-275	9	IGLVNIVLM	1.127039	0.054902	-4.646865	1.181941	-3.464925	44347.125555
HLA A*2403	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.396793	0.931448	-3.465345	24934.079524
HLA A*1101	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.436793	0.971364	-3.465429	27339.673416
HLA A*0211	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.530470	1.064763	-3.465706	33921.077486
HLA B*3501	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.401046	0.935291	-3.465755	25179.430788
HLA A*0216	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.216931	0.750956	-3.465975	16479.000443
HLA A*0212	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.328738	0.862516	-3.466223	21317.592577
HLA B*4402	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.409809	0.943496	-3.466314	25692.684694
HLA B*4403	1:295-303	9	GIEVTLADR	0.657184	0.545986	-4.669688	1.203170	-3.466519	46739.963914
HLA B*3501	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.410181	0.943496	-3.466685	25714.655226
HLA B*0702	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.459555	0.992668	-3.466887	28810.787758
HLA B*0702	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.365778	0.898490	-3.467287	23215.486481
HLA B*5701	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.402881	0.935291	-3.467590	25286.042055
HLA B*5801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.357940	0.890279	-3.467661	22800.265635
HLA A*1101	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.135573	0.667908	-3.467665	13663.844117
HLA A*2902	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.316121	0.848433	-3.467689	20707.202150

HLA B*1517	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.439176	0.971364	-3.467812	27490.060790
HLA A*0206	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.328719	0.860615	-3.468104	21316.669991
HLA B*5101	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.403706	0.935291	-3.468415	25334.102605
HLA A*2902	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.412206	0.943496	-3.468710	25834.851044
HLA A*3201	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.511545	1.042623	-3.468921	32474.654349
HLA B*5301	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.553741	1.084809	-3.468933	35788.318021
HLA A*0250	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.475217	1.005856	-3.469361	29868.732964
HLA B*5701	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.400945	0.931448	-3.469497	25173.574098
HLA B*5401	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.534405	1.064763	-3.469642	34229.852390
HLA A*3001	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.258684	0.789030	-3.469654	18141.933195
HLA B*5801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.351848	0.882099	-3.469749	22482.659968
HLA A*2603	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.238598	0.768800	-3.469798	17321.991298
HLA A*0201	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.401692	0.931448	-3.470244	25216.918597
HLA A*0212	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.348049	0.877206	-3.470842	22286.844090
HLA B*1801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.442207	0.971364	-3.470843	27682.578229
HLA B*1509	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.353713	0.882099	-3.471614	22579.440864
HLA B*1509	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.290268	0.818322	-3.471946	19510.468147
HLA A*3201	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.611358	1.139383	-3.471974	40865.583897
HLA B*2705	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.411553	0.939568	-3.471985	25796.025944
HLA B*5801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.354752	0.882547	-3.472204	22633.496771
HLA B*1502	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.165604	0.693390	-3.472214	14642.121829
HLA A*0202	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.351982	0.879222	-3.472759	22489.593873
HLA B*4501	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.408740	0.935815	-3.472925	25629.519934
HLA A*2301	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.505683	1.032607	-3.473076	32039.267038
HLA B*2705	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.478978	1.005856	-3.473123	30128.556577
HLA B*5101	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.466004	0.992668	-3.473337	29241.824714
HLA B*1801	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.291694	0.818322	-3.473372	19574.641985
HLA B*0803	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.506124	1.032607	-3.473517	32071.869445
HLA A*3001	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.257817	0.784035	-3.473781	18105.753501
HLA A*6901	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.355929	0.882099	-3.473830	22694.924778
HLA B*4403	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.056560	0.581978	-3.474581	11390.944035
HLA A*0206	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.467783	0.992668	-3.475115	29361.823899
HLA A*3001	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.090430	0.615291	-3.475139	12314.871766
HLA A*2501	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.481013	1.005856	-3.475157	30270.038941
HLA B*4801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.415037	0.939568	-3.475469	26003.816416
HLA B*5801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.278299	0.802529	-3.475771	18980.140094
HLA A*0301	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.366215	0.890279	-3.475936	23238.858575
HLA A*6901	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.296132	0.820012	-3.476120	19775.706360
HLA B*5701	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.278673	0.802529	-3.476144	18996.473310
HLA A*6801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.324925	0.848433	-3.476492	21131.238100
HLA A*3002	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.172577	0.695802	-3.476776	14879.121411
HLA B*5801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.339630	0.862516	-3.477115	21859.004031
HLA A*0301	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.356815	0.879222	-3.477592	22741.258951
HLA B*4801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.413414	0.935815	-3.477598	25906.789549
HLA B*1509	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.503342	1.025655	-3.477687	31867.095738
HLA A*2603	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.417274	0.939568	-3.477706	26138.087112
HLA B*0702	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.280637	0.802529	-3.478108	19082.582614
HLA B*5301	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.598501	1.120296	-3.478205	39673.574087
HLA B*7301	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.618239	1.139383	-3.478856	41518.279686
HLA A*2602	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.414755	0.935815	-3.478940	25986.940563
HLA B*0702	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.024240	0.545171	-3.479069	10574.021825
HLA B*4403	1:92-100	9	PVTGPAAAV	1.144634	0.038149	-4.661956	1.182783	-3.479173	45915.172219
HLA B*4801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.369744	0.890279	-3.479465	23428.458757
HLA B*5801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.172150	0.692679	-3.479470	14864.478640

HLA B*5401	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.173014	0.693390	-3.479624	14894.100904
HLA B*1517	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.328118	0.848433	-3.479685	21287.168294
HLA B*0803	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.477329	0.997451	-3.479878	30014.353082
HLA B*1517	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.325047	0.844974	-3.480074	21137.183454
HLA B*1502	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.487566	1.007379	-3.480187	30730.221692
HLA B*1503	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.342863	0.862516	-3.480348	22022.329765
HLA A*0301	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.363179	0.882547	-3.480632	23076.995126
HLA B*4801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.379760	0.898490	-3.481269	23975.052895
HLA B*5801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.358494	0.877206	-3.481288	22829.394096
HLA B*3501	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.358678	0.877206	-3.481471	22839.029479
HLA A*0212	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.263956	0.782174	-3.481782	18363.514732
HLA A*2602	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.542668	1.060834	-3.481834	34887.364689
HLA A*0101	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.361215	0.879222	-3.481993	22972.861214
HLA A*1101	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.474749	0.992668	-3.482081	29836.594546
HLA B*5701	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.380742	0.898490	-3.482251	24029.329835
HLA A*0101	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.359606	0.877206	-3.482399	22887.886526
HLA B*4501	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.640418	1.157848	-3.482570	43693.666407
HLA B*4402	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.414022	0.931448	-3.482574	25943.114582
HLA B*1517	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.488928	1.005856	-3.483073	30826.796439
HLA A*3301	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.626815	1.143634	-3.483181	42346.251297
HLA A*2301	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.544031	1.060834	-3.483196	34997.003938
HLA B*4001	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.361307	0.877206	-3.484100	22977.708670
HLA B*1502	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.329076	0.844974	-3.484103	21334.205964
HLA B*3901	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.509921	1.025655	-3.484266	32353.483135
HLA B*0801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.415991	0.931448	-3.484543	26060.994359
HLA A*0101	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.374830	0.890279	-3.484551	23704.475728
HLA A*2601	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.333132	0.848433	-3.484699	21534.346392
HLA B*5701	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.333284	0.848433	-3.484852	21541.920122
HLA A*3101	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.375199	0.890279	-3.484920	23724.617739
HLA B*0801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.278781	0.793787	-3.484994	19001.201264
HLA A*0301	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.367108	0.882099	-3.485008	23286.681181
HLA B*1509	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.517627	1.032607	-3.485020	32932.701210
HLA B*0803	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.362228	0.877206	-3.485021	23026.488663
HLA A*2403	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.269183	0.784035	-3.485148	18585.892114
HLA B*5401	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.516495	1.030229	-3.486266	32846.938864
HLA B*4501	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.518952	1.032607	-3.486346	33033.338179
HLA A*2301	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.493752	1.007379	-3.486373	31171.082697
HLA B*5801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.331452	0.844974	-3.486478	21451.210908
HLA A*0301	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.347308	0.860615	-3.486694	22248.897085
HLA A*1101	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.174057	0.687090	-3.486968	14929.919397
HLA B*1509	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.369605	0.882547	-3.487058	23420.981974
HLA A*2603	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.517352	1.030229	-3.487124	32911.862821
HLA B*4402	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.422941	0.935815	-3.487126	26481.388872
HLA A*8001	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.364643	0.877206	-3.487437	23154.904146
HLA A*0201	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.350046	0.862516	-3.487530	22389.564036
HLA A*2602	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.459036	0.971364	-3.487672	28776.362581
HLA A*2602	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.513354	1.025655	-3.487698	32610.213392
HLA B*1517	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.423009	0.935291	-3.487718	26485.543778
HLA B*0803	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.518029	1.030229	-3.487800	32963.181053
HLA A*0201	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.378157	0.890279	-3.487878	23886.758855
HLA A*3002	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.336320	0.848433	-3.487887	21693.016461
HLA B*1509	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.258806	0.770901	-3.487905	18147.037497
HLA A*2602	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.306653	0.818322	-3.488331	20260.632479
HLA B*1509	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.428027	0.939568	-3.488459	26793.373234

HLA B*4403	1:222-230	9	FLYLVLGGM	0.909808	0.248040	-4.646365	1.157848	-3.488517	44296.053510
HLA B*4501	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.629980	1.141236	-3.488743	42655.960614
HLA B*5701	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.333888	0.844974	-3.488915	21571.891578
HLA B*5401	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.420685	0.931448	-3.489237	26344.214465
HLA A*2403	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.337845	0.848433	-3.489412	21769.314897
HLA B*4801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.368738	0.879222	-3.489516	23374.274495
HLA A*0301	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.308133	0.818322	-3.489811	20329.803186
HLA B*4002	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.610122	1.120296	-3.489826	40749.462020
HLA B*1801	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.510097	1.020231	-3.489867	32366.612956
HLA A*0101	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.388387	0.898490	-3.489896	24456.082059
HLA B*3901	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.426042	0.935815	-3.490227	26671.170706
HLA B*1509	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.462290	0.971364	-3.490926	28992.784912
HLA B*4402	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.335949	0.844974	-3.490975	21674.482006
HLA A*0202	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.336186	0.844974	-3.491213	21686.328154
HLA A*3002	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.258669	0.767455	-3.491215	18141.344329
HLA B*0802	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.497398	1.005856	-3.491543	31433.901508
HLA A*8001	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.352188	0.860615	-3.491573	22500.303048
HLA A*0101	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.352252	0.860615	-3.491637	22503.589840
HLA B*0802	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.484338	0.992668	-3.491670	30502.645044
HLA B*1503	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.497835	1.005856	-3.491980	31465.547457
HLA A*6901	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.352769	0.860615	-3.492154	22530.389009
HLA A*2402	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.524871	1.032607	-3.492264	33486.581626
HLA B*2705	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.423822	0.931448	-3.492374	26535.166420
HLA B*4001	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.372056	0.879222	-3.492833	23553.508742
HLA B*3901	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.499031	1.005856	-3.493176	31552.311448
HLA B*1801	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.500601	1.007379	-3.493222	31666.541657
HLA A*0211	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.485916	0.992668	-3.493249	30613.737561
HLA A*6801	1:69-77	9	GRPTNPPAA	1.486407	-0.298880	-4.680863	1.187527	-3.493335	47958.161232
HLA A*2402	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.558137	1.064763	-3.493374	36152.403399
HLA A*0201	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.180523	0.687090	-3.493434	15153.859133
HLA B*4002	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.523832	1.030229	-3.493604	33406.605140
HLA B*0702	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-3.347043	-0.146721	-3.493764	2223.532293
HLA A*2902	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.338773	0.844974	-3.493799	21815.883620
HLA B*0801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.231040	0.737162	-3.493878	17023.134199
HLA A*3001	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.279143	0.785097	-3.494046	19017.038196
HLA A*2602	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.524337	1.030229	-3.494109	33445.483842
HLA B*1517	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.373477	0.879222	-3.494255	23630.725269
HLA A*0301	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.356932	0.862516	-3.494416	22747.411168
HLA A*0101	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.376806	0.882099	-3.494707	23812.570092
HLA A*2403	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.373956	0.879222	-3.494734	23656.818944
HLA A*3001	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.107064	0.612174	-3.494890	12795.705846
HLA B*5101	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.372479	0.877206	-3.495272	23576.455849
HLA B*0802	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.434900	0.939568	-3.495332	27220.721831
HLA B*0802	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.466700	0.971364	-3.495336	29288.687954
HLA B*4002	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.438917	0.943496	-3.495421	27473.706657
HLA A*6802	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.281854	0.786144	-3.495710	19136.133164
HLA B*4601	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.386030	0.890279	-3.495751	24323.739829
HLA A*6801	1:290-298	9	TDLIGGIEV	1.158088	0.004287	-4.658303	1.162375	-3.495928	45530.536571
HLA B*1502	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.298507	0.802529	-3.495978	19884.163896
HLA B*0802	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.439984	0.943496	-3.496488	27541.267478
HLA A*8001	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.375921	0.879222	-3.496698	23764.053176
HLA B*4001	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.387069	0.890279	-3.496790	24381.971644
HLA A*2602	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.636532	1.139383	-3.497149	43304.441356
HLA B*4801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.428610	0.931448	-3.497162	26829.344756

HLA A*0211	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.387475	0.890279	-3.497196	24404.801676
HLA B*0801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.395788	0.898490	-3.497297	24876.413132
HLA A*2902	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.299828	0.802529	-3.497299	19944.710862
HLA A*0216	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.342377	0.844974	-3.497403	21997.681927
HLA B*0803	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.503509	1.005856	-3.497654	31879.338309
HLA A*6802	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.358452	0.860615	-3.497837	22827.171124
HLA A*2403	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.235381	0.737162	-3.498220	17194.176129
HLA B*4402	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.433570	0.935291	-3.498279	27137.499534
HLA A*0212	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.397115	0.898490	-3.498625	24952.566387
HLA B*4402	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.397768	0.898490	-3.499278	24990.122012
HLA A*3301	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.619579	1.120296	-3.499282	41646.504579
HLA B*4501	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.584113	1.084809	-3.499304	38380.716724
HLA B*1517	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.492114	0.992668	-3.499447	31053.767441
HLA A*3201	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.519963	1.020231	-3.499732	33110.271507
HLA A*0203	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.431387	0.931448	-3.499939	27001.454395
HLA A*2603	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.532619	1.032607	-3.500012	34089.404737
HLA A*8001	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.348488	0.848433	-3.500055	22309.401968
HLA A*2602	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.626947	1.126836	-3.500110	42359.082198
HLA A*3201	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.530425	1.030229	-3.500196	33917.590989
HLA B*5301	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.561323	1.060834	-3.500489	36418.585687
HLA B*0801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.383632	0.882547	-3.501084	24189.758094
HLA B*3801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.531454	1.030229	-3.501225	33998.055081
HLA A*3301	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.508868	1.007379	-3.501490	32275.165197
HLA A*0203	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.252833	0.750956	-3.501877	17899.188666
HLA B*3501	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-3.684726	0.182632	-3.502094	4838.664638
HLA B*1509	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.499708	0.997451	-3.502257	31601.509783
HLA B*4501	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.522542	1.020231	-3.502312	33307.533744
HLA B*4601	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.350929	0.848433	-3.502496	22435.153409
HLA B*1502	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.508439	1.005856	-3.502583	32243.228282
HLA A*2402	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.563419	1.060834	-3.502584	36594.752699
HLA A*6802	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.434155	0.931448	-3.502707	27174.080072
HLA B*0803	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.446234	0.943496	-3.502738	27940.460083
HLA A*2602	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.365374	0.862516	-3.502858	23193.894497
HLA A*1101	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.401469	0.898490	-3.502978	25203.961957
HLA A*0201	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.401617	0.898490	-3.503126	25212.553512
HLA B*4001	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.363922	0.860615	-3.503307	23116.479566
HLA A*2403	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.385455	0.882099	-3.503356	24291.521944
HLA B*4001	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.321680	0.818322	-3.503359	20973.953690
HLA B*4501	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.509277	1.005856	-3.503422	32305.560783
HLA A*2601	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.393718	0.890279	-3.503439	24758.131448
HLA B*3901	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.438837	0.935291	-3.503547	27468.653711
HLA B*1502	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.568346	1.064763	-3.503582	37012.267020
HLA A*3002	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.321969	0.818322	-3.503648	20987.914746
HLA A*2601	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.402275	0.898490	-3.503784	25250.773645
HLA B*7301	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.536935	1.032607	-3.504328	34429.873074
HLA B*4002	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.643813	1.139383	-3.504430	44036.571006
HLA B*5301	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.524744	1.020231	-3.504513	33476.800485
HLA B*2705	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.497234	0.992668	-3.504566	31421.999987
HLA B*3801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.475992	0.971364	-3.504628	29922.104147
HLA B*1501	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.386777	0.882099	-3.504678	24365.621062
HLA A*3101	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.323226	0.818322	-3.504905	21048.747864
HLA A*2403	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.382685	0.877206	-3.505478	24137.077386
HLA A*0202	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.175237	0.669638	-3.505599	14970.520647
HLA A*0211	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.535866	1.030229	-3.505638	34345.228176

HLA A*0211	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.477080	0.971364	-3.505716	29997.146338
HLA B*3801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.531447	1.025655	-3.505792	33997.503308
HLA A*2403	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.396084	0.890279	-3.505805	24893.375820
HLA B*1801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.350788	0.844974	-3.505815	22427.872289
HLA B*7301	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.632707	1.126836	-3.505871	42924.720781
HLA B*5701	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.368513	0.862516	-3.505997	23362.138232
HLA B*0802	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.404565	0.898490	-3.506075	25384.314314
HLA B*4501	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.645512	1.139383	-3.506129	44209.150731
HLA B*4001	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.404655	0.898490	-3.506164	25389.533251
HLA A*8001	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.300110	0.793787	-3.506322	19957.662907
HLA B*0803	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.477726	0.971364	-3.506362	30041.806891
HLA B*1501	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.291468	0.785097	-3.506372	19564.478546
HLA B*3501	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.437907	0.931448	-3.506459	27409.870161
HLA A*3101	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.367079	0.860615	-3.506464	23285.169489
HLA A*2601	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.389021	0.882547	-3.506474	24491.830428
HLA A*0206	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.536933	1.030229	-3.506704	34429.686813
HLA B*0803	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.442636	0.935815	-3.506821	27709.997821
HLA B*1501	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.293249	0.786144	-3.507105	19644.871245
HLA A*2601	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.386437	0.879222	-3.507214	24346.515336
HLA B*5401	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.514735	1.007379	-3.507356	32714.112128
HLA A*3001	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.278525	0.770901	-3.507624	18989.999978
HLA A*2501	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.356248	0.848433	-3.507815	22711.628598
HLA B*5701	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.398149	0.890279	-3.507870	25012.033006
HLA B*5101	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.387146	0.879222	-3.507924	24386.324856
HLA B*5301	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.550574	1.042623	-3.507951	35528.279938
HLA A*3301	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.505417	0.997451	-3.507966	32019.686860
HLA A*0206	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.123276	0.615291	-3.507985	13282.373678
HLA B*4403	1:224-232	9	YLVLGGMGV	0.951226	0.190010	-4.649288	1.141236	-3.508051	44595.166987
HLA B*3801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.540786	1.032607	-3.508179	34736.513611
HLA A*0219	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.371015	0.862516	-3.508499	23497.128440
HLA B*0702	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.357165	0.848433	-3.508732	22759.597467
HLA B*3901	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.448461	0.939568	-3.508893	28084.122903
HLA A*3002	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.448466	0.939568	-3.508898	28084.426769
HLA A*0211	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.295686	0.786144	-3.509541	19755.389772
HLA B*1502	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.260566	0.750956	-3.509609	18220.718597
HLA B*5101	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.445618	0.935815	-3.509803	27900.885580
HLA A*3101	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.392372	0.882547	-3.509824	24681.503376
HLA A*2501	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.453851	0.943496	-3.510355	28434.826557
HLA A*2301	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.536649	1.025655	-3.510993	34407.156632
HLA B*5101	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.202538	0.691047	-3.511491	15941.820701
HLA B*0801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.393661	0.882099	-3.511562	24754.917127
HLA A*3101	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.374126	0.862516	-3.511610	23666.035354
HLA B*1517	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.296964	0.785097	-3.511867	19813.615119
HLA B*3901	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.455451	0.943496	-3.511955	28539.777491
HLA A*1101	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.443532	0.931448	-3.512084	27767.171677
HLA B*4002	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.047472	0.535260	-3.512212	11155.059989
HLA A*3101	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.279744	0.767455	-3.512290	19043.393740
HLA A*0203	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.297544	0.785097	-3.512447	19840.108612
HLA A*0212	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.444490	0.931448	-3.513042	27828.528033
HLA A*3001	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.280583	0.767455	-3.513129	19080.208365
HLA B*3801	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.556039	1.042623	-3.513416	35978.171217
HLA B*5101	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.332201	0.818322	-3.513880	21488.262396

HLA A*0203	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.199070	0.685107	-3.513963	15815.032198
HLA A*6901	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.359009	0.844974	-3.514035	22856.457609
HLA A*2402	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.556664	1.042623	-3.514041	36029.982173
HLA B*4601	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.396699	0.882547	-3.514152	24928.684483
HLA A*0101	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.376961	0.862516	-3.514446	23821.073952
HLA B*3801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.413134	0.898490	-3.514644	25890.116726
HLA B*5401	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-3.697338	0.182632	-3.514706	4981.241048
HLA A*6802	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.396852	0.882099	-3.514753	24937.452017
HLA A*0206	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-3.833058	0.318175	-3.514883	6808.601386
HLA A*0201	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.396998	0.882099	-3.514899	24945.817769
HLA A*0201	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.397526	0.882547	-3.514979	24976.200931
HLA A*6901	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.397679	0.882547	-3.515132	24984.985176
HLA A*0201	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.375751	0.860615	-3.515136	23754.798594
HLA A*0202	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.579983	1.064763	-3.515219	38017.423953
HLA B*4002	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.642110	1.126836	-3.515274	43864.190379
HLA A*0211	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.360376	0.844974	-3.515403	22928.535845
HLA B*4501	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.405914	0.890279	-3.515635	25463.262139
HLA B*1801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.459196	0.943496	-3.515700	28786.950560
HLA A*0201	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.309552	0.793787	-3.515765	20396.340952
HLA B*7301	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.536113	1.020231	-3.515883	34364.743125
HLA B*0702	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.451236	0.935291	-3.515945	28264.129010
HLA A*2501	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.487474	0.971364	-3.516110	30723.738739
HLA B*1509	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.361271	0.844974	-3.516298	22975.844143
HLA A*6901	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.007103	0.490659	-3.516444	10164.898791
HLA A*0202	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.299121	0.782174	-3.516946	19912.259790
HLA B*7301	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.559613	1.042623	-3.516989	36275.436829
HLA A*3201	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.577896	1.060834	-3.517062	37835.226935
HLA B*4403	1:47-55	9	QRAATRQSQ	1.089348	0.030948	-4.637399	1.120296	-3.517103	43390.974149
HLA A*0219	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.408132	0.890279	-3.517853	25593.633990
HLA A*2603	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.380495	0.862516	-3.517979	24015.684130
HLA B*0801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.363210	0.844974	-3.518236	23078.618155
HLA A*0206	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.300483	0.782174	-3.518309	19974.837323
HLA B*4501	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.645167	1.126836	-3.518331	44174.007216
HLA B*4501	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.544101	1.025655	-3.518446	35002.684296
HLA A*2902	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.449915	0.931448	-3.518467	28178.326449
HLA A*2902	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.032567	0.514013	-3.518554	10778.709748
HLA A*0212	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.363706	0.844974	-3.518732	23104.977130
HLA A*2602	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.539377	1.020231	-3.519146	34623.943994
HLA B*4403	1:4-12	9	PNEPGALSK	1.207092	-0.067709	-4.658575	1.139383	-3.519192	45559.118096
HLA B*1801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.511878	0.992668	-3.519210	32499.611101
HLA A*0202	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.380018	0.860615	-3.519403	23989.324402
HLA A*3001	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-3.671451	0.152039	-3.519412	4693.004087
HLA B*4002	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.455232	0.935815	-3.519417	28525.422178
HLA B*5801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.206687	0.687090	-3.519598	16094.856570
HLA A*3101	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.402160	0.882099	-3.520060	25244.080942
HLA A*3201	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.585072	1.064763	-3.520308	38465.525539
HLA B*4402	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.383481	0.862516	-3.520966	24181.384253
HLA A*2601	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.341134	0.820012	-3.521122	21934.818267
HLA A*2301	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.541937	1.020231	-3.521707	34828.716902
HLA B*1502	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.547522	1.025655	-3.521867	35279.482100
HLA A*0101	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.209018	0.687090	-3.521928	16181.463574
HLA A*8001	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.342403	0.820012	-3.522391	21998.991022
HLA B*4601	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.404939	0.882099	-3.522840	25406.158594
HLA A*2603	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.587776	1.064763	-3.523013	38705.789255

HLA A*0101	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.405606	0.882547	-3.523059	25445.222834
HLA A*3201	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.383878	0.860615	-3.523263	24203.502708
HLA B*1801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.462887	0.939568	-3.523319	29032.651626
HLA A*0203	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.405430	0.882099	-3.523331	25434.900740
HLA B*5401	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.529342	1.005856	-3.523486	33833.107305
HLA B*0802	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.341872	0.818322	-3.523550	21972.110722
HLA A*2601	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.405674	0.882099	-3.523575	25449.215166
HLA A*0216	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.193234	0.669638	-3.523596	15603.928789
HLA B*7301	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.588556	1.064763	-3.523793	38775.370541
HLA B*5301	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.588925	1.064763	-3.524161	38808.318492
HLA A*0203	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.313387	0.789030	-3.524357	20577.216297
HLA B*1517	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.046997	0.522301	-3.524696	11142.876424
HLA B*5801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.344820	0.820012	-3.524808	22121.795972
HLA A*8001	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.423420	0.898490	-3.524930	26510.630326
HLA A*2301	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.530881	1.005856	-3.525025	33953.206815
HLA B*3901	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.407145	0.882099	-3.525046	25535.547342
HLA B*4002	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.585943	1.060834	-3.525109	38542.806025
HLA B*5701	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.407321	0.882099	-3.525222	25545.910281
HLA A*3001	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.066319	0.540972	-3.525347	11649.827072
HLA A*6901	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.311538	0.786144	-3.525393	20489.793334
HLA B*1501	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.218167	0.692679	-3.525487	16525.959897
HLA B*5701	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.405007	0.879222	-3.525785	25410.144797
HLA A*3001	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.294633	0.768800	-3.525833	19707.567984
HLA A*2902	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.388455	0.862516	-3.525939	24459.919196
HLA A*0216	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.416294	0.890279	-3.526015	26079.188041
HLA A*2501	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.424632	0.898490	-3.526142	26584.738213
HLA B*5701	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.408698	0.882547	-3.526151	25627.024304
HLA A*6802	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.424818	0.898490	-3.526328	26596.102460
HLA B*3901	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.519190	0.992668	-3.526522	33051.392487
HLA B*5301	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.552219	1.025655	-3.526563	35663.077850
HLA A*6801	1:22-30	9	VDRGGAHRA	1.439692	-0.296058	-4.670201	1.143634	-3.526567	46795.119481
HLA A*0203	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.425309	0.898490	-3.526819	26626.190797
HLA B*7301	1:211-219	9	ALFFVVWMIT	0.834379	-0.166471	-4.194850	0.667908	-3.526942	15662.114888
HLA A*3001	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-3.540199	0.013159	-3.527040	3468.960081
HLA A*3001	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.278454	0.750956	-3.527498	18986.918214
HLA B*5701	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.388521	0.860615	-3.527906	24463.624589
HLA A*2402	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.535399	1.007379	-3.528020	34308.273100
HLA A*3101	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.322150	0.793787	-3.528363	20996.659324
HLA B*5401	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.419175	0.890279	-3.528896	26252.733771
HLA B*5101	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.500443	0.971364	-3.529079	31655.065801
HLA B*4801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.411182	0.882099	-3.529082	25773.985890
HLA B*0802	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.464383	0.935291	-3.529093	29132.873617
HLA B*1501	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.198736	0.669638	-3.529099	15802.887688
HLA A*2902	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.419445	0.890279	-3.529166	26269.071656
HLA B*4801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.406534	0.877206	-3.529328	25499.655026
HLA A*0219	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.427875	0.898490	-3.529384	26783.953194
HLA A*0211	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.297112	0.767455	-3.529657	19820.369206
HLA A*2403	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.412215	0.882547	-3.529668	25835.410105
HLA B*0802	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.465650	0.935815	-3.529835	29217.947018
HLA B*4001	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.392390	0.862516	-3.529875	24682.571593
HLA A*0101	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.374884	0.844974	-3.529911	23707.425399
HLA B*0702	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.374929	0.844974	-3.529956	23709.862360
HLA A*0219	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.407176	0.877206	-3.529969	25537.343284
HLA A*0250	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.594784	1.064763	-3.530021	39335.478849
HLA B*0802	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.409347	0.879222	-3.530124	25665.317349
HLA B*4402	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.409647	0.879222	-3.530425	25683.095858

HLA B*5401	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.465854	0.935291	-3.530564	29231.701984
HLA A*8001	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.462095	0.931448	-3.530647	28979.769471
HLA B*1503	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-3.902777	0.371790	-3.530987	7994.227933
HLA A*3001	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.014429	0.483198	-3.531231	10337.814930
HLA B*3501	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.376266	0.844974	-3.531292	23782.959144
HLA B*4801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.393913	0.862516	-3.531397	24769.250860
HLA A*6802	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.320738	0.789030	-3.531709	20928.502835
HLA B*0801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.320856	0.789030	-3.531826	20934.164644
HLA A*0203	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.147193	0.615291	-3.531902	14034.387113
HLA A*0201	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.376966	0.844974	-3.531993	23821.331692
HLA A*8001	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.414562	0.882547	-3.532015	25975.415029
HLA B*3501	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.299703	0.767455	-3.532249	19938.993052
HLA A*2601	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.393349	0.860615	-3.532734	24737.111992
HLA B*0803	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.431399	0.898490	-3.532908	27002.184779
HLA B*1501	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.270140	0.737162	-3.532978	18626.860079
HLA B*3501	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.395651	0.862516	-3.533136	24868.608795
HLA B*0803	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.526205	0.992668	-3.533538	33589.638020
HLA B*2705	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.382043	0.848433	-3.533610	24101.455654
HLA A*2402	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.531132	0.997451	-3.533681	33972.866594
HLA A*3002	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.598511	1.064763	-3.533747	39674.432615
HLA B*0801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.304677	0.770901	-3.533776	20168.661719
HLA B*3501	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.394479	0.860615	-3.533864	24801.565656
HLA B*3901	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.416447	0.882547	-3.533899	26088.360212
HLA B*0702	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.416073	0.882099	-3.533974	26065.929374
HLA A*2301	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.531912	0.997451	-3.534461	34033.939519
HLA B*1502	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.577137	1.042623	-3.534514	37769.171609
HLA B*7301	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.564746	1.030229	-3.534518	36706.778880
HLA A*2601	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.397162	0.862516	-3.534647	24955.266345
HLA B*4601	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.355447	0.820012	-3.535435	22669.769439
HLA B*0702	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.398100	0.862516	-3.535584	25009.191609
HLA B*1517	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.426496	0.890279	-3.536217	26699.032848
HLA A*0301	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.330148	0.793787	-3.536361	21386.900488
HLA A*0216	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.330279	0.793787	-3.536492	21393.380712
HLA B*1801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.542353	1.005856	-3.536498	34862.083126
HLA A*1101	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.415944	0.879222	-3.536722	26058.174769
HLA A*1101	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.414170	0.877206	-3.536964	25951.958099
HLA B*1502	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.567239	1.030229	-3.537010	36918.077676
HLA A*2603	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.562958	1.025655	-3.537303	36555.970447
HLA B*4801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.213919	0.676597	-3.537322	16365.106112
HLA B*0801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.214478	0.676597	-3.537881	16386.190634
HLA A*0212	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.420211	0.882099	-3.538111	26315.441295
HLA B*3801	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.535634	0.997451	-3.538183	34326.838517
HLA A*0202	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.544057	1.005856	-3.538201	34999.086629
HLA A*2603	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.436706	0.898490	-3.538216	27334.201493
HLA A*0250	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.305793	0.767455	-3.538339	20220.555723
HLA A*0206	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.127871	0.589436	-3.538435	13423.670611
HLA A*0203	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.421127	0.882547	-3.538579	26371.021719
HLA A*0216	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.327620	0.789030	-3.538590	21262.768110
HLA A*0219	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.470180	0.931448	-3.538732	29524.292842
HLA A*0101	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.359152	0.820012	-3.539140	22864.001558
HLA B*1502	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.207162	0.667908	-3.539253	16112.454604
HLA B*4402	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.421378	0.882099	-3.539279	26386.291219
HLA A*2602	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.571886	1.032607	-3.539279	37315.250427
HLA B*4601	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.400703	0.860615	-3.540088	25159.550822

HLA B*0702	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.423061	0.882547	-3.540513	26488.696211
HLA B*5101	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.480238	0.939568	-3.540670	30216.047157
HLA B*4801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.401286	0.860615	-3.540671	25193.328851
HLA A*6802	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.234305	0.693390	-3.540915	17151.626351
HLA B*1509	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.547038	1.005856	-3.541183	35240.187234
HLA A*0202	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.326292	0.785097	-3.541196	21197.875827
HLA B*4001	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.423366	0.882099	-3.541267	26507.331881
HLA B*3901	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.402049	0.860615	-3.541434	25237.663077
HLA A*1101	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.335234	0.793787	-3.541447	21638.865313
HLA B*1503	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.234162	0.692679	-3.541483	17145.967193
HLA B*0702	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.234895	0.693390	-3.541505	17174.932059
HLA A*2402	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.567183	1.025655	-3.541527	36913.284642
HLA B*1502	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.562141	1.020231	-3.541910	36487.213406
HLA A*2602	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.606743	1.064763	-3.541980	40433.684691
HLA A*2403	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.402752	0.860615	-3.542137	25278.519467
HLA A*0212	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.403031	0.860615	-3.542416	25294.798431
HLA B*1517	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.441130	0.898490	-3.542640	27614.073199
HLA A*0211	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.324988	0.782174	-3.542814	21134.324902
HLA A*2501	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.478114	0.935291	-3.542823	30068.635132
HLA B*1503	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.478490	0.935291	-3.543199	30094.673277
HLA A*8001	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.388286	0.844974	-3.543312	24450.393619
HLA B*7301	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.549430	1.005856	-3.543574	35434.799759
HLA B*4501	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.586202	1.042623	-3.543578	38565.749205
HLA B*4601	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.406252	0.862516	-3.543737	25483.106361
HLA A*3002	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.573973	1.030229	-3.543744	37494.943477
HLA A*0202	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.574109	1.030229	-3.543880	37506.710246
HLA B*3801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.487888	0.943496	-3.544392	30753.005986
HLA B*1503	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.312452	0.767455	-3.544997	20532.958419
HLA A*2602	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.552552	1.007379	-3.545174	35690.484905
HLA A*0211	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.405860	0.860615	-3.545245	25460.094008
HLA B*0801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.365284	0.820012	-3.545272	23189.126884
HLA B*5801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-3.971800	0.426351	-3.545448	9371.296897
HLA B*4403	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-3.510633	-0.034919	-3.545552	3240.659362
HLA A*0211	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.339426	0.793787	-3.545639	21848.718285
HLA A*0219	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.406262	0.860615	-3.545647	25483.657810
HLA B*1502	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.543286	0.997451	-3.545835	34937.037790
HLA A*6801	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.606715	1.060834	-3.545881	40431.059875
HLA B*4002	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.630962	1.084809	-3.546153	42752.529119
HLA B*4403	1:195-203	9	RIDPWSTLK	0.781325	0.345511	-4.673126	1.126836	-3.546290	47111.363013
HLA A*2501	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.423603	0.877206	-3.546397	26521.819413
HLA A*2402	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.330825	0.784035	-3.546789	21420.248279
HLA A*8001	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.437421	0.890279	-3.547142	27379.192479
HLA B*0801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.409955	0.862516	-3.547440	25701.303803
HLA B*0801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.217161	0.669638	-3.547523	16487.739417
HLA A*8001	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.350182	0.802529	-3.547653	22396.590391
HLA B*1503	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.540366	0.992668	-3.547698	34702.892089
HLA A*3002	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.446741	0.898490	-3.548251	27973.128601
HLA A*0216	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.330442	0.782174	-3.548267	21401.367975
HLA B*5701	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.366739	0.818322	-3.548417	23266.910975
HLA B*5101	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.479918	0.931448	-3.548470	30193.824030
HLA B*0802	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.480285	0.931448	-3.548837	30219.316643
HLA B*3901	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.426207	0.877206	-3.549000	26681.272784
HLA B*5301	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.581618	1.032607	-3.549011	38160.840139
HLA A*2902	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.428514	0.879222	-3.549291	26823.394520

HLA A*0216	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.480809	0.931448	-3.549361	30255.795386
HLA A*0202	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.316824	0.767455	-3.549369	20740.724331
HLA B*1801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.484681	0.935291	-3.549390	30526.746887
HLA A*2301	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.542476	0.992668	-3.549808	34871.891705
HLA B*3801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.555708	1.005856	-3.549852	35950.737735
HLA B*4801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.432621	0.882547	-3.550073	27078.252713
HLA A*2402	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.490007	0.939568	-3.550439	30903.438781
HLA A*0301	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.335632	0.785097	-3.550535	21658.658152
HLA B*1517	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.370857	0.820012	-3.550845	23488.613153
HLA B*4402	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.428380	0.877206	-3.551173	26815.124435
HLA B*4501	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.219309	0.667908	-3.551400	16569.467221
HLA A*0212	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.434084	0.882547	-3.551537	27169.670167
HLA B*0702	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.318997	0.767455	-3.551543	20844.774097
HLA B*0803	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.491146	0.939568	-3.551578	30984.629575
HLA B*1509	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.483240	0.931448	-3.551792	30425.679870
HLA B*4402	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.400353	0.848433	-3.551920	25139.278547
HLA B*4601	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.354608	0.802529	-3.552079	22626.028876
HLA A*2501	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.442364	0.890279	-3.552085	27692.613946
HLA B*1509	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.429522	0.877206	-3.552315	26885.719688
HLA B*7301	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.550036	0.997451	-3.552585	35484.292462
HLA A*3301	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.585250	1.032607	-3.552643	38481.343952
HLA A*3001	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.189578	0.636799	-3.552779	15473.129525
HLA B*5101	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.496414	0.943496	-3.552918	31362.729609
HLA A*3001	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.229529	0.676597	-3.552931	16964.021101
HLA A*2902	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.413759	0.860615	-3.553144	25927.400213
HLA A*2902	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.435327	0.882099	-3.553228	27247.536548
HLA B*5301	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.550725	0.997451	-3.553273	35540.583127
HLA B*7301	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.413987	0.860615	-3.553372	25941.009427
HLA A*2402	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.559483	1.005856	-3.553628	36264.644900
HLA B*3501	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.033657	0.480013	-3.553644	10805.800329
HLA A*0219	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.435870	0.882099	-3.553771	27281.608654
HLA B*5401	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.525160	0.971364	-3.553796	33508.871560
HLA B*0801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.239131	0.685107	-3.554024	17343.276547
HLA B*0803	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.489422	0.935291	-3.554131	30861.837946
HLA A*2403	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.372979	0.818322	-3.554657	23603.638809
HLA A*2601	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.348554	0.793787	-3.554766	22312.781583
HLA A*2402	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.491085	0.935815	-3.555270	30980.271672
HLA A*3301	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.403769	0.848433	-3.555336	25337.803352
HLA B*3801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.400538	0.844974	-3.555565	25150.024900
HLA A*1101	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.323438	0.767455	-3.555983	21058.998785
HLA A*3201	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.563372	1.007379	-3.555993	36590.793442
HLA B*5801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.341644	0.785097	-3.556547	21960.583679
HLA B*4001	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.405270	0.848433	-3.556837	25425.545662
HLA A*0216	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.417476	0.860615	-3.556861	26150.250699
HLA B*1509	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.492279	0.935291	-3.556988	31065.529489
HLA A*2601	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.402261	0.844974	-3.557287	25249.954035
HLA A*3001	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-3.980380	0.422812	-3.557568	9558.285895
HLA B*5801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.351380	0.793787	-3.557593	22458.468881
HLA B*0802	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.402597	0.844974	-3.557623	25269.495314
HLA A*3001	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-3.787741	0.229292	-3.558450	6133.961448
HLA B*5101	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.243941	0.685107	-3.558833	17536.404117
HLA B*4601	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.404128	0.844974	-3.559155	25358.784464
HLA B*4403	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.624369	1.064763	-3.559606	42108.440410
HLA B*4403	1:271-279	9	NIVLMTALA	1.190155	-0.105346	-4.644424	1.084809	-3.559616	44098.555160

HLA A*2603	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.620502	1.060834	-3.559668	41735.142841
HLA A*2602	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.503216	0.943496	-3.559720	31857.787635
HLA A*8001	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.378059	0.818322	-3.559737	23881.332034
HLA A*6901	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.348815	0.789030	-3.559785	22326.184381
HLA B*5401	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.499478	0.939568	-3.559910	31584.760078
HLA A*0206	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-3.947722	0.387714	-3.560009	8865.886657
HLA B*5401	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.552682	0.992668	-3.560014	35701.105971
HLA A*6901	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.362665	0.802529	-3.560136	23049.670483
HLA B*0702	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.342325	0.782174	-3.560151	21995.063973
HLA B*3501	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.442282	0.882099	-3.560183	27687.370954
HLA A*1101	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.405350	0.844974	-3.560377	25430.222771
HLA B*3901	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.492020	0.931448	-3.560572	31047.048271
HLA A*0250	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.591190	1.030229	-3.560961	39011.237706
HLA A*0212	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.150417	0.589436	-3.560981	14138.943044
HLA A*2902	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.354904	0.793787	-3.561117	22641.457077
HLA A*0301	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.347316	0.786144	-3.561171	22249.258180
HLA A*6901	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.346340	0.785097	-3.561244	22199.362314
HLA B*1503	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.332218	0.770901	-3.561317	21489.076155
HLA A*0101	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.363856	0.802529	-3.561327	23112.978219
HLA B*0802	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.443962	0.882547	-3.561414	27794.675059
HLA B*0803	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.379738	0.818322	-3.561417	23973.885602
HLA B*4002	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.587654	1.025655	-3.561998	38694.902297
HLA A*0219	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.231956	0.669638	-3.562318	17059.088490
HLA A*6802	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.445641	0.882547	-3.563094	27902.395028
HLA A*6802	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-3.881669	0.318175	-3.563494	7614.979763
HLA B*1509	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.499489	0.935815	-3.563674	31585.614440
HLA A*0212	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.350003	0.786144	-3.563859	22387.383891
HLA A*3301	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.624961	1.060834	-3.564127	42165.885661
HLA A*6901	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.346312	0.782174	-3.564138	22197.921207
HLA B*1503	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.104654	0.540487	-3.564166	12724.879433
HLA B*0802	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.446767	0.882099	-3.564668	27974.793298
HLA B*0802	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.455199	0.890279	-3.564920	28523.261789
HLA A*0219	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.409953	0.844974	-3.564979	25701.164763
HLA A*8001	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.427623	0.862516	-3.565108	26768.453571
HLA B*2705	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.427818	0.862516	-3.565303	26780.475862
HLA A*1101	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.425972	0.860615	-3.565357	26666.842415
HLA B*5301	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.413846	0.848433	-3.565413	25932.590514
HLA A*2501	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.496907	0.931448	-3.565459	31398.380324
HLA A*2402	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.410869	0.844974	-3.565896	25755.447784
HLA B*4801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.385981	0.820012	-3.565969	24320.976622
HLA A*0201	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.348389	0.782174	-3.566215	22304.333505
HLA B*1501	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.318074	0.751562	-3.566512	20800.503384
HLA A*0202	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.214201	0.647511	-3.566689	16375.733571
HLA B*7301	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.538237	0.971364	-3.566873	34533.216897
HLA A*2902	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.444462	0.877206	-3.567256	27826.721501
HLA B*4001	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.361274	0.793787	-3.567487	22975.968440
HLA A*2403	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.361337	0.793787	-3.567550	22979.324716
HLA B*5801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.352423	0.784035	-3.568388	22512.478756
HLA B*3801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.450575	0.882099	-3.568476	28221.195120
HLA B*5801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.357766	0.789030	-3.568737	22791.139790
HLA B*1509	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.512419	0.943496	-3.568923	32540.074707
HLA A*2501	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.448209	0.879222	-3.568987	28067.870884
HLA B*4801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.417448	0.848433	-3.569015	26148.553114
HLA B*1517	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.205945	0.636799	-3.569146	16067.365516
HLA A*2501	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.431758	0.862516	-3.569243	27024.544092

HLA B*5401	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.512773	0.943496	-3.569278	32566.667335
HLA A*2601	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.355785	0.786144	-3.569641	22687.436615
HLA B*1801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.446999	0.877206	-3.569793	27989.780023
HLA A*0301	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.343963	0.773810	-3.570152	22078.157162
HLA B*5801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.352419	0.782174	-3.570244	22512.235177
HLA A*2301	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.505668	0.935291	-3.570378	32038.227082
HLA A*2603	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.415657	0.844974	-3.570684	26040.981879
HLA B*4402	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.373625	0.802529	-3.571096	23638.780537
HLA A*2902	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.453672	0.882547	-3.571125	28423.137936
HLA A*1101	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.461641	0.890279	-3.571362	28949.527236
HLA A*2501	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.416350	0.844974	-3.571377	26082.574313
HLA A*0250	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.564241	0.992668	-3.571573	36664.109085
HLA A*3201	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.597315	1.025655	-3.571659	39565.334043
HLA A*1101	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.391874	0.820012	-3.571861	24653.212473
HLA A*3001	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.137481	0.565473	-3.572007	13723.999090
HLA A*0101	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.323663	0.751562	-3.572102	21069.938603
HLA A*1101	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.390581	0.818322	-3.572260	24579.967364
HLA B*0802	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.374805	0.802529	-3.572276	23703.065145
HLA B*3501	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.265246	0.692679	-3.572566	18418.135979
HLA B*1501	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.258825	0.686161	-3.572663	18147.822902
HLA B*4501	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.452117	0.879222	-3.572894	28321.526888
HLA B*0803	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.463314	0.890279	-3.573035	29061.251247
HLA A*0219	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.455639	0.882547	-3.573091	28552.131927
HLA B*3501	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.455803	0.882547	-3.573256	28562.946445
HLA A*6801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.375935	0.802529	-3.573406	23764.824554
HLA B*4501	1:127-135	9	PDLSGPTPR	0.734090	0.330673	-4.638428	1.064763	-3.573665	43493.912336
HLA A*0212	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.341174	0.767455	-3.573719	21936.835664
HLA A*0250	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-3.555100	-0.018628	-3.573728	3590.043709
HLA A*2403	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.393983	0.820012	-3.573971	24773.271153
HLA B*4501	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.419102	0.844974	-3.574128	26248.331384
HLA A*0211	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.347962	0.773810	-3.574151	22282.383470
HLA B*0803	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.419348	0.844974	-3.574375	26263.245679
HLA B*5801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.360708	0.786144	-3.574563	22946.032275
HLA A*0219	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.360961	0.786144	-3.574817	22959.442826
HLA A*3301	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.595111	1.020231	-3.574880	39365.069253
HLA A*0301	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.363955	0.789030	-3.574925	23118.230439
HLA A*0301	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.262032	0.687090	-3.574942	18282.331504
HLA A*2602	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.452373	0.877206	-3.575166	28338.232392
HLA B*5701	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.395379	0.820012	-3.575367	24853.007467
HLA A*0212	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.349806	0.773810	-3.575996	22377.212688
HLA B*1517	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-3.792905	0.216823	-3.576082	6207.335371
HLA A*2501	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.458209	0.882099	-3.576110	28721.616444
HLA B*0801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.244027	0.667908	-3.576119	17539.914658
HLA A*2402	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.568851	0.992668	-3.576183	37055.342003
HLA B*5801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.350024	0.773810	-3.576214	22388.473937
HLA A*3001	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.261649	0.685107	-3.576541	18266.217032
HLA B*3501	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.379151	0.802529	-3.576622	23941.483502
HLA B*1517	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.437329	0.860615	-3.576714	27373.416471
HLA B*1509	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.437383	0.860615	-3.576768	27376.822688
HLA B*3501	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.345690	0.768800	-3.576890	22166.120610
HLA B*4002	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.244836	0.667908	-3.576927	17572.586864
HLA B*1509	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.569899	0.992668	-3.577231	37144.857471
HLA B*5101	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.467541	0.890279	-3.577262	29345.467503
HLA A*2403	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.366396	0.789030	-3.577366	23248.541005
HLA A*0301	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.247728	0.669638	-3.578090	17690.003336

HLA B*0702	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.000999	0.422812	-3.578187	10023.031536
HLA B*1502	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.509895	0.931448	-3.578447	32351.557876
HLA B*1501	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.069209	0.490659	-3.578550	11727.605416
HLA B*1801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.510022	0.931448	-3.578574	32361.010247
HLA A*0202	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.455791	0.877206	-3.578585	28562.173843
HLA B*4001	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.398743	0.820012	-3.578731	25046.290464
HLA B*2705	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.461454	0.882547	-3.578906	28937.000848
HLA B*1503	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.330587	0.751562	-3.579026	21408.547478
HLA A*3002	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.399227	0.820012	-3.579215	25074.218540
HLA A*8001	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.461517	0.882099	-3.579418	28941.227898
HLA B*4002	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.469733	0.890279	-3.579454	29493.961035
HLA A*0250	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.368590	0.789030	-3.579561	23366.309362
HLA A*0202	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.572283	0.992668	-3.579616	37349.382289
HLA B*1501	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-3.898261	0.318175	-3.580086	7911.536146
HLA A*0101	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.227715	0.647511	-3.580204	16893.319722
HLA A*6801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.272938	0.692679	-3.580259	18747.263728
HLA A*6801	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.612883	1.032607	-3.580276	41009.315875
HLA B*1517	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.463133	0.882547	-3.580586	29049.147971
HLA A*0301	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.362956	0.782174	-3.580782	23065.137995
HLA B*1801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.332439	0.751562	-3.580877	21500.006765
HLA B*1517	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.463117	0.882099	-3.581018	29048.047923
HLA B*3501	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.071864	0.490659	-3.581205	11799.517900
HLA B*4002	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.460530	0.879222	-3.581308	28875.543638
HLA A*0201	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.196730	0.615291	-3.581439	15730.046026
HLA A*0203	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.384026	0.802529	-3.581497	24211.753224
HLA B*0801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.384029	0.802529	-3.581500	24211.884208
HLA B*4002	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.624167	1.042623	-3.581544	42088.853995
HLA A*3201	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.480221	0.898490	-3.581731	30214.902920
HLA A*3301	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.459163	0.877206	-3.581956	28784.770364
HLA A*1101	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.464106	0.882099	-3.582007	29114.282089
HLA B*3801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.521605	0.939568	-3.582037	33235.715448
HLA A*0206	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.513795	0.931448	-3.582347	32643.396780
HLA B*5801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.349952	0.767455	-3.582497	22384.719557
HLA A*0202	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.096510	0.514013	-3.582497	12488.502385
HLA A*0216	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.464863	0.882099	-3.582763	29165.042911
HLA A*3301	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.608618	1.025655	-3.582963	40608.617938
HLA B*0801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.333954	0.750956	-3.582998	21575.159468
HLA B*1503	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-3.893308	0.310085	-3.583223	7821.825128
HLA A*0301	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.367702	0.784035	-3.583667	23318.575529
HLA A*0201	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.218270	0.634444	-3.583826	16529.894124
HLA B*0702	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.377647	0.793787	-3.583860	23858.733545
HLA A*0203	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.572336	-0.011592	-3.583927	3735.386614
HLA B*1503	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.176210	0.592259	-3.583951	15004.087610
HLA B*1801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.482524	0.898490	-3.584033	30375.518401
HLA A*0216	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.466594	0.882547	-3.584047	29281.558637
HLA B*5801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.355074	0.770901	-3.584173	22650.277914
HLA A*3001	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.106505	0.522301	-3.584204	12779.241290
HLA B*5801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.353469	0.768800	-3.584669	22566.740601
HLA B*1503	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.022144	0.436810	-3.585335	10523.118520
HLA A*0211	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.516880	0.931448	-3.585432	32876.094316
HLA B*5701	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.281579	0.695802	-3.585778	19124.024647
HLA B*0801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.258350	0.672009	-3.586341	18128.001836

HLA B*1503	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.323926	0.737162	-3.586765	21082.708907
HLA A*0101	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.369361	0.782174	-3.587186	23407.808369
HLA B*0802	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.447869	0.860615	-3.587254	28045.862128
HLA B*4002	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.580382	0.992668	-3.587714	38052.403944
HLA B*4601	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.369967	0.782174	-3.587793	23440.502661
HLA A*0201	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.376961	0.789030	-3.587932	23821.073952
HLA B*7301	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.580810	0.992668	-3.588142	38089.888785
HLA A*0216	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.486640	0.898490	-3.588150	30664.790096
HLA B*1503	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.370416	0.782174	-3.588241	23464.735988
HLA B*3801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.450961	0.862516	-3.588445	28246.244691
HLA B*3801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.581310	0.992668	-3.588642	38133.805305
HLA A*1101	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.451351	0.862516	-3.588835	28271.622387
HLA B*1503	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.373973	0.785097	-3.588876	23657.714827
HLA B*4002	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.621820	1.032607	-3.589213	41861.999225
HLA B*2705	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.391787	0.802529	-3.589258	24648.278234
HLA B*3501	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.134694	0.545171	-3.589523	13636.226030
HLA A*6901	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.360574	0.770901	-3.589673	22938.957643
HLA A*2301	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.533270	0.943496	-3.589774	34140.527345
HLA B*1502	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.529459	0.939568	-3.589891	33842.260210
HLA A*0219	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.383735	0.793787	-3.589948	24195.516791
HLA B*0803	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.521546	0.931448	-3.590098	33231.220713
HLA A*2402	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.525477	0.935291	-3.590186	33533.353202
HLA B*4001	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.392851	0.802529	-3.590322	24708.757348
HLA A*0211	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.237949	0.647511	-3.590438	17296.146623
HLA A*0212	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.384616	0.793787	-3.590829	24244.652264
HLA B*4801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.183423	0.592259	-3.591164	15255.361743
HLA B*4501	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.621759	1.030229	-3.591530	41856.111451
HLA A*0101	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.377692	0.786144	-3.591548	23861.186060
HLA A*3001	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.251428	0.659875	-3.591554	17841.376320
HLA A*6801	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.617751	1.025655	-3.592095	41471.587229
HLA A*2603	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.386040	0.793787	-3.592252	24324.266189
HLA A*8001	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.378486	0.786144	-3.592342	23904.857168
HLA B*4403	1:90-98	9	SAPVTGPAA	1.186011	-0.125177	-4.653449	1.060834	-3.592614	45024.482766
HLA A*0250	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.343587	0.750956	-3.592631	22059.054969
HLA A*2403	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.395290	0.802529	-3.592761	24847.898815
HLA A*0216	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.280099	0.687090	-3.593010	19058.956516
HLA A*2501	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.475673	0.882547	-3.593125	29900.097207
HLA A*2301	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.529083	0.935815	-3.593268	33812.979624
HLA A*0216	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.367122	0.773810	-3.593311	23287.437063
HLA A*2601	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.378411	0.785097	-3.593314	23900.719203
HLA A*6802	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.438426	0.844974	-3.593453	27442.660603
HLA A*0101	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.383171	0.789030	-3.594141	24164.122361
HLA B*7301	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.533773	0.939568	-3.594205	34180.075277
HLA A*2402	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.537730	0.943496	-3.594234	34492.887156
HLA A*3001	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.273267	0.679020	-3.594247	18761.467993
HLA B*4402	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.414320	0.820012	-3.594308	25960.945077
HLA A*3002	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.600207	1.005856	-3.594351	39829.701605
HLA A*0301	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.363485	0.768800	-3.594685	23093.230553
HLA B*1502	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.473948	0.879222	-3.594726	29781.603564
HLA B*7301	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.439733	0.844974	-3.594759	27525.329604
HLA A*6802	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.379858	0.785097	-3.594762	23980.501014
HLA B*1801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.455758	0.860615	-3.595143	28560.010671
HLA B*3801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.526633	0.931448	-3.595185	33622.726658
HLA A*0201	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.397731	0.802529	-3.595202	24987.959005
HLA A*8001	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.362902	0.767455	-3.595447	23062.268237

HLA B*5101	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.494231	0.898490	-3.595741	31205.502636
HLA A*3002	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.347001	0.750956	-3.596045	22233.134978
HLA B*4403	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.602333	1.005856	-3.596478	40025.183965
HLA A*0206	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-3.886203	0.289672	-3.596531	7694.904949
HLA B*0803	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.479249	0.882547	-3.596701	30147.306506
HLA A*0301	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.367629	0.770901	-3.596728	23314.665178
HLA B*1509	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.399523	0.802529	-3.596995	25091.316108
HLA B*4002	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.594470	0.997451	-3.597018	39306.973904
HLA B*1501	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.386202	0.789030	-3.597172	24333.347704
HLA B*3801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.480139	0.882547	-3.597592	30209.182387
HLA A*0250	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.366452	0.768800	-3.597652	23251.559729
HLA A*2501	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.458270	0.860615	-3.597655	28725.656628
HLA A*0101	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.368846	0.770901	-3.597945	23380.092022
HLA B*5301	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.590661	0.992668	-3.597993	38963.781138
HLA A*2403	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.380361	0.782174	-3.598187	24008.279707
HLA A*0250	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.569835	0.971364	-3.598471	37139.432230
HLA A*2603	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.606295	1.007379	-3.598916	40391.926594
HLA A*0216	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.384282	0.785097	-3.599186	24226.034571
HLA A*2402	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.417575	0.818322	-3.599253	26156.193112
HLA A*3301	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.417647	0.818322	-3.599326	26160.580045
HLA A*3002	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.460152	0.860615	-3.599537	28850.404215
HLA B*4601	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.393417	0.793787	-3.599630	24740.993223
HLA A*3002	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.489946	0.890279	-3.599667	30899.092298
HLA A*0101	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.384816	0.785097	-3.599719	24255.803503
HLA B*1501	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.113906	0.514013	-3.599893	12998.880404
HLA A*3101	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.287338	0.687090	-3.600248	19379.290925
HLA A*2301	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.539976	0.939568	-3.600408	34671.741438
HLA B*3501	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.352146	0.751562	-3.600584	22498.112120
HLA B*4403	1:239-247	9	NVGDLLNNA	1.244897	-0.202274	-4.643219	1.042623	-3.600596	43976.339294
HLA B*3501	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.296750	0.695802	-3.600948	19803.863278
HLA A*0212	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-3.783878	0.182878	-3.601001	6079.648750
HLA B*5301	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.607098	1.005856	-3.601242	40466.728190
HLA A*6802	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.122618	0.521317	-3.601301	13262.269182
HLA B*4002	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.621674	1.020231	-3.601444	41847.960515
HLA B*3501	1:122-130	9	YASELPDLS	0.787644	-0.897152	-3.492477	-0.109508	-3.601984	3107.968174
HLA B*4403	1:275-283	9	MTALATIGA	1.189575	-0.192124	-4.599505	0.997451	-3.602053	39765.326877
HLA A*2601	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.391556	0.789030	-3.602527	24635.213941
HLA A*1101	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.485334	0.882547	-3.602786	30572.692104
HLA A*0301	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.353958	0.750956	-3.603001	22592.148275
HLA A*2603	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.574372	0.971364	-3.603008	37529.442732
HLA A*0216	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.370484	0.767455	-3.603029	23468.417584
HLA A*0206	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.486015	0.882547	-3.603468	30620.694262
HLA A*3001	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.106369	0.502834	-3.603535	12775.232131
HLA B*4403	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.448531	0.844974	-3.603558	28088.681233
HLA A*6901	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.355419	0.751562	-3.603857	22668.297796
HLA B*4601	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.389214	0.785097	-3.604117	24502.697681
HLA A*3002	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.272402	0.667908	-3.604494	18724.154082
HLA A*3101	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.389693	0.785097	-3.604597	24529.754211
HLA A*0203	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.222104	0.617415	-3.604689	16676.481706
HLA B*3501	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.386897	0.782174	-3.604723	24372.344570
HLA B*4403	1:226-234	9	VLGGMGVWA	1.278102	-0.245495	-4.637364	1.032607	-3.604757	43387.453187
HLA A*2603	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.481974	0.877206	-3.604767	30337.089934

HLA B*4402	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.387170	0.782174	-3.604996	24387.644165
HLA B*4001	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.387398	0.782174	-3.605223	24400.445165
HLA A*2902	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.374302	0.768800	-3.605502	23675.639600
HLA A*3001	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.296588	0.691047	-3.605541	19796.472225
HLA B*4001	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.390786	0.785097	-3.605689	24591.538903
HLA A*2601	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.389771	0.784035	-3.605735	24534.133810
HLA B*0803	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.454384	0.848433	-3.605951	28469.767249
HLA A*3101	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.394982	0.789030	-3.605952	24830.295460
HLA A*2301	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.390189	0.784035	-3.606154	24557.770585
HLA B*7301	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.613688	1.007379	-3.606310	41085.483079
HLA B*5801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.358168	0.751562	-3.606606	22812.233425
HLA A*0216	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.375782	0.768800	-3.606982	23756.469293
HLA A*3301	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.578392	0.971364	-3.607028	37878.439999
HLA A*0201	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.392144	0.785097	-3.607047	24668.554926
HLA B*0801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.358814	0.751562	-3.607252	22846.196888
HLA A*2902	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.391726	0.784035	-3.607690	24644.811522
HLA B*0803	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.489983	0.882099	-3.607884	30901.766984
HLA A*0101	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.381768	0.773810	-3.607958	24086.205295
HLA B*5401	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.081859	0.473842	-3.608017	12074.216884
HLA A*8001	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.277902	0.669638	-3.608265	18962.795028
HLA B*0803	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.487700	0.879222	-3.608477	30739.699237
HLA A*6901	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.304318	0.695802	-3.608516	20151.974762
HLA B*4403	1:10-18	9	LSKGDGPNA	1.171694	-0.146039	-4.634350	1.025655	-3.608694	43087.348445
HLA A*3101	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.131104	0.522301	-3.608803	13523.969364
HLA B*0803	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.469677	0.860615	-3.609062	29490.131866
HLA B*4001	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.395240	0.786144	-3.609096	24845.076063
HLA A*0219	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.391425	0.782174	-3.609250	24627.751740
HLA A*0250	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.597837	-0.011592	-3.609429	3961.292105
HLA B*3801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.545711	0.935815	-3.609896	35132.636975
HLA B*3801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.500241	0.890279	-3.609962	31640.341692
HLA B*4402	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.378848	0.768800	-3.610048	23924.781151
HLA B*5801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.361034	0.750956	-3.610078	22963.293598
HLA A*3301	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.553715	0.943496	-3.610220	35786.188365
HLA B*3501	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.206156	0.595896	-3.610260	16075.190460
HLA A*6802	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.045964	0.435662	-3.610302	11116.384008
HLA A*0250	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.280092	0.669638	-3.610454	19058.647197
HLA A*6802	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.258012	0.647511	-3.610500	18113.885187
HLA B*3501	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-3.302056	-0.308836	-3.610891	2004.728214
HLA B*4601	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.397068	0.786144	-3.610924	24949.866721
HLA A*0203	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.247744	0.636799	-3.610946	17690.673256
HLA A*3001	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.179997	0.568895	-3.611102	15135.506579
HLA A*3001	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.091252	0.480013	-3.611239	12338.211588
HLA B*7301	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.473784	0.862516	-3.611268	29770.327637
HLA A*0211	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.599966	-0.011592	-3.611557	3980.755481
HLA B*5401	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.393889	0.782174	-3.611715	24767.910907
HLA A*6901	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.298195	0.686161	-3.612034	19869.862083
HLA A*0201	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.385861	0.773810	-3.612051	24314.267285
HLA B*4801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.414962	0.802529	-3.612433	25999.315117
HLA B*5101	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.494565	0.882099	-3.612466	31229.484046
HLA B*1517	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.298651	0.686161	-3.612489	19890.726817
HLA A*2902	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.398797	0.786144	-3.612653	25049.407104
HLA B*2705	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.380182	0.767455	-3.612728	23998.410694
HLA B*4402	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.406842	0.793787	-3.613055	25517.732921

HLA B*5101	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.473683	0.860615	-3.613068	29763.403114
HLA B*0802	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.475823	0.862516	-3.613307	29910.451397
HLA B*4001	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.384301	0.770901	-3.613400	24227.083075
HLA B*1502	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.548763	0.935291	-3.613472	35380.399232
HLA A*3201	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.458472	0.844974	-3.613499	28739.024363
HLA B*0802	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.461996	0.848433	-3.613563	28973.185571
HLA B*0801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.381169	0.767455	-3.613715	24053.000760
HLA B*4601	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.402766	0.789030	-3.613736	25279.340004
HLA B*4501	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.621268	1.007379	-3.613889	41808.812878
HLA A*0202	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-3.595299	-0.018628	-3.613928	3938.215023
HLA A*3101	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.396103	0.782174	-3.613928	24894.453207
HLA A*6901	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.381411	0.767455	-3.613957	24066.407274
HLA B*0702	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.305109	0.691047	-3.614062	20188.747996
HLA A*3301	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.644342	1.030229	-3.614113	44090.206060
HLA A*3201	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.301653	0.687090	-3.614564	20028.724584
HLA A*2902	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.307334	0.692679	-3.614655	20292.443682
HLA A*6801	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.554286	0.939568	-3.614718	35833.263934
HLA B*5701	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.400101	0.785097	-3.615005	25124.730682
HLA B*5301	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.586698	0.971364	-3.615334	38609.796626
HLA B*4402	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.401788	0.786144	-3.615644	25222.512468
HLA A*0101	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.399754	0.784035	-3.615718	25104.622276
HLA A*0206	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.300864	0.685107	-3.615757	19992.350984
HLA A*6901	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.399798	0.784035	-3.615763	25107.202860
HLA A*2403	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.400886	0.785097	-3.615789	25170.169672
HLA B*4001	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.389609	0.773810	-3.615798	24524.977360
HLA A*0206	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.353286	0.737162	-3.616124	22557.220092
HLA A*0201	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.400193	0.784035	-3.616158	25130.032200
HLA A*3101	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.353445	0.737162	-3.616284	22565.519798
HLA A*3201	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.495556	0.879222	-3.616334	31300.861567
HLA B*4801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.401481	0.785097	-3.616384	25204.643720
HLA A*2902	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.367382	0.750956	-3.616426	23301.425315
HLA A*0212	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.401962	0.785097	-3.616866	25232.611863
HLA B*4002	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.588471	0.971364	-3.617107	38767.819540
HLA A*0219	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.386171	0.768800	-3.617371	24331.636435
HLA A*2301	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.548897	0.931448	-3.617449	35391.310945
HLA B*5701	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.411445	0.793787	-3.617657	25789.607275
HLA A*3002	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.500349	0.882547	-3.617802	31648.216526
HLA A*6901	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.391655	0.773810	-3.617845	24640.812076
HLA A*2601	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.386756	0.768800	-3.617956	24364.434753
HLA A*0201	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.385412	0.767455	-3.617958	24289.156600
HLA A*0101	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.385492	0.767455	-3.618038	24293.624666
HLA B*4801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.385495	0.767455	-3.618040	24293.756093
HLA B*4402	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.403402	0.785097	-3.618306	25316.428718
HLA B*1502	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.611045	0.992668	-3.618377	40836.191062
HLA B*4801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.370073	0.751562	-3.618511	23446.209829
HLA B*4402	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.312087	0.693390	-3.618697	20515.748076
HLA A*2601	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.400950	0.782174	-3.618775	25173.846472
HLA A*0101	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.369965	0.750956	-3.619008	23440.375851
HLA A*0206	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.236530	0.617415	-3.619115	17239.722436
HLA A*2601	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.392926	0.773810	-3.619116	24713.035211
HLA B*3501	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.439145	0.820012	-3.619133	27488.127522
HLA B*4402	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.393060	0.773810	-3.619250	24720.656989
HLA B*1509	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-3.732735	0.113485	-3.619250	5404.243380
HLA B*5101	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.481770	0.862516	-3.619254	30322.814828
HLA A*3201	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.612056	0.992668	-3.619388	40931.296924

HLA A*2301	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.498620	0.879222	-3.619398	31522.454045
HLA A*0216	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.371137	0.751562	-3.619575	23503.739446
HLA B*1801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.499017	0.879222	-3.619795	31551.287298
HLA A*3101	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.388713	0.768800	-3.619913	24474.479327
HLA B*4402	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.438241	0.818322	-3.619919	27430.934630
HLA B*4501	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.497671	0.877206	-3.620464	31453.633954
HLA B*1509	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.468920	0.848433	-3.620487	29438.805237
HLA B*4501	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.591939	0.971364	-3.620575	39078.619655
HLA A*3002	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.552115	0.931448	-3.620667	35654.589796
HLA B*3501	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.314402	0.693390	-3.621011	20625.362975
HLA A*2603	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.641285	1.020231	-3.621055	43780.976967
HLA A*3001	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.268758	0.647511	-3.621247	18567.701903
HLA A*0201	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.372850	0.751562	-3.621288	23596.616734
HLA B*4001	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.372248	0.750956	-3.621292	23563.959653
HLA A*0212	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.290980	0.669638	-3.621342	19542.475863
HLA A*6901	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.314862	0.693390	-3.621472	20647.244436
HLA B*5101	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.504320	0.882547	-3.621772	31938.893841
HLA B*0801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.406144	0.784035	-3.622109	25476.765554
HLA A*1101	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.407453	0.785097	-3.622356	25553.650683
HLA A*0301	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.359559	0.737162	-3.622397	22885.410242
HLA A*0201	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.393347	0.770901	-3.622446	24736.978168
HLA A*0211	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.411710	0.789030	-3.622681	25805.377733
HLA B*1503	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.416611	0.793787	-3.622824	26098.241542
HLA A*3001	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.257457	0.634444	-3.623014	18090.773333
HLA B*4001	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.390779	0.767455	-3.623324	24591.139794
HLA A*8001	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.291264	0.667908	-3.623356	19555.272489
HLA B*5701	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.407420	0.784035	-3.623385	25551.715363
HLA A*2501	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.417370	0.793787	-3.623583	26143.885325
HLA B*0702	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.443764	0.820012	-3.623752	27782.047175
HLA A*3201	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.629653	1.005856	-3.623798	42623.896473
HLA B*4501	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.309059	0.685107	-3.623952	20373.182301
HLA A*3201	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.138012	0.514013	-3.623999	13740.788792
HLA B*5701	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.410665	0.786144	-3.624520	25743.328568
HLA A*3002	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.617222	0.992668	-3.624554	41421.137684
HLA A*6802	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.427247	0.802529	-3.624719	26745.293297
HLA B*4001	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.414492	0.789030	-3.625462	25971.199648
HLA B*7301	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.561332	0.935815	-3.625517	36419.373778
HLA A*2301	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.524081	0.898490	-3.625591	33425.767593
HLA B*1517	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.393051	0.767455	-3.625596	24720.122050
HLA B*5701	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.407949	0.782174	-3.625774	25582.836488
HLA A*2601	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.396826	0.770901	-3.625925	24935.968064
HLA A*2301	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.471411	0.844974	-3.626437	29608.106514
HLA A*2501	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.393929	0.767455	-3.626475	24770.188870
HLA A*6802	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.397477	0.770901	-3.626576	24973.363604
HLA B*4601	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.411160	0.784035	-3.627125	25772.731010
HLA A*2603	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.570662	0.943496	-3.627166	37210.223526
HLA A*1101	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.296851	0.669638	-3.627213	19808.470692
HLA B*0803	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.429773	0.802529	-3.627244	26901.287211
HLA A*0219	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.416334	0.789030	-3.627304	26081.586605
HLA B*5801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.364751	0.737162	-3.627589	23160.667075
HLA A*2601	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.217062	0.589436	-3.627626	16483.993575
HLA B*4001	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.379424	0.751562	-3.627862	23956.512627
HLA B*1503	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.245289	0.617415	-3.627874	17590.944135

HLA A*0250	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.472900	0.844974	-3.627927	29709.832816
HLA B*3801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.505685	0.877206	-3.628478	32039.440368
HLA B*4601	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.402369	0.773810	-3.628558	25256.238392
HLA A*0211	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.527091	0.898490	-3.628601	33658.214942
HLA B*4601	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.397407	0.768800	-3.628606	24969.310839
HLA B*7301	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.477049	0.848433	-3.628616	29995.036756
HLA B*3901	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.491139	0.862516	-3.628624	30984.126709
HLA A*2501	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.448644	0.820012	-3.628632	28095.976099
HLA A*2602	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.634542	1.005856	-3.628687	43106.466703
HLA B*5401	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.507976	0.879222	-3.628753	32208.883425
HLA A*2602	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.568327	0.939568	-3.628759	37010.665197
HLA B*1503	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.414962	0.786144	-3.628818	25999.315117
HLA A*6801	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.600411	0.971364	-3.629047	39848.452279
HLA A*3301	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.397905	0.768800	-3.629104	24997.964483
HLA B*1501	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.301200	0.672009	-3.629191	20007.823334
HLA B*0702	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.400120	0.770901	-3.629219	25125.818082
HLA A*0202	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.088682	0.459317	-3.629365	12265.404549
HLA B*5301	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.569043	0.939568	-3.629475	37071.783803
HLA A*0203	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.308584	0.679020	-3.629564	20350.930697
HLA B*1517	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.423364	0.793787	-3.629576	26507.188480
HLA A*6901	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.366821	0.737162	-3.629659	23271.316891
HLA A*6901	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.119300	0.489523	-3.629778	13161.347792
HLA B*7301	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.573439	0.943496	-3.629944	37448.926267
HLA B*3801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.565263	0.935291	-3.629973	36750.492401
HLA A*2402	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.509270	0.879222	-3.630048	32305.036478
HLA A*0206	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.381099	0.750956	-3.630143	24049.097355
HLA A*0202	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.245515	0.615291	-3.630224	17600.082353
HLA B*0801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.195837	0.565473	-3.630364	15697.742076
HLA A*0101	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.399227	0.768800	-3.630427	25074.218540
HLA A*0101	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.323168	0.692679	-3.630488	21045.901272
HLA B*0803	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.493082	0.862516	-3.630567	31123.059579
HLA A*3101	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.416731	0.786144	-3.630587	26105.443154
HLA A*0202	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.381691	0.750956	-3.630735	24081.905657
HLA B*4402	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.420091	0.789030	-3.631061	26308.181752
HLA A*0206	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.310231	0.679020	-3.631211	20428.254715
HLA A*2902	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.382774	0.751562	-3.631212	24142.039895
HLA A*0201	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.400045	0.768800	-3.631245	25121.468766
HLA B*0702	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.417520	0.786144	-3.631376	26152.938766
HLA B*4801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.425666	0.793787	-3.631879	26648.094602
HLA B*5401	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.492601	0.860615	-3.631986	31088.562390
HLA A*0250	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.522524	0.890279	-3.632245	33306.092255
HLA B*5701	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.421599	0.789030	-3.632570	26399.712841
HLA B*3501	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.370402	0.737162	-3.633240	23463.974351
HLA A*0203	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.280764	0.647511	-3.633253	19088.158100
HLA B*4601	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.384931	0.751562	-3.633369	24262.234194
HLA B*0801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.418545	0.785097	-3.633448	26214.698816
HLA B*5301	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.568769	0.935291	-3.633478	37048.326382
HLA B*7301	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.516194	0.882547	-3.633647	32824.201355
HLA A*2603	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.626331	0.992668	-3.633663	42299.085347
HLA A*2403	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.320957	0.687090	-3.633867	20939.035026
HLA A*2501	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.402709	0.768800	-3.633909	25276.058015
HLA A*0206	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.419095	0.785097	-3.633998	26247.905386
HLA B*1501	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.418258	0.784035	-3.634223	26197.402654
HLA B*1501	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.405183	0.770901	-3.634282	25420.456844

HLA A*6801	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.524650	0.890279	-3.634371	33469.557037
HLA B*4001	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.418512	0.784035	-3.634477	26212.713431
HLA A*6801	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.570420	0.935815	-3.634605	37189.495073
HLA A*3301	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.640578	1.005856	-3.634723	43709.743060
HLA B*5701	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.408731	0.773810	-3.634921	25628.965329
HLA A*0212	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.386521	0.751562	-3.634960	24351.257428
HLA B*1501	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.250491	0.615291	-3.635200	17802.906427
HLA B*2705	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.419609	0.784035	-3.635574	26279.021433
HLA A*6901	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.326732	0.691047	-3.635685	21219.331493
HLA A*0212	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.438271	0.802529	-3.635742	27432.863876
HLA A*0211	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.387355	0.751562	-3.635794	24398.069214
HLA A*6801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.303897	0.667908	-3.635989	20132.469636
HLA A*0203	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.312874	0.676597	-3.636277	20552.962742
HLA A*2601	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.323414	0.687090	-3.636325	21057.859547
HLA B*0802	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.430142	0.793787	-3.636355	26924.145595
HLA A*3101	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.407375	0.770901	-3.636474	25549.089091
HLA B*2705	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.430274	0.793787	-3.636486	26932.303603
HLA B*4002	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.644128	1.007379	-3.636750	44068.505797
HLA A*6901	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.387727	0.750956	-3.636770	24418.932684
HLA A*0219	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.407686	0.770901	-3.636785	25567.340348
HLA B*3501	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.423035	0.786144	-3.636890	26487.119948
HLA B*1517	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.309216	0.672009	-3.637207	20380.568156
HLA A*2603	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.643109	1.005856	-3.637253	43965.159081
HLA A*2301	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.527735	0.890279	-3.637456	33708.143834
HLA B*5301	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.573369	0.935815	-3.637554	37442.848924
HLA A*0202	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.500070	0.862516	-3.637554	31627.848695
HLA B*4501	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.572873	0.935291	-3.637583	37400.132798
HLA B*4403	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.630475	0.992668	-3.637808	42704.679623
HLA A*2403	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.389068	0.750956	-3.638112	24494.480533
HLA A*2601	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.389275	0.750956	-3.638319	24506.144402
HLA B*4801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.427583	0.789030	-3.638554	26765.991840
HLA A*2402	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.487009	0.848433	-3.638576	30690.846379
HLA B*4403	1:48-56	9	RAATRQSQA	1.136689	-0.116458	-4.658817	1.020231	-3.638587	45584.511557
HLA B*1501	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.323915	0.685107	-3.638807	21082.138639
HLA A*2602	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.570305	0.931448	-3.638857	37179.638019
HLA B*4402	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.409845	0.770901	-3.638944	25694.769698
HLA A*6901	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.306864	0.667908	-3.638956	20270.499581
HLA B*3501	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.432825	0.793787	-3.639038	27091.000373
HLA B*3901	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.487918	0.848433	-3.639485	30755.168877
HLA A*6802	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.421747	0.782174	-3.639573	26408.712004
HLA A*0203	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.161878	0.522301	-3.639577	14517.028614
HLA A*0206	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.521929	0.882099	-3.639830	33260.537324
HLA A*3101	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.423967	0.784035	-3.639932	26544.068156
HLA A*0250	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.571492	0.931448	-3.640044	37281.351444
HLA B*3901	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.460124	0.820012	-3.640112	28848.531346
HLA B*0702	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.424191	0.784035	-3.640155	26557.713707
HLA B*7301	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.517428	0.877206	-3.640221	32917.560899
HLA B*3501	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.287845	0.647511	-3.640334	19401.949561
HLA A*0301	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.336233	0.695802	-3.640431	21688.674693
HLA B*1503	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.295970	0.654994	-3.640976	19768.325816
HLA A*2403	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.408618	0.767455	-3.641164	25622.310999
HLA A*6801	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.584764	0.943496	-3.641268	38438.274852
HLA B*3801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.502121	0.860615	-3.641506	31777.575038
HLA A*0101	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.378855	0.737162	-3.641693	23925.169446

HLA B*3801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.520971	0.879222	-3.641748	33187.204471
HLA A*0203	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.425784	0.784035	-3.641748	26655.303739
HLA B*1801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.224120	0.581978	-3.642142	16754.068607
HLA A*0211	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.524302	0.882099	-3.642203	33442.769907
HLA A*0219	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.427325	0.785097	-3.642228	26750.068463
HLA A*0211	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.319002	0.676597	-3.642405	20844.999634
HLA A*0212	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.413313	0.770901	-3.642412	25900.763677
HLA A*0219	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.394082	0.751562	-3.642520	24778.900660
HLA A*6802	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.327629	0.685107	-3.642522	21263.228232
HLA A*3001	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.200625	0.557970	-3.642656	15871.772853
HLA A*2301	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.491177	0.848433	-3.642744	30986.808756
HLA A*3101	1:282-290	9	GAFVVYNLIT	0.924708	-0.309417	-4.258059	0.615291	-3.642767	18115.845175
HLA B*5301	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.586265	0.943496	-3.642769	38571.382800
HLA A*3002	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.394467	0.751562	-3.642906	24800.894797
HLA B*2705	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.235191	0.592259	-3.642932	17186.643274
HLA B*3501	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.432160	0.789030	-3.643131	27049.555823
HLA B*5801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.312823	0.669638	-3.643185	20550.516724
HLA B*1801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.525503	0.882099	-3.643404	33535.348790
HLA B*4801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.380817	0.737162	-3.643655	24033.490067
HLA A*6901	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.233145	0.589436	-3.643709	17105.850079
HLA A*0101	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.337217	0.693390	-3.643827	21737.893118
HLA A*0203	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.339823	0.695802	-3.644021	21868.703075
HLA B*3501	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-3.636749	-0.007282	-3.644031	4332.604425
HLA A*8001	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.414953	0.770901	-3.644052	25998.752510
HLA B*5301	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.575559	0.931448	-3.644111	37632.113129
HLA A*8001	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.395675	0.751562	-3.644113	24869.954196
HLA A*2602	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.637143	0.992668	-3.644476	43365.394993
HLA A*0203	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.415382	0.770901	-3.644482	26024.504272
HLA B*4801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.426698	0.782174	-3.644523	26711.457476
HLA B*1517	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.418484	0.773810	-3.644673	26211.011792
HLA B*0702	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.337363	0.692679	-3.644684	21745.185516
HLA B*4001	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.381874	0.737162	-3.644712	24092.069676
HLA B*4001	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.332058	0.687090	-3.644968	21481.172370
HLA B*4601	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.395952	0.750956	-3.644996	24885.835420
HLA B*0702	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.265032	0.620011	-3.645021	18409.070964
HLA B*4403	1:168-176	9	TAESRDARV	0.917270	0.090109	-4.652455	1.007379	-3.645076	44921.567301
HLA A*0201	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.396234	0.750956	-3.645278	24901.996219
HLA A*2301	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.527690	0.882099	-3.645591	33704.679223
HLA A*3002	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.263110	0.617415	-3.645695	18327.785487
HLA A*0301	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.338477	0.692679	-3.645798	21801.017977
HLA A*0212	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.435057	0.789030	-3.646028	27230.590113
HLA A*2403	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.432755	0.786144	-3.646610	27086.603951
HLA A*3001	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.187125	0.540487	-3.646638	15385.984786
HLA A*6901	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.635072	-0.011592	-3.646663	4315.901324
HLA A*6802	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.169274	0.522301	-3.646973	14766.375621
HLA A*3001	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.246953	0.599894	-3.647059	17658.450194
HLA A*2902	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.429411	0.782174	-3.647237	26878.884465
HLA B*4601	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.418237	0.770901	-3.647336	26196.127159
HLA B*5701	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.416209	0.768800	-3.647409	26074.109457
HLA A*0219	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.450303	0.802529	-3.647774	28203.490546
HLA B*4403	1:84-92	9	RFISGASAP	0.656730	0.314634	-4.619167	0.971364	-3.647803	41607.095217
HLA A*3301	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.587485	0.939568	-3.647917	38679.833102

HLA A*6801	1:38-46	9	PDAGDPPPW	0.977783	0.052446	-4.678440	1.030229	-3.648212	47691.414592
HLA A*2501	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.437277	0.789030	-3.648248	27370.158748
HLA A*1101	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.430497	0.782174	-3.648322	26946.148734
HLA B*4002	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.525552	0.877206	-3.648346	33539.158880
HLA A*6802	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.417361	0.768800	-3.648561	26143.319589
HLA A*0202	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.580180	0.931448	-3.648732	38034.704163
HLA B*5701	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.419764	0.770901	-3.648863	26288.406104
HLA B*5101	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.325585	0.676597	-3.648988	21163.385790
HLA A*0211	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.531647	0.882547	-3.649099	34013.140335
HLA A*2403	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.400698	0.751562	-3.649137	25159.278603
HLA A*8001	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.400195	0.750956	-3.649239	25130.168151
HLA A*6901	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.328271	0.679020	-3.649251	21294.655089
HLA A*0206	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.547832	0.898490	-3.649342	35304.684365
HLA A*6801	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.584637	0.935291	-3.649346	38427.047365
HLA A*3002	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.531745	0.882099	-3.649646	34020.869520
HLA A*0212	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.334821	0.685107	-3.649714	21618.271878
HLA B*1517	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.435882	0.786144	-3.649737	27282.346617
HLA B*4001	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.418629	0.768800	-3.649829	26219.804784
HLA B*5701	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.342619	0.692679	-3.649940	22009.942860
HLA A*2902	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.337340	0.687090	-3.650250	21744.009157
HLA A*2601	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.401958	0.751562	-3.650396	25232.338853
HLA B*4801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.436547	0.786144	-3.650402	27324.147843
HLA B*4402	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.434441	0.784035	-3.650406	27192.021061
HLA B*4801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.434564	0.784035	-3.650528	27199.671639
HLA B*1501	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.327354	0.676597	-3.650757	21249.773781
HLA B*1501	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.419706	0.768800	-3.650905	26284.850910
HLA A*6802	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.424743	0.773810	-3.650932	26591.498635
HLA A*0206	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.285383	0.634444	-3.650939	19292.260209
HLA A*2403	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.263289	0.612174	-3.651114	18335.322535
HLA B*0802	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.471234	0.820012	-3.651222	29596.095708
HLA B*1517	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-3.919745	0.268222	-3.651522	8312.745940
HLA B*4801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.422443	0.770901	-3.651542	26451.034870
HLA A*2402	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.425629	0.773810	-3.651818	26645.788090
HLA B*3801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.454375	0.802529	-3.651846	28469.151182
HLA A*6901	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.299391	0.647511	-3.651879	19924.651803
HLA A*1101	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.438302	0.786144	-3.652157	27434.793258
HLA A*2603	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.542520	0.890279	-3.652241	34875.476298
HLA B*5701	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.339355	0.687090	-3.652266	21845.172599
HLA B*4402	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.419755	0.767455	-3.652300	26287.837241
HLA B*0801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.421113	0.768800	-3.652313	26370.165748
HLA A*0201	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.348455	0.695802	-3.652653	22307.712353
HLA B*4403	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.513342	0.860615	-3.652727	32609.331315
HLA B*5101	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.473048	0.820012	-3.653036	29719.960337
HLA B*5401	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.551552	0.898490	-3.653061	35608.326865
HLA A*1101	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.442221	0.789030	-3.653191	27683.476802
HLA A*0211	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.346629	0.693390	-3.653239	22214.139048
HLA A*0250	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.435656	0.782174	-3.653482	27268.181226
HLA B*0801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.427304	0.773810	-3.653493	26748.766060
HLA A*2403	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.346387	0.692679	-3.653708	22201.764365
HLA B*5801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.347264	0.693390	-3.653874	22246.610285
HLA B*5701	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.421378	0.767455	-3.653924	26386.291219
HLA A*3301	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.646858	0.992668	-3.654191	44346.405822
HLA A*0219	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.302017	0.647511	-3.654506	20045.526370
HLA A*3301	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.590374	0.935815	-3.654559	38938.073275

HLA B*2705	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.331278	0.676597	-3.654681	21442.625025
HLA B*1501	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.220464	0.565473	-3.654991	16613.628345
HLA B*3501	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.426037	0.770901	-3.655136	26670.882132
HLA A*2601	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.392437	0.737162	-3.655276	24685.242337
HLA B*3901	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.429573	0.773810	-3.655763	26888.919752
HLA B*2705	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.324194	0.667908	-3.656286	21095.715201
HLA B*4801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.349714	0.693390	-3.656324	22372.491914
HLA A*0206	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.408036	0.751562	-3.656474	25587.957812
HLA B*5101	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.501451	0.844974	-3.656478	31728.617539
HLA B*1501	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.249112	0.592259	-3.656853	17746.461102
HLA A*2402	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.519519	0.862516	-3.657003	33076.434581
HLA A*8001	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.344214	0.687090	-3.657125	22090.940982
HLA A*3301	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.408778	0.751562	-3.657216	25631.738476
HLA A*3101	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.408332	0.750956	-3.657375	25605.405688
HLA B*3501	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.442484	0.785097	-3.657387	27700.255513
HLA A*2902	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.272867	0.615291	-3.657576	18744.221357
HLA B*4501	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.650448	0.992668	-3.657781	44714.506307
HLA A*2902	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.447338	0.789030	-3.658308	28011.593230
HLA A*0201	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.395581	0.737162	-3.658419	24864.573030
HLA A*2602	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.351328	0.692679	-3.658649	22455.796088
HLA B*4002	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.503937	0.844974	-3.658963	31910.742157
HLA A*6802	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.410019	0.750956	-3.659062	25705.058190
HLA B*1502	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.594923	0.935815	-3.659108	39348.036087
HLA A*2301	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.536421	0.877206	-3.659214	34389.105895
HLA A*2402	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.519951	0.860615	-3.659336	33109.375905
HLA B*0801	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.082193	0.422812	-3.659380	12083.495913
HLA B*5401	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.150041	0.490659	-3.659382	14126.709920
HLA B*1501	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.296320	0.636799	-3.659521	19784.266963
HLA A*2402	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.591131	0.931448	-3.659683	39005.961901
HLA A*3201	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.397129	0.737162	-3.659968	24953.376344
HLA A*2403	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.143209	0.483198	-3.660011	13906.208129
HLA A*2902	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.445256	0.785097	-3.660159	27877.650393
HLA A*0219	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.345267	0.685107	-3.660160	22144.546190
HLA B*3501	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.411139	0.750956	-3.660183	25771.476192
HLA A*6802	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.149759	0.489523	-3.660237	14117.542024
HLA B*1501	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.315539	0.654994	-3.660545	20679.438909
HLA A*0212	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.444598	0.784035	-3.660563	27835.454160
HLA A*2603	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.596403	0.935815	-3.660588	39482.372044
HLA A*3201	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.592228	0.931448	-3.660780	39104.631862
HLA A*0219	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.411854	0.750956	-3.660897	25813.894996
HLA B*4601	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.398161	0.737162	-3.660999	25012.709577
HLA A*6802	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.445042	0.784035	-3.661007	27863.929606
HLA A*0212	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.348136	0.687090	-3.661046	22291.305603
HLA B*7301	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.540316	0.879222	-3.661094	34698.949799
HLA B*2705	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.447601	0.786144	-3.661457	28028.570810
HLA A*0211	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.430377	0.768800	-3.661577	26938.715200
HLA A*0219	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.429038	0.767455	-3.661583	26855.773933
HLA B*5301	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.338211	0.676597	-3.661614	21787.694706
HLA B*4801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.430422	0.768800	-3.661621	26941.484316
HLA B*1801	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.464188	0.802529	-3.661659	29119.795287
HLA A*8001	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.443858	0.782174	-3.661684	27788.059738
HLA B*4002	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.355355	0.693390	-3.661965	22664.986947
HLA B*5401	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.455829	0.793787	-3.662042	28564.646242
HLA B*2705	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.447199	0.785097	-3.662103	28002.653819

HLA B*5701	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.413790	0.751562	-3.662228	25929.223714
HLA B*4501	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.593683	0.931448	-3.662235	39235.801882
HLA A*2301	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.544853	0.882547	-3.662306	35063.332182
HLA A*0201	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.309973	0.647511	-3.662461	20416.101726
HLA B*5301	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.480942	0.818322	-3.662621	30265.126613
HLA A*0203	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.282653	0.620011	-3.662642	19171.363837
HLA B*3901	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.433612	0.770901	-3.662711	27140.142258
HLA B*0702	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.414046	0.750956	-3.663089	25944.518114
HLA B*7301	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.595059	0.931448	-3.663611	39360.384398
HLA B*1502	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.483724	0.820012	-3.663712	30459.606279
HLA A*2402	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.562463	0.898490	-3.663972	36514.266104
HLA B*0702	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.401229	0.737162	-3.664067	25190.058028
HLA A*0206	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.431601	0.767455	-3.664146	27014.750481
HLA B*7301	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.599563	0.935291	-3.664273	39770.705391
HLA A*0202	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.546517	0.882099	-3.664417	35197.889336
HLA A*0211	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.449934	0.785097	-3.664837	28179.546008
HLA A*2602	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.547400	0.882547	-3.664853	35269.558875
HLA B*5801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.355938	0.691047	-3.664891	22695.415892
HLA A*0301	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.358290	0.693390	-3.664900	22818.651734
HLA A*3201	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.600195	0.935291	-3.664905	39828.624248
HLA A*6901	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.264971	0.599894	-3.665077	18406.481779
HLA B*0702	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.454602	0.789030	-3.665573	28484.094553
HLA A*2602	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.564229	0.898490	-3.665739	36663.117354
HLA A*6802	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.417509	0.751562	-3.665947	26152.231353
HLA B*5401	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.146136	0.480013	-3.666123	14000.262652
HLA A*0216	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.468767	0.802529	-3.666239	29428.455114
HLA A*3101	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.359674	0.693390	-3.666284	22891.477615
HLA A*0206	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.359834	0.693390	-3.666443	22899.900308
HLA B*0802	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.418021	0.751562	-3.666459	26183.092334
HLA A*2403	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.437531	0.770901	-3.666630	27386.154929
HLA A*2902	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.301263	0.634444	-3.666820	20010.746030
HLA B*5801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.334971	0.667908	-3.667063	21625.758131
HLA B*4403	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.606687	0.939568	-3.667119	40428.435229
HLA A*0219	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.360647	0.693390	-3.667256	22942.804980
HLA B*1801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.529927	0.862516	-3.667411	33878.713321
HLA B*2705	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.456888	0.789030	-3.667859	28634.425070
HLA A*2501	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.419748	0.751562	-3.668186	26287.410601
HLA B*2705	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.419764	0.751562	-3.668203	26288.406104
HLA B*4002	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.603635	0.935291	-3.668344	40145.322529
HLA A*3201	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.454527	0.786144	-3.668383	28479.163915
HLA B*1501	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.190767	0.522301	-3.668466	15515.543756
HLA A*3001	1:163-171	9	GGRSITAES	1.149832	-1.125937	-3.692582	0.023895	-3.668688	4926.995896
HLA A*8001	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.457833	0.789030	-3.668803	28696.766279
HLA A*2602	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.353972	0.685107	-3.668864	22592.881613
HLA A*2301	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.529499	0.860615	-3.668884	33845.372762
HLA A*0301	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.324091	0.654994	-3.669097	21090.694277
HLA B*1501	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.209709	0.540487	-3.669221	16207.220789
HLA B*4601	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.362651	0.693390	-3.669260	23048.922319
HLA A*6901	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.183277	0.514013	-3.669264	15250.245752
HLA B*5801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.341331	0.672009	-3.669322	21944.788387

HLA A*0212	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.345967	0.676597	-3.669370	22180.275246
HLA A*6802	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.339045	0.669638	-3.669408	21829.578412
HLA B*4501	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.517992	0.848433	-3.669559	32960.327942
HLA B*1801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.489591	0.820012	-3.669579	30873.861345
HLA A*1101	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.362348	0.692679	-3.669668	23032.842647
HLA A*0301	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.341717	0.672009	-3.669707	21964.266921
HLA A*3002	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.455859	0.786144	-3.669715	28566.655223
HLA A*0101	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.365919	0.695802	-3.670117	23223.023297
HLA A*1101	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.444023	0.773810	-3.670212	27798.584853
HLA A*8001	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.362916	0.692679	-3.670237	23063.016835
HLA B*4402	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.421858	0.751562	-3.670296	26415.427664
HLA B*5401	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.552430	0.882099	-3.670331	35680.446075
HLA A*0203	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.129727	0.459317	-3.670410	13481.163631
HLA A*0201	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.259999	0.589436	-3.670563	18196.978208
HLA A*3101	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.357028	0.686161	-3.670867	22752.457227
HLA A*2602	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.550541	0.879222	-3.671319	35525.589183
HLA B*1509	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.533923	0.862516	-3.671408	34191.911593
HLA A*3101	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.348072	0.676597	-3.671475	22288.049816
HLA B*5801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.357642	0.686161	-3.671480	22784.605958
HLA B*4601	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.367324	0.695802	-3.671522	23298.274075
HLA B*4002	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.491790	0.820012	-3.671778	31030.592447
HLA B*1517	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.155215	0.483430	-3.671784	14296.001773
HLA A*6802	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.264423	0.592259	-3.672165	18383.294949
HLA B*1517	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.409368	0.737162	-3.672206	25666.566998
HLA B*5401	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.359512	0.687090	-3.672422	22882.934225
HLA B*1517	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.366013	0.693390	-3.672623	23228.049200
HLA A*0203	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.441899	0.768800	-3.673099	27662.966661
HLA B*1502	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.459259	0.786144	-3.673115	28791.155691
HLA B*5801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.358313	0.685107	-3.673206	22819.886231
HLA B*0702	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.424879	0.751562	-3.673317	26599.843654
HLA B*5101	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.455538	0.782174	-3.673363	28545.490753
HLA B*0801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.360670	0.687090	-3.673580	22944.046194
HLA A*6801	1:41-49	9	GDPPPWQRA	1.388208	-0.382352	-4.679502	1.005856	-3.673647	47808.175670
HLA B*1502	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.447610	0.773810	-3.673800	28029.177342
HLA B*5801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.353342	0.679020	-3.674322	22560.149051
HLA B*5401	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.071531	0.397004	-3.674527	11790.456941
HLA B*3801	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.493031	0.818322	-3.674709	31119.355609
HLA B*3801	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.523149	0.848433	-3.674716	33354.055240
HLA B*4002	1:161-169	9	SSGGRSITA	1.214584	-0.275016	-4.614389	0.939568	-3.674820	41151.772335
HLA A*2402	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.552242	0.877206	-3.675036	35665.007236
HLA A*3201	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.552435	0.877206	-3.675229	35680.832132
HLA A*6802	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.442834	0.767455	-3.675379	27722.592956
HLA A*6802	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.352078	0.676597	-3.675481	22494.582741
HLA B*0702	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.267910	0.592259	-3.675651	18531.475125
HLA B*5401	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.538235	0.862516	-3.675719	34533.030076
HLA A*2301	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.494046	0.818322	-3.675724	31192.168839
HLA A*0250	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.574264	0.898490	-3.675774	37520.104508
HLA A*0219	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.371633	0.695802	-3.675831	23530.583968
HLA A*2602	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.520846	0.844974	-3.675873	33177.690263
HLA A*2403	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.354893	0.679020	-3.675873	22640.844646
HLA A*2301	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.538392	0.862516	-3.675876	34545.549276
HLA B*2705	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.413066	0.737162	-3.675904	25886.055227
HLA A*0301	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.362211	0.686161	-3.676050	23025.616684
HLA A*0216	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.446997	0.770901	-3.676096	27989.628602

HLA A*0211	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.198478	0.522301	-3.676177	15793.486380
HLA A*2301	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.496498	0.820012	-3.676486	31368.838284
HLA A*0203	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.428175	0.751562	-3.676614	26802.506589
HLA A*6901	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.348739	0.672009	-3.676730	22322.319685
HLA A*0301	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.367951	0.691047	-3.676904	23331.951360
HLA A*2501	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.364100	0.687090	-3.677011	23125.985897
HLA A*2501	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.427973	0.750956	-3.677017	26790.039610
HLA B*1517	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.445836	0.768800	-3.677036	27914.926597
HLA A*0212	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.445865	0.768800	-3.677064	27916.738856
HLA B*5701	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.428100	0.750956	-3.677144	26797.867035
HLA A*0219	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.451106	0.773810	-3.677296	28255.720441
HLA B*3901	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.479841	0.802529	-3.677312	30188.434118
HLA A*0206	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.373315	0.695802	-3.677513	23621.905982
HLA B*3901	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.462673	0.785097	-3.677576	29018.362372
HLA B*4001	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.345575	0.667908	-3.677666	22160.245492
HLA A*8001	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.461733	0.784035	-3.677698	28955.635816
HLA A*0212	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.371323	0.693390	-3.677932	23513.786650
HLA A*0301	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.363558	0.685107	-3.678450	23097.103764
HLA B*1503	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.350640	0.672009	-3.678631	22420.229657
HLA B*0702	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.452699	0.773810	-3.678889	28359.550037
HLA B*2705	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.461080	0.782174	-3.678906	28912.120741
HLA B*4402	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.416228	0.737162	-3.679066	26075.237946
HLA A*3101	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.348782	0.669638	-3.679144	22324.493494
HLA B*4601	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.347212	0.667908	-3.679304	22243.962706
HLA A*0301	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.356023	0.676597	-3.679425	22699.836391
HLA B*3901	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.447162	0.767455	-3.679707	28000.230064
HLA A*3001	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.197233	0.517364	-3.679868	15748.267502
HLA A*2902	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.450841	0.770901	-3.679940	28238.452504
HLA A*0216	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.327467	0.647511	-3.679956	21255.292525
HLA A*8001	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.453797	0.773810	-3.679986	28431.288704
HLA B*4403	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.570376	0.890279	-3.680097	37185.672640
HLA A*3301	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.570514	0.890279	-3.680235	37197.543586
HLA B*5801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.356930	0.676597	-3.680332	22747.288107
HLA B*0801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.297814	0.617415	-3.680399	19852.455723
HLA B*0801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.371527	0.691047	-3.680480	23524.856262
HLA B*0803	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.464649	0.784035	-3.680613	29150.688497
HLA A*0101	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.348659	0.667908	-3.680751	22318.214180
HLA B*3501	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.348920	0.667908	-3.681012	22331.620240
HLA A*2601	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.373827	0.692679	-3.681148	23649.781049
HLA A*2603	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.499501	0.818322	-3.681179	31586.468825
HLA B*5401	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.563839	0.882547	-3.681292	36630.207129
HLA A*2403	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.349207	0.667908	-3.681299	22346.364119
HLA A*0202	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.107750	0.426351	-3.681399	12815.935038
HLA B*0803	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.501566	0.820012	-3.681554	31737.029421
HLA A*0216	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.377819	0.695802	-3.682017	23868.157742
HLA A*3002	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.337055	0.654994	-3.682061	21729.780261
HLA A*0101	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.367260	0.685107	-3.682153	23294.871214
HLA B*5101	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.451478	0.768800	-3.682677	28279.882696
HLA A*2301	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.434406	0.751562	-3.682845	27189.814563
HLA B*4601	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.352548	0.669638	-3.682910	22518.934552
HLA A*2501	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.469181	0.786144	-3.683037	29456.488481
HLA B*1517	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.465375	0.782174	-3.683201	29199.459165
HLA A*8001	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.468375	0.785097	-3.683278	29401.879939
HLA A*3201	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-3.993547	0.310085	-3.683462	9852.501970

HLA B*1503	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.174128	0.490659	-3.683469	14932.342670
HLA A*3101	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.379299	0.695802	-3.683497	23949.644702
HLA B*0801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.369685	0.686161	-3.683524	23425.290337
HLA B*5101	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.468650	0.785097	-3.683553	29420.495956
HLA A*2902	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.286227	0.602429	-3.683798	19329.765085
HLA A*3101	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.369093	0.685107	-3.683986	23393.376583
HLA A*0250	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.544646	0.860615	-3.684031	35046.643546
HLA B*5701	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.421296	0.737162	-3.684134	26381.295550
HLA A*0203	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.421686	0.737162	-3.684524	26404.997692
HLA A*0219	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.468662	0.784035	-3.684626	29421.291775
HLA A*0203	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.277287	0.592259	-3.685028	18935.936373
HLA B*1801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.354740	0.669638	-3.685102	22632.884556
HLA B*1502	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.547621	0.862516	-3.685105	35287.499050
HLA B*5101	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.474174	0.789030	-3.685144	29797.074638
HLA B*1503	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.202749	0.517364	-3.685385	15949.584505
HLA A*0101	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.355386	0.669638	-3.685748	22666.580999
HLA A*2403	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.454617	0.768800	-3.685816	28485.019143
HLA A*2602	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.621211	0.935291	-3.685921	41803.384886
HLA B*3901	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.355738	0.669638	-3.686101	22684.982018
HLA A*3301	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.621479	0.935291	-3.686189	41829.174129
HLA A*3001	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.288684	0.602429	-3.686255	19439.457345
HLA A*8001	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.455093	0.768800	-3.686293	28516.318788
HLA A*0301	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.365494	0.679020	-3.686474	23200.294676
HLA A*0201	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.208952	0.522301	-3.686651	16179.012641
HLA A*3002	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.460478	0.773810	-3.686668	28872.107145
HLA B*3501	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.083856	0.397004	-3.686852	12129.866885
HLA B*5301	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.564168	0.877206	-3.686962	36657.960789
HLA A*3301	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.585492	0.898490	-3.687002	38502.792447
HLA A*2403	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.363724	0.676597	-3.687127	23105.977115
HLA B*5101	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.347151	0.659875	-3.687276	22240.834154
HLA B*0801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.383124	0.695802	-3.687322	24161.507998
HLA B*4002	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.302664	0.615291	-3.687372	20075.370686
HLA B*1501	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.366400	0.679020	-3.687380	23248.792550
HLA A*2902	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.299555	0.612174	-3.687381	19932.198543
HLA B*0802	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.471474	0.784035	-3.687439	29612.431598
HLA B*5401	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.472813	0.785097	-3.687717	29703.886516
HLA A*2902	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.461606	0.773810	-3.687796	28947.178125
HLA B*0702	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.177351	0.489523	-3.687829	15043.588354
HLA B*1503	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.374257	0.686161	-3.688096	23673.206156
HLA A*0101	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.379146	0.691047	-3.688099	23941.224462
HLA A*3101	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.360120	0.672009	-3.688111	22915.019379
HLA A*0201	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.381548	0.693390	-3.688157	24073.959861
HLA B*3501	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.472353	0.784035	-3.688317	29672.407041
HLA A*2403	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.384177	0.695802	-3.688375	24220.137581
HLA A*3201	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.490933	0.802529	-3.688404	30969.379598
HLA A*0202	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.587156	0.898490	-3.688665	38650.548688
HLA A*1101	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.382318	0.693390	-3.688928	24116.715669
HLA A*0211	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.203008	0.514013	-3.688995	15959.078733
HLA B*0802	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.474120	0.785097	-3.689023	29793.367295
HLA B*4402	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.440118	0.750956	-3.689162	27549.761514
HLA B*1801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.458033	0.768800	-3.689232	28709.965251
HLA A*2602	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.323701	0.634444	-3.689257	21071.762458
HLA B*0702	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.458178	0.768800	-3.689378	28719.596565
HLA B*5801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.326302	0.636799	-3.689503	21198.334544
HLA B*4601	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.382447	0.692679	-3.689768	24123.892518
HLA A*3201	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.572380	0.882547	-3.689832	37357.667504

HLA B*4403	1:81-89	9	RLNRFISGA	1.033741	-0.090245	-4.633490	0.943496	-3.689994	43002.119064
HLA B*5101	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.483957	0.793787	-3.690170	30475.924175
HLA B*4002	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.538690	0.848433	-3.690258	34569.292155
HLA A*2501	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.472809	0.782174	-3.690634	29703.565128
HLA B*4403	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.626040	0.935291	-3.690749	42270.719525
HLA B*2705	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.377842	0.687090	-3.690753	23869.449018
HLA B*5701	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.384313	0.693390	-3.690923	24227.738413
HLA A*2902	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.040682	0.349724	-3.690957	10982.011610
HLA B*1801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.376271	0.685107	-3.691163	23783.216471
HLA A*6901	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.351321	0.659875	-3.691447	22455.431641
HLA A*2501	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.465394	0.773810	-3.691583	29200.722919
HLA B*5301	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.581994	0.890279	-3.691715	38193.885785
HLA A*2601	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.385344	0.693390	-3.691954	24285.346251
HLA B*0803	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.478226	0.786144	-3.692082	30076.444209
HLA A*2402	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.574297	0.882099	-3.692198	37522.946330
HLA B*1501	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.326661	0.634444	-3.692218	21215.887946
HLA B*5801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.307546	0.615291	-3.692255	20302.326276
HLA A*2501	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.463204	0.770901	-3.692303	29053.862933
HLA B*4801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.443405	0.750956	-3.692449	27759.061127
HLA A*6801	1:105-113	9	PDPDASLGC	1.356894	-0.364226	-4.685251	0.992668	-3.692584	48445.267848
HLA A*0201	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.377781	0.685107	-3.692674	23866.091846
HLA A*0250	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.575432	0.882547	-3.692884	37621.121114
HLA B*3901	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.430177	0.737162	-3.693015	26926.330534
HLA A*0211	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-3.674595	-0.018628	-3.693223	4727.097319
HLA A*0206	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.464517	0.770901	-3.693616	29141.858522
HLA B*0702	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.478894	0.785097	-3.693797	30122.689431
HLA B*0802	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.467696	0.773810	-3.693886	29355.947252
HLA A*0101	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.380070	0.686161	-3.693908	23992.179723
HLA A*0206	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.341616	0.647511	-3.694104	21959.158073
HLA B*5301	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.592957	0.898490	-3.694466	39170.267919
HLA A*2402	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.585079	0.890279	-3.694800	38466.149826
HLA B*1509	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.446396	0.751562	-3.694834	27950.891710
HLA A*3001	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.290963	0.595896	-3.695067	19541.735818
HLA A*3002	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.432522	0.737162	-3.695360	27072.100818
HLA B*1509	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.380544	0.685107	-3.695437	24018.412651
HLA A*6801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.489666	0.793787	-3.695879	30879.206581
HLA B*5801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.343434	0.647511	-3.695923	22051.299425
HLA A*2601	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.330545	0.634444	-3.696101	21406.462858
HLA A*2402	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.578679	0.882547	-3.696131	37903.448267
HLA A*6802	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.433351	0.737162	-3.696190	27123.849558
HLA B*1502	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.579059	0.882547	-3.696512	37936.681487
HLA A*0206	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.373136	0.676597	-3.696539	23612.195795
HLA A*2603	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.210573	0.514013	-3.696560	16239.518900
HLA B*4001	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.333501	0.636799	-3.696702	21552.644415
HLA B*5701	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.364779	0.667908	-3.696871	23162.170683
HLA A*0202	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.579463	0.882547	-3.696916	37971.998033
HLA B*4001	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.388058	0.691047	-3.697011	24437.566414
HLA B*3501	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.376059	0.679020	-3.697039	23771.639479
HLA A*2902	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.180251	0.483198	-3.697053	15144.352355
HLA A*3002	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.481156	0.784035	-3.697121	30280.029800
HLA A*0301	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.312454	0.615291	-3.697163	20533.069500
HLA B*1517	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.486201	0.789030	-3.697171	30633.783770
HLA B*0803	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.449182	0.751562	-3.697620	28130.804779

HLA B*0801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.390304	0.692679	-3.697625	24564.281333
HLA A*3001	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.285388	0.587655	-3.697732	19292.468948
HLA B*1517	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.449321	0.751562	-3.697759	28139.785100
HLA A*0212	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.434965	0.737162	-3.697804	27224.845454
HLA B*3901	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.480050	0.782174	-3.697875	30202.972749
HLA A*0206	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.124559	0.426351	-3.698207	13321.665148
HLA A*2403	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.384421	0.686161	-3.698260	24233.768355
HLA B*4601	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.383526	0.685107	-3.698419	24183.869935
HLA B*7301	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-3.978923	0.280375	-3.698548	9526.279855
HLA B*0802	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.484866	0.786144	-3.698722	30539.796234
HLA A*6801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.518765	0.820012	-3.698752	33019.044736
HLA B*0802	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.481039	0.782174	-3.698865	30271.840328
HLA B*5801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.353997	0.654994	-3.699004	22594.226128
HLA B*0802	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.469919	0.770901	-3.699018	29506.568895
HLA A*2601	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.385234	0.686161	-3.699073	24279.172127
HLA B*1501	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.009171	0.310085	-3.699086	10213.406222
HLA A*0216	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.483200	0.784035	-3.699165	30422.881806
HLA B*1801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.493113	0.793787	-3.699326	31125.248496
HLA B*5301	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.578651	0.879222	-3.699428	37900.987705
HLA B*5801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.359354	0.659875	-3.699480	22874.641521
HLA B*1509	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.392888	0.693390	-3.699498	24710.896187
HLA A*0202	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.473661	0.773810	-3.699851	29761.953998
HLA A*2403	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.393271	0.693390	-3.699881	24732.696160
HLA A*2602	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.548345	0.848433	-3.699912	35346.345712
HLA B*0802	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.467395	0.767455	-3.699941	29335.626298
HLA B*1501	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.289506	0.589436	-3.700070	19476.300073
HLA A*0250	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.582177	0.882099	-3.700078	38210.005911
HLA A*2601	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.396121	0.695802	-3.700320	24895.530640
HLA A*8001	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.396239	0.695802	-3.700437	24902.265654
HLA A*2602	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.494391	0.793787	-3.700604	31216.984393
HLA B*1509	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.386848	0.686161	-3.700687	24369.575842
HLA B*5101	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.370467	0.669638	-3.700830	23467.528870
HLA A*0301	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.335352	0.634444	-3.700908	21644.719297
HLA B*3901	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.494809	0.793787	-3.701022	31247.059587
HLA A*0202	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.318581	0.617415	-3.701166	20824.823729
HLA B*3501	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.475003	0.773810	-3.701193	29854.032208
HLA A*0211	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.397005	0.695802	-3.701203	24946.222634
HLA A*0202	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.452819	0.751562	-3.701258	28367.375640
HLA A*0201	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.392308	0.691047	-3.701261	24677.898486
HLA A*0211	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.503913	0.802529	-3.701385	31909.015868
HLA A*0212	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.392665	0.691047	-3.701618	24698.199545
HLA B*0802	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.490909	0.789030	-3.701879	30967.704235
HLA A*3001	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.056033	0.353947	-3.702086	11377.148677
HLA A*1101	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.439491	0.737162	-3.702329	27509.996251
HLA A*6801	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.601020	0.898490	-3.702530	39904.325522
HLA B*4002	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.633993	0.931448	-3.702545	43051.932146
HLA B*0702	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.320205	0.617415	-3.702790	20902.817469
HLA B*3901	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.489006	0.786144	-3.702862	30832.300326
HLA A*0212	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.399411	0.695802	-3.703609	25084.801374
HLA B*5101	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.506181	0.802529	-3.703652	32076.033841
HLA A*3101	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.272581	0.568895	-3.703686	18731.854131
HLA A*0101	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.380406	0.676597	-3.703808	24010.747594
HLA A*2602	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.594843	0.890279	-3.704564	39340.799223
HLA A*2601	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.383723	0.679020	-3.704703	24194.862325

HLA B*0802	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.473511	0.768800	-3.704711	29751.651214
HLA A*2603	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.636173	0.931448	-3.704725	43268.612535
HLA A*3201	1:83-91	9	NRFISGASA	0.946143	-0.055864	-4.595031	0.890279	-3.704752	39357.829257
HLA B*4001	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.389891	0.685107	-3.704783	24540.903818
HLA A*2601	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.219304	0.514013	-3.705291	16569.287944
HLA A*2601	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.373315	0.667908	-3.705407	23621.905982
HLA B*4402	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.390617	0.685107	-3.705509	24581.962069
HLA A*2403	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.396676	0.691047	-3.705629	24927.335906
HLA A*3101	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.317844	0.612174	-3.705669	20789.478522
HLA A*0201	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.391848	0.686161	-3.705686	24651.745434
HLA B*4001	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.375331	0.669638	-3.705693	23731.806290
HLA B*4001	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.401525	0.695802	-3.705724	25207.234585
HLA A*0301	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.365620	0.659875	-3.705746	23207.073261
HLA A*2601	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.391004	0.685107	-3.705897	24603.914504
HLA A*0219	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.393004	0.687090	-3.705914	24717.447533
HLA A*2501	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.443116	0.737162	-3.705954	27740.595937
HLA B*4001	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.392306	0.686161	-3.706145	24677.764982
HLA A*2603	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.585426	0.879222	-3.706204	38496.960605
HLA A*2603	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.477230	0.770901	-3.706329	30007.534135
HLA B*2705	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.399787	0.693390	-3.706396	25106.523733
HLA A*2601	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.397731	0.691047	-3.706684	24987.959005
HLA B*0803	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.500497	0.793787	-3.706710	31659.004805
HLA B*3901	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.458402	0.751562	-3.706840	28734.360493
HLA B*0803	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.480719	0.773810	-3.706909	30249.576166
HLA A*0211	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.392026	0.685107	-3.706919	24661.883122
HLA B*1501	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.398274	0.691047	-3.707226	25019.205588
HLA B*2705	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.079373	0.371790	-3.707584	12005.305540
HLA B*1501	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.276662	0.568895	-3.707767	18908.706579
HLA B*4601	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.323189	0.615291	-3.707898	21046.926001
HLA B*1517	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.393088	0.685107	-3.707981	24722.261873
HLA B*1509	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.490190	0.782174	-3.708016	30916.481899
HLA A*2402	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.528071	0.820012	-3.708059	33734.231021
HLA A*1101	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.323468	0.615291	-3.708177	21060.479886
HLA A*3301	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.639669	0.931448	-3.708221	43618.326887
HLA A*6901	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.323522	0.615291	-3.708231	21063.100551
HLA B*3901	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.497300	0.789030	-3.708270	31426.760055
HLA A*3201	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.502067	0.793787	-3.708279	31773.621281
HLA B*4801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.393838	0.685107	-3.708730	24764.963266
HLA B*3901	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.399874	0.691047	-3.708826	25111.549706
HLA B*1502	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.591173	0.882099	-3.709074	39009.760408
HLA B*1517	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.493414	0.784035	-3.709378	31146.809131
HLA A*0301	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.223434	0.514013	-3.709421	16727.623305
HLA B*5401	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.554643	0.844974	-3.709670	35862.741858
HLA A*2501	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.402531	0.692679	-3.709852	25265.667860
HLA A*6802	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.405966	0.695802	-3.710164	25466.292895
HLA B*4001	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.403229	0.692679	-3.710549	25306.295775
HLA B*1503	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.279599	0.568895	-3.710703	19037.007407
HLA A*2902	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.395962	0.685107	-3.710854	24886.373944
HLA A*6801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.397947	0.687090	-3.710857	25000.398853
HLA A*3301	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.378874	0.667908	-3.710966	23926.204928
HLA A*6801	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.588243	0.877206	-3.711037	38747.481105
HLA A*0101	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.390090	0.679020	-3.711070	24552.191316
HLA B*3501	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.300573	0.589436	-3.711137	19978.944088
HLA A*2601	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.380923	0.669638	-3.711285	24039.341613
HLA B*5701	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.380965	0.669638	-3.711327	24041.682630

HLA A*0211	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.326673	0.615291	-3.711382	21216.461832
HLA B*4601	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.383422	0.672009	-3.711413	24178.114009
HLA B*5101	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.405353	0.693390	-3.711962	25430.360346
HLA A*0301	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.348859	0.636799	-3.712060	22328.479360
HLA A*0201	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.388948	0.676597	-3.712351	24487.723331
HLA A*1101	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.463331	0.750956	-3.712375	29062.351795
HLA A*1101	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.496463	0.784035	-3.712428	31366.292859
HLA A*0201	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.391556	0.679020	-3.712536	24635.213941
HLA B*4001	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.389150	0.676597	-3.712553	24499.118907
HLA B*4403	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.644102	0.931448	-3.712655	44065.883412
HLA A*2603	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.480158	0.767455	-3.712703	30210.489842
HLA A*2403	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.226761	0.514013	-3.712748	16856.255700
HLA A*3101	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.349834	0.636799	-3.713035	22378.665434
HLA B*3901	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.497116	0.784035	-3.713081	31413.501660
HLA A*0202	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.003142	0.289672	-3.713470	10072.605552
HLA B*0801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.235776	0.522301	-3.713475	17209.810355
HLA B*5101	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.499900	0.786144	-3.713756	31615.531667
HLA A*0216	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.407352	0.693390	-3.713962	25547.706951
HLA A*0206	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.306519	0.592259	-3.714260	20254.385799
HLA B*1502	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.303742	0.589436	-3.714306	20125.282567
HLA A*3002	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.483597	0.768800	-3.714797	30450.709292
HLA B*5701	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.401076	0.686161	-3.714915	25181.201683
HLA B*5301	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.597132	0.882099	-3.715032	39548.642127
HLA B*0803	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.504080	0.789030	-3.715051	31921.274543
HLA A*0216	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.297201	0.581978	-3.715223	19824.444212
HLA B*4601	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.401605	0.686161	-3.715444	25211.871535
HLA B*1509	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.482909	0.767455	-3.715454	30402.480182
HLA A*2501	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.305098	0.589436	-3.715662	20188.201909
HLA A*3001	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-3.887448	0.171766	-3.715682	7716.999758
HLA B*2705	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.401856	0.686161	-3.715695	25226.469857
HLA A*3301	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.518417	0.802529	-3.715888	32992.618170
HLA B*4402	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.394935	0.679020	-3.715915	24827.609022
HLA A*0219	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.392531	0.676597	-3.715934	24690.584692
HLA B*5701	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.406997	0.691047	-3.715950	25526.845723
HLA A*2501	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.230187	0.514013	-3.716174	16989.737146
HLA B*4601	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.392778	0.676597	-3.716181	24704.613875
HLA A*2602	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.598356	0.882099	-3.716256	39660.269281
HLA B*4402	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.403543	0.687090	-3.716454	25324.647597
HLA A*0301	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.364004	0.647511	-3.716492	23120.856996
HLA A*3101	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.371748	0.654994	-3.716754	23536.822390
HLA B*0702	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.412756	0.695802	-3.716954	25867.576455
HLA B*0801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.351472	0.634444	-3.717028	22463.207796
HLA A*6802	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.143415	0.426351	-3.717064	13912.830037
HLA A*6802	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.403337	0.686161	-3.717175	25312.594155
HLA B*1801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.484941	0.767455	-3.717487	30545.083633
HLA B*0801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.332822	0.615291	-3.717530	21518.974089
HLA B*4501	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.335108	0.617415	-3.717692	21632.544787
HLA A*0250	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.154665	0.436810	-3.717855	14277.915714
HLA A*6901	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.310170	0.592259	-3.717912	20425.381538
HLA A*6801	1:30-38	9	AATGPGRIP	0.760169	0.171279	-4.649377	0.931448	-3.717929	44604.335616
HLA B*3801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.491900	0.773810	-3.718090	31038.483437
HLA B*5301	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.600642	0.882547	-3.718094	39869.584299
HLA A*0212	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.365616	0.647511	-3.718104	23206.822167
HLA A*3001	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.195020	0.476646	-3.718373	15668.216658
HLA A*2902	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.414210	0.695802	-3.718408	25954.344962
HLA B*1801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.502445	0.784035	-3.718410	31801.307912

HLA B*4601	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.397740	0.679020	-3.718720	24988.499740
HLA A*3002	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.232799	0.514013	-3.718786	17092.251996
HLA A*1101	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.489701	0.770901	-3.718800	30881.712479
HLA A*0203	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.405230	0.686161	-3.719069	25423.207430
HLA B*5801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.353685	0.634444	-3.719241	22577.975085
HLA A*3101	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.411924	0.692679	-3.719245	25818.084845
HLA B*5401	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.539266	0.820012	-3.719254	34615.141463
HLA A*3201	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.601466	0.882099	-3.719367	39945.363425
HLA B*4001	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.412876	0.693390	-3.719485	25874.714416
HLA A*3001	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.308951	0.589436	-3.719515	20368.112966
HLA B*1517	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.285068	0.565473	-3.719595	19278.279833
HLA B*1503	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.503634	0.784035	-3.719598	31888.480195
HLA A*6901	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.339640	0.620011	-3.719629	21859.477055
HLA B*3501	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.379623	0.659875	-3.719749	23967.531337
HLA B*4501	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.522399	0.802529	-3.719870	33296.543964
HLA B*1509	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.488818	0.768800	-3.720018	30818.959267
HLA B*1501	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.367531	0.647511	-3.720019	23309.368330
HLA A*0206	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.315943	0.595896	-3.720047	20698.690101
HLA A*0201	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.392191	0.672009	-3.720181	24671.224154
HLA B*5101	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.494360	0.773810	-3.720550	31214.789024
HLA B*4601	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.411694	0.691047	-3.720647	25804.400522
HLA A*3101	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.380617	0.659875	-3.720743	24022.441034
HLA A*0203	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.392823	0.672009	-3.720813	24707.153341
HLA B*1801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.310321	0.589436	-3.720885	20432.454701
HLA A*2601	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.392997	0.672009	-3.720987	24717.046380
HLA B*4501	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.491903	0.770901	-3.721002	31038.651352
HLA A*3101	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.412150	0.691047	-3.721102	25831.496934
HLA B*5101	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.472686	0.751562	-3.721125	29695.210268
HLA B*1503	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.472261	0.750956	-3.721305	29666.147248
HLA A*2601	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.376332	0.654994	-3.721338	23786.561985
HLA B*4402	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.417267	0.695802	-3.721465	26137.662903
HLA A*0206	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.118633	0.397004	-3.721630	13141.142112
HLA A*3001	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.303690	0.581978	-3.721712	20122.887448
HLA B*2705	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.472670	0.750956	-3.721714	29694.085755
HLA B*1801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.415211	0.693390	-3.721821	26014.228655
HLA B*1501	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.257149	0.535260	-3.721889	18077.957026
HLA B*1503	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.287418	0.565473	-3.721944	19382.855807
HLA A*2902	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.408231	0.686161	-3.722069	25599.449917
HLA A*0219	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.459487	0.737162	-3.722325	28806.268081
HLA A*2902	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.459612	0.737162	-3.722450	28814.528717
HLA A*0101	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.394531	0.672009	-3.722522	24804.517654
HLA A*2603	1:262-270	9	GGAFLIGLV	1.032037	-0.096746	-4.658242	0.935291	-3.722951	45524.132827
HLA A*0202	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.206278	0.483198	-3.723080	16079.713277
HLA B*4001	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.402263	0.679020	-3.723243	25250.090635
HLA A*2601	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.319171	0.595896	-3.723275	20853.120594
HLA A*0216	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.319211	0.595896	-3.723315	20855.038504
HLA B*1801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.512374	0.789030	-3.723344	32536.730153
HLA B*0802	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.474336	0.750956	-3.723380	29808.199437
HLA A*6901	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.319519	0.595896	-3.723623	20869.823614
HLA B*4402	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.395673	0.672009	-3.723663	24869.819652
HLA A*0202	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.512839	0.789030	-3.723810	32571.600807
HLA A*3101	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.402841	0.679020	-3.723821	25283.716652
HLA A*8001	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.461421	0.737162	-3.724259	28934.809287
HLA A*6901	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.379426	0.654994	-3.724432	23956.642229
HLA B*0803	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.509571	0.785097	-3.724474	32327.414359

HLA A*6802	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.341996	0.617415	-3.724581	21978.411560
HLA B*3501	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.344607	0.620011	-3.724596	22110.908094
HLA A*1101	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.493430	0.768800	-3.724630	31147.988659
HLA A*3002	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.507052	0.782174	-3.724878	32140.477300
HLA A*0206	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.527483	0.802529	-3.724955	33688.637247
HLA B*1801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.510109	0.785097	-3.725012	32367.488467
HLA B*4501	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.623599	0.898490	-3.725108	42033.787609
HLA B*5301	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.585936	0.860615	-3.725321	38542.180493
HLA A*8001	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.418834	0.693390	-3.725444	26232.148311
HLA B*0802	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.412789	0.687090	-3.725699	25869.535699
HLA A*2501	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.510097	0.784035	-3.726062	32366.612956
HLA B*1509	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.515442	0.789030	-3.726413	32767.426419
HLA B*5101	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.510452	0.784035	-3.726417	32393.063826
HLA A*0216	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.463674	0.737162	-3.726512	29085.315581
HLA A*2501	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.511676	0.785097	-3.726579	32484.494159
HLA B*4403	1:203-211	9	KVSLLLSVA	1.041697	-0.105882	-4.662668	0.935815	-3.726853	45990.497924
HLA B*4402	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.403489	0.676597	-3.726892	25321.496711
HLA A*0216	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.412131	0.685107	-3.727024	25830.378994
HLA A*0216	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.406090	0.679020	-3.727070	25473.595743
HLA B*0803	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.509298	0.782174	-3.727124	32307.133746
HLA A*3001	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.210578	0.483430	-3.727148	16239.694608
HLA B*4801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.414250	0.687090	-3.727160	25956.732044
HLA A*2403	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.374786	0.647511	-3.727274	23702.039320
HLA A*2403	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.399328	0.672009	-3.727319	25080.052114
HLA B*4801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.423159	0.695802	-3.727358	26494.715533
HLA A*2602	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.414461	0.687090	-3.727372	25969.373195
HLA B*1502	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.576205	0.848433	-3.727772	37688.140824
HLA B*4001	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.343082	0.615291	-3.727791	22033.412420
HLA B*1503	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.516876	0.789030	-3.727846	32875.738606
HLA A*2601	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.404598	0.676597	-3.728001	25386.236955
HLA B*1509	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.514176	0.786144	-3.728032	32672.018059
HLA B*1801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.419118	0.691047	-3.728071	26249.325407
HLA B*4002	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.626648	0.898490	-3.728158	42329.989135
HLA A*2403	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.413606	0.685107	-3.728499	25918.284633
HLA B*3901	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.497396	0.768800	-3.728596	31433.731455
HLA B*4801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.396509	0.667908	-3.728601	24917.763101
HLA B*3801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.515231	0.786144	-3.729087	32751.476170
HLA B*3801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.466531	0.737162	-3.729369	29277.281880
HLA B*1801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.515520	0.786144	-3.729376	32773.276790
HLA A*2601	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.389705	0.659875	-3.729830	24530.417737
HLA A*0250	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.523713	0.793787	-3.729925	33397.389383
HLA B*1509	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.523849	0.793787	-3.730061	33407.870246
HLA A*2602	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.590884	0.860615	-3.730269	38983.811310
HLA B*1509	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.423025	0.692679	-3.730346	26486.546784
HLA B*5701	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.415587	0.685107	-3.730480	26036.755858
HLA A*0216	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.345922	0.615291	-3.730631	22177.995499
HLA B*1501	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.350642	0.620011	-3.730631	22420.350948
HLA B*5801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.348077	0.617415	-3.730661	22288.290969
HLA A*0101	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.390609	0.659875	-3.730735	24581.563115
HLA B*5301	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.593300	0.862516	-3.730784	39201.218534
HLA B*0801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.390706	0.659875	-3.730831	24587.016044
HLA B*5101	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.426749	0.695802	-3.730948	26714.636797
HLA B*5701	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.410115	0.679020	-3.731095	25710.760345
HLA A*0101	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.348648	0.617415	-3.731232	22317.610492
HLA A*2902	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.424691	0.693390	-3.731301	26588.333968
HLA B*7301	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.505274	0.773810	-3.731463	32009.122003

HLA B*4801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.424207	0.692679	-3.731528	26558.719446
HLA B*0801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.410637	0.679020	-3.731617	25741.657399
HLA B*1517	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.408282	0.676597	-3.731685	25602.496882
HLA B*7301	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.550057	0.818322	-3.731736	35486.020199
HLA B*0803	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.499348	0.767455	-3.731894	31575.363623
HLA A*1101	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.428260	0.695802	-3.732458	26807.727046
HLA B*3901	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.400369	0.667908	-3.732461	25140.230570
HLA A*6901	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.249939	0.517364	-3.732574	17780.287547
HLA B*1503	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.502135	0.768800	-3.733335	31778.606534
HLA B*5701	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.410141	0.676597	-3.733543	25712.290406
HLA A*0212	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.251088	0.517364	-3.733723	17827.386427
HLA A*0211	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.504729	0.770901	-3.733828	31968.972738
HLA A*3001	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.215629	0.481784	-3.733845	16429.685521
HLA B*0803	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.484866	0.750956	-3.733910	30539.796234
HLA B*5701	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.406299	0.672009	-3.734290	25485.863726
HLA B*3901	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.371207	0.636799	-3.734409	23507.554334
HLA B*5301	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.349973	0.615291	-3.734682	22385.809474
HLA A*0101	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.371492	0.636799	-3.734693	23522.947337
HLA B*5401	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.523781	0.789030	-3.734751	33402.629403
HLA B*4402	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.421421	0.686161	-3.735259	26388.860789
HLA B*3901	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.486255	0.750956	-3.735298	30637.595690
HLA A*8001	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.420469	0.685107	-3.735362	26331.105954
HLA A*6901	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.372655	0.636799	-3.735856	23586.023741
HLA B*4402	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.428650	0.692679	-3.735971	26831.812313
HLA B*4801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.422692	0.686161	-3.736531	26466.207520
HLA A*6901	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.338998	0.602429	-3.736570	21827.216628
HLA B*1509	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.556800	0.820012	-3.736788	36041.289203
HLA B*0702	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.404775	0.667908	-3.736866	25396.539300
HLA A*0212	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.423350	0.686161	-3.737188	26506.328088
HLA A*3002	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.526297	0.789030	-3.737267	33596.725700
HLA A*2403	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.319267	0.581978	-3.737289	20857.746443
HLA B*5701	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.352600	0.615291	-3.737308	22521.614860
HLA A*0101	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.333338	0.595896	-3.737442	21544.600695
HLA B*2705	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.506244	0.768800	-3.737444	32080.719434
HLA B*3501	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.409560	0.672009	-3.737551	25677.955493
HLA B*1517	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.428685	0.691047	-3.737638	26833.989759
HLA A*0101	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.393004	0.654994	-3.738010	24717.447533
HLA B*5801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.350189	0.612174	-3.738015	22396.953883
HLA B*0801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.385755	0.647511	-3.738244	24308.348818
HLA B*5301	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.558534	0.820012	-3.738522	36185.471617
HLA A*0201	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.398560	0.659875	-3.738686	25035.723876
HLA B*0702	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.410728	0.672009	-3.738719	25747.089093
HLA B*5701	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.252840	0.514013	-3.738827	17899.479166
HLA B*4801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.430107	0.691047	-3.739060	26921.960834
HLA B*4501	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.521304	0.782174	-3.739130	33212.708818
HLA A*6802	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.375972	0.636799	-3.739173	23766.881684
HLA B*4001	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.411205	0.672009	-3.739196	25775.380271
HLA A*3101	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.222650	0.483430	-3.739219	16697.425403
HLA B*5401	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.490827	0.751562	-3.739265	30961.841175
HLA B*0801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.229975	0.490659	-3.739316	16981.467026
HLA B*4501	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.621456	0.882099	-3.739357	41826.911278
HLA B*4801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.409051	0.669638	-3.739413	25647.828648
HLA B*5101	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.507031	0.767455	-3.739577	32138.912450
HLA B*3501	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.262386	0.522301	-3.740085	18297.272319
HLA A*2902	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.387616	0.647511	-3.740105	24412.724598

HLA B*0702	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.376992	0.636799	-3.740193	23822.749312
HLA B*1517	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.491151	0.750956	-3.740195	30984.964823
HLA B*3901	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.257657	0.517364	-3.740293	18099.094118
HLA A*0101	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.355668	0.615291	-3.740377	22681.300619
HLA B*0702	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.419407	0.679020	-3.740387	26266.797950
HLA A*2602	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.507976	0.767455	-3.740521	32208.883425
HLA B*3501	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.374990	0.634444	-3.740547	23713.197556
HLA A*0219	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.419734	0.679020	-3.740714	26286.557343
HLA B*1801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.408834	0.667908	-3.740926	25635.066649
HLA B*1502	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.601570	0.860615	-3.740955	39954.872956
HLA A*2301	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.530026	0.789030	-3.740996	33886.411959
HLA A*3201	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.514824	0.773810	-3.741014	32720.838048
HLA B*4402	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.432184	0.691047	-3.741137	27051.019213
HLA B*4002	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.603712	0.862516	-3.741197	40152.490166
HLA B*0801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.378040	0.636799	-3.741241	23880.298493
HLA B*5801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.341155	0.599894	-3.741262	21935.886277
HLA A*0211	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.178146	0.436810	-3.741336	15071.121360
HLA A*0301	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.358767	0.617415	-3.741352	22843.725113
HLA A*2402	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.492974	0.751562	-3.741413	31115.315417
HLA B*4001	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.388934	0.647511	-3.741423	24486.928489
HLA B*0802	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.478656	0.737162	-3.741495	30106.234925
HLA B*5101	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.512449	0.770901	-3.741548	32542.363284
HLA B*3901	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.428706	0.687090	-3.741617	26835.296311
HLA B*2705	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.411503	0.669638	-3.741866	25793.095484
HLA A*0101	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.376313	0.634444	-3.741869	23785.532546
HLA A*6802	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.414093	0.672009	-3.742083	25947.325405
HLA B*3801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.531151	0.789030	-3.742121	33974.336942
HLA B*4403	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.621395	0.879222	-3.742172	41821.028439
HLA A*2301	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.544919	0.802529	-3.742390	35068.643869
HLA A*3101	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.390083	0.647511	-3.742572	24551.792845
HLA A*2403	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.412457	0.669638	-3.742820	25849.810087
HLA A*2602	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.562857	0.820012	-3.742845	36547.467595
HLA B*5801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.362970	0.620011	-3.742959	23065.886686
HLA A*0250	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.545532	0.802529	-3.743003	35118.195105
HLA B*1517	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.410963	0.667908	-3.743055	25761.021751
HLA A*0219	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.415126	0.672009	-3.743117	26009.162721
HLA B*4402	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.411088	0.667908	-3.743179	25768.409117
HLA B*1501	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.169570	0.426351	-3.743218	14776.444494
HLA B*5401	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.413270	0.669638	-3.743632	25898.241635
HLA A*2602	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.398868	0.654994	-3.743874	25053.472869
HLA A*0201	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.380758	0.636799	-3.743959	24030.239824
HLA A*1101	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.416148	0.672009	-3.744139	26070.442206
HLA A*2403	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.381017	0.636799	-3.744218	24044.544183
HLA A*0201	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.399213	0.654994	-3.744219	25073.404660
HLA B*1502	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-3.986146	0.241837	-3.744308	9686.026494
HLA A*0216	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.416383	0.672009	-3.744374	26084.549842
HLA A*3001	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.170834	0.426351	-3.744482	14819.514283
HLA A*0250	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.431613	0.687090	-3.744523	27015.481225
HLA A*2902	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.423754	0.679020	-3.744734	26531.003730
HLA B*3801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.512285	0.767455	-3.744830	32530.042077
HLA A*0301	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.364852	0.620011	-3.744841	23166.055457
HLA A*0301	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.357134	0.612174	-3.744960	22757.996874
HLA B*4601	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.362378	0.617415	-3.744963	23034.462571
HLA B*3801	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.564977	0.820012	-3.744964	36726.244841
HLA A*6801	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.590140	0.844974	-3.745166	38917.013906

HLA A*0212	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.424202	0.679020	-3.745182	26558.432088
HLA B*1517	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.516152	0.770901	-3.745251	32821.005155
HLA B*1503	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.382149	0.636799	-3.745350	24107.323748
HLA A*2902	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.417434	0.672009	-3.745424	26147.704363
HLA A*2301	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.539534	0.793787	-3.745747	34636.496152
HLA A*0216	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.422520	0.676597	-3.745923	26455.757498
HLA A*2603	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.628509	0.882547	-3.745961	42511.746673
HLA A*6802	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.437031	0.691047	-3.745983	27354.615863
HLA B*1503	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.282148	0.535260	-3.746888	19149.078085
HLA A*0219	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.433130	0.686161	-3.746969	27110.059785
HLA B*5801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.349418	0.602429	-3.746989	22357.246990
HLA B*1503	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.269423	0.522301	-3.747122	18596.150801
HLA A*2501	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.416961	0.669638	-3.747323	26119.287124
HLA B*4403	1:58-66	9	HRQPPPVSH	1.107246	-0.208756	-4.646177	0.898490	-3.747687	44276.886719
HLA A*2603	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.596248	0.848433	-3.747815	39468.277273
HLA A*1101	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.424506	0.676597	-3.747908	26576.973041
HLA A*0203	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.439037	0.691047	-3.747990	27481.287818
HLA B*4501	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.610613	0.862516	-3.748097	40795.562142
HLA B*1501	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.360341	0.612174	-3.748167	22926.675308
HLA A*3001	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.146235	0.397920	-3.748315	14003.444088
HLA A*2601	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.385128	0.636799	-3.748329	24273.262203
HLA B*2705	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.433499	0.685107	-3.748392	27133.095566
HLA B*4801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.427755	0.679020	-3.748735	26776.564404
HLA B*3901	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.444711	0.695802	-3.748909	27842.683262
HLA B*5401	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.486370	0.737162	-3.749208	30645.718321
HLA B*1509	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.440308	0.691047	-3.749261	27561.836493
HLA B*4801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.421423	0.672009	-3.749414	26389.003550
HLA B*1801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.531607	0.782174	-3.749432	34010.012354
HLA A*0216	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.349578	0.599894	-3.749684	22365.473119
HLA B*3501	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.386676	0.636799	-3.749878	24359.953663
HLA B*1801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.500951	0.750956	-3.749995	31692.077507
HLA B*4601	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.397837	0.647511	-3.750325	24994.042940
HLA A*0219	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.441387	0.691047	-3.750339	27630.361410
HLA A*0203	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.350250	0.599894	-3.750356	22400.104396
HLA A*3002	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.308457	0.557970	-3.750488	20344.986366
HLA B*5301	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.595778	0.844974	-3.750805	39425.596566
HLA B*0702	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.436972	0.686161	-3.750811	27350.916477
HLA A*2902	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.441979	0.691047	-3.750932	27668.055351
HLA B*1509	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.524812	0.773810	-3.751002	33482.052965
HLA A*2902	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.234526	0.483430	-3.751096	17160.350679
HLA A*2501	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.444551	0.693390	-3.751161	27832.442589
HLA A*8001	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.427839	0.676597	-3.751242	26781.779809
HLA A*0219	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.351580	0.599894	-3.751686	22468.798571
HLA A*3001	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.297210	0.545171	-3.752039	19824.873209
HLA A*2402	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.546002	0.793787	-3.752215	35156.212777
HLA B*0803	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.523163	0.770901	-3.752262	33355.137908
HLA A*3301	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.634448	0.882099	-3.752349	43097.139664
HLA A*3101	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.369873	0.617415	-3.752458	23435.430789
HLA B*3901	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.438901	0.686161	-3.752740	27472.666268
HLA B*7301	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.546528	0.793787	-3.752741	35198.841433
HLA B*1501	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.413028	0.659875	-3.753154	25883.814673
HLA B*4402	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.365465	0.612174	-3.753291	23198.788593
HLA B*4601	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.413402	0.659875	-3.753527	25906.088794
HLA B*5701	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.413691	0.659875	-3.753816	25923.332866

HLA B*1509	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.430485	0.676597	-3.753888	26945.419866
HLA A*2902	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.430492	0.676597	-3.753895	26945.857185
HLA A*1101	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.322874	0.568895	-3.753979	21031.674084
HLA A*3002	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.447404	0.693390	-3.754013	28015.836661
HLA B*2705	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.369318	0.615291	-3.754027	23405.529074
HLA B*2705	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.450004	0.695802	-3.754203	28184.119826
HLA B*1509	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.538404	0.784035	-3.754368	34546.483726
HLA B*4601	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.391190	0.636799	-3.754391	24614.432003
HLA B*0803	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.523593	0.768800	-3.754793	33388.176170
HLA A*2402	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.543824	0.789030	-3.754795	34980.346871
HLA B*3801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.538876	0.784035	-3.754841	34584.069580
HLA B*1502	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.372302	0.617415	-3.754887	23566.891839
HLA A*3001	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-3.715678	-0.039278	-3.754955	5196.101646
HLA B*0803	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.448428	0.693390	-3.755038	28081.995936
HLA B*5701	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.402561	0.647511	-3.755050	25267.444820
HLA B*5101	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.447812	0.692679	-3.755133	28042.220964
HLA B*4601	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.410582	0.654994	-3.755589	25738.454630
HLA A*0211	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.539741	0.784035	-3.755705	34652.989483
HLA A*8001	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.442023	0.686161	-3.755862	27670.899438
HLA A*2601	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.403496	0.647511	-3.755985	25321.907674
HLA A*1101	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.442390	0.686161	-3.756229	27694.261949
HLA B*5801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.352155	0.595896	-3.756259	22498.598975
HLA A*2603	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.638431	0.882099	-3.756332	43494.147634
HLA B*0803	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.325233	0.568895	-3.756337	21146.219021
HLA A*2501	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.391002	0.634444	-3.756558	24603.781400
HLA A*3001	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.277914	0.521317	-3.756597	18963.307968
HLA B*4402	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.426357	0.669638	-3.756719	26690.512318
HLA A*6801	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.619292	0.862516	-3.756776	41619.026685
HLA A*0212	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.338874	0.581978	-3.756896	21820.959136
HLA B*5101	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.494135	0.737162	-3.756973	31198.581853
HLA A*2501	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.448066	0.691047	-3.757019	28058.609924
HLA A*0202	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.559615	0.802529	-3.757086	36275.633076
HLA A*0216	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.374508	0.617415	-3.757093	23686.913551
HLA A*2301	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.543347	0.786144	-3.757203	34941.952278
HLA A*6802	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-3.731617	-0.025677	-3.757294	5390.344777
HLA A*0206	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.541461	0.784035	-3.757425	34790.488739
HLA A*3001	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.292695	0.535260	-3.757435	19619.805977
HLA B*4402	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.417633	0.659875	-3.757759	26159.730904
HLA A*0202	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.429919	0.672009	-3.757909	26910.311769
HLA A*0203	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.076512	0.318175	-3.758337	11926.459693
HLA B*4001	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.392827	0.634444	-3.758384	24707.420668
HLA B*0802	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.444850	0.686161	-3.758688	27851.571604
HLA B*0802	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.451459	0.692679	-3.758780	28278.658794
HLA B*2705	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.450054	0.691047	-3.759007	28187.321940
HLA B*5301	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.510835	0.751562	-3.759273	32421.641014
HLA B*4002	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.641412	0.882099	-3.759313	43793.768747
HLA B*4001	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.371581	0.612174	-3.759407	23527.783582
HLA A*0212	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.376830	0.617415	-3.759414	23813.858360
HLA A*8001	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.450498	0.691047	-3.759451	28216.157343
HLA A*2501	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.436305	0.676597	-3.759707	27308.926561
HLA B*5401	1:3-11	9	APNEPGALS	0.822079	-1.082447	-3.499445	-0.260368	-3.759813	3158.240042
HLA A*8001	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.438863	0.679020	-3.759843	27470.288386
HLA A*3301	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.639133	0.879222	-3.759911	43564.558823
HLA A*2301	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.542313	0.782174	-3.760139	34858.877073
HLA B*1801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.533954	0.773810	-3.760144	34194.316345

HLA A*0206	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.528989	0.768800	-3.760189	33805.663437
HLA B*5801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.352719	0.592259	-3.760461	22527.829529
HLA B*3501	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.446654	0.686161	-3.760493	27967.529895
HLA A*3301	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.643151	0.882547	-3.760603	43969.440529
HLA A*2501	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.445773	0.685107	-3.760666	27910.849445
HLA A*0301	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.363097	0.602429	-3.760668	23072.626001
HLA B*1509	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.545781	0.785097	-3.760685	35138.339348
HLA B*1503	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.342830	0.581978	-3.760852	22020.661891
HLA B*1502	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.437533	0.676597	-3.760936	27386.303086
HLA B*1503	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.073438	0.312492	-3.760947	11842.364340
HLA B*5801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.350452	0.589436	-3.761016	22410.528480
HLA A*0211	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.498385	0.737162	-3.761223	31505.405359
HLA A*0301	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.330134	0.568895	-3.761239	21386.206295
HLA B*4001	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.416322	0.654994	-3.761328	26080.881122
HLA B*4501	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.454790	0.693390	-3.761400	28496.424885
HLA B*5401	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.563940	0.802529	-3.761412	36638.729231
HLA B*0702	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.416682	0.654994	-3.761688	26102.477544
HLA A*0219	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.379156	0.617415	-3.761740	23941.742545
HLA B*0802	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.433762	0.672009	-3.761753	27149.540696
HLA A*2902	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.416785	0.654994	-3.761791	26108.691590
HLA A*0203	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.416804	0.654994	-3.761810	26109.821575
HLA B*1517	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.409335	0.647511	-3.761823	25664.623126
HLA B*1503	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.276072	0.514013	-3.762059	18883.048208
HLA B*7301	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.564765	0.802529	-3.762236	36708.367551
HLA B*5801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.116331	0.353947	-3.762383	13071.656191
HLA A*2902	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.399397	0.636799	-3.762598	25083.987152
HLA B*5101	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.513795	0.750956	-3.762839	32643.396780
HLA A*1101	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.399841	0.636799	-3.763042	25109.647868
HLA A*2301	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.536888	0.773810	-3.763078	34426.148040
HLA B*0702	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.410606	0.647511	-3.763094	25739.847089
HLA B*1501	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.345100	0.581978	-3.763122	22136.042056
HLA A*6901	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.380615	0.617415	-3.763199	24022.311076
HLA B*0802	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.459010	0.695802	-3.763208	28774.650186
HLA B*7301	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.583364	0.820012	-3.763352	38314.538145
HLA B*4001	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.380908	0.617415	-3.763493	24038.561324
HLA A*2601	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.383561	0.620011	-3.763550	24185.832495
HLA B*3901	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.456987	0.693390	-3.763597	28640.931990
HLA B*5701	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.400435	0.636799	-3.763636	25144.039023
HLA B*1501	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.366118	0.602429	-3.763690	23233.704641
HLA A*1101	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.411266	0.647511	-3.763755	25779.006017
HLA A*0250	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.548852	0.785097	-3.763755	35387.673333
HLA A*0301	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.363689	0.599894	-3.763795	23104.102179
HLA B*5401	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.534854	0.770901	-3.763953	34265.239994
HLA B*1502	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.546167	0.782174	-3.763992	35169.528683
HLA A*2301	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.549092	0.785097	-3.763995	35407.205948
HLA B*0801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.356258	0.592259	-3.763999	22712.120073
HLA B*3501	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.199719	0.435662	-3.764057	15838.663725
HLA A*0201	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.381479	0.617415	-3.764064	24070.183271
HLA B*1502	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.398532	0.634444	-3.764088	25034.098643
HLA B*4801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.411792	0.647511	-3.764281	25810.264343
HLA A*0212	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.379783	0.615291	-3.764492	23976.349954
HLA A*2403	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.352266	0.587655	-3.764611	22504.320304
HLA B*5801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.352301	0.587655	-3.764646	22506.146566
HLA A*3301	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.287124	0.522301	-3.764823	19369.752850
HLA B*1509	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.451931	0.687090	-3.764842	28309.425385
HLA A*6901	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.377076	0.612174	-3.764902	23827.389388

HLA B*4402	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.420049	0.654994	-3.765055	26305.620038
HLA B*0802	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.450199	0.685107	-3.765092	28196.777923
HLA B*3801	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.559115	0.793787	-3.765327	36233.856506
HLA B*5701	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.420392	0.654994	-3.765398	26326.405577
HLA B*4001	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.425380	0.659875	-3.765505	26630.512490
HLA B*4403	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.647789	0.882099	-3.765690	44441.511678
HLA A*0216	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.202571	0.436810	-3.765761	15943.028156
HLA B*7301	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.554799	0.789030	-3.765769	35875.549032
HLA B*5401	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.552301	0.786144	-3.766157	35669.831155
HLA B*1509	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.503519	0.737162	-3.766357	31880.028171
HLA A*2301	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.535248	0.768800	-3.766448	34296.396503
HLA A*0212	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.438485	0.672009	-3.766476	27446.372397
HLA B*5101	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.381869	0.615291	-3.766578	24091.809006
HLA B*2705	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.459266	0.692679	-3.766587	28791.622966
HLA B*3801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.537516	0.770901	-3.766615	34475.910489
HLA B*1501	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.189470	0.422812	-3.766658	15469.279440
HLA B*0803	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.503869	0.737162	-3.766707	31905.736176
HLA A*0216	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.457791	0.691047	-3.766744	28693.971981
HLA A*0250	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.518487	0.751562	-3.766926	32997.973197
HLA A*0101	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.386954	0.620011	-3.766943	24375.509216
HLA A*0203	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.284342	0.517364	-3.766978	19246.080107
HLA A*2501	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.434921	0.667908	-3.767013	27222.047213
HLA A*2601	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.369495	0.602429	-3.767066	23415.027600
HLA A*0202	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-3.983890	0.216823	-3.767067	9635.852579
HLA A*3301	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.629630	0.862516	-3.767114	42621.590630
HLA B*5701	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.387363	0.620011	-3.767352	24398.465190
HLA B*0801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.422461	0.654994	-3.767468	26452.179672
HLA A*0219	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.404831	0.636799	-3.768032	25399.836933
HLA B*1501	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.368026	0.599894	-3.768133	23335.990854
HLA A*2601	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.380333	0.612174	-3.768159	24006.721172
HLA B*7301	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.179452	0.411293	-3.768159	15116.522007
HLA A*0203	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.364246	0.595896	-3.768350	23133.743957
HLA A*3002	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.438062	0.669638	-3.768424	27419.658676
HLA B*1502	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.438069	0.669638	-3.768431	27420.103692
HLA A*2601	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.383726	0.615291	-3.768434	24194.993217
HLA A*2602	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.554580	0.786144	-3.768436	35857.503877
HLA A*1101	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.459785	0.691047	-3.768738	28826.066399
HLA B*1501	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.252204	0.483430	-3.768773	17873.256325
HLA A*0212	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.405771	0.636799	-3.768972	25454.860567
HLA B*3801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.551225	0.782174	-3.769051	35581.560373
HLA B*5101	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.437049	0.667908	-3.769141	27355.799772
HLA A*0203	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.166455	0.397004	-3.769451	14670.824762
HLA B*5801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.351787	0.581978	-3.769808	22479.497844
HLA B*4801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.406790	0.636799	-3.769992	25514.696044
HLA A*2501	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.449029	0.679020	-3.770009	28120.914524
HLA B*1517	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.425412	0.654994	-3.770419	26632.529520
HLA A*2501	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.466491	0.695802	-3.770689	29274.589427
HLA B*3801	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.522366	0.751562	-3.770805	33294.022231
HLA B*3901	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.386258	0.615291	-3.770967	24336.507286
HLA A*6801	1:169-177	9	AESRDARVQ	0.923606	-0.041059	-4.653522	0.882547	-3.770974	45032.034301
HLA A*0212	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.383401	0.612174	-3.771227	24176.936830
HLA B*4403	1:179-187	9	SARRSRGPV	0.654360	0.222846	-4.648527	0.877206	-3.771320	44517.068861
HLA A*6901	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.353344	0.581978	-3.771366	22560.271100
HLA B*4501	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.589888	0.818322	-3.771566	38894.492994

HLA A*0206	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.443694	0.672009	-3.771684	27777.538607
HLA B*1503	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.463016	0.691047	-3.771969	29041.291400
HLA A*0201	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.392029	0.620011	-3.772018	24662.016540
HLA A*0101	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.384285	0.612174	-3.772110	24226.165631
HLA A*2603	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.523741	0.751562	-3.772179	33399.557568
HLA B*4002	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.590504	0.818322	-3.772182	38949.660785
HLA A*6802	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.248886	0.476646	-3.772240	17737.246881
HLA A*0301	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.364509	0.592259	-3.772250	23147.765116
HLA A*1101	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.294626	0.522301	-3.772325	19707.248140
HLA B*4001	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.368280	0.595896	-3.772384	23349.629311
HLA B*1517	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.392477	0.620011	-3.772466	24687.512696
HLA B*3801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.557710	0.785097	-3.772613	36116.825267
HLA B*4601	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.407065	0.634444	-3.772622	25530.850862
HLA B*5401	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.444648	0.672009	-3.772638	27838.616661
HLA A*0301	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.368541	0.595896	-3.772645	23363.654920
HLA A*3301	1:52-60	9	RQSQAGHRQ	0.751084	0.093890	-4.617628	0.844974	-3.772655	41459.922322
HLA A*3301	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.592867	0.820012	-3.772855	39162.216288
HLA A*2601	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.390558	0.617415	-3.773142	24578.637651
HLA A*2902	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.362613	0.589436	-3.773177	23046.927331
HLA A*6801	1:138-146	9	QRNPAPARP	0.846785	0.035314	-4.655772	0.882099	-3.773673	45266.026474
HLA B*4501	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.291205	0.517364	-3.773841	19552.627871
HLA A*6802	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.433739	0.659875	-3.773864	27148.071975
HLA A*2301	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.544830	0.770901	-3.773929	35061.435346
HLA A*0212	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.433861	0.659875	-3.773987	27155.710189
HLA B*4801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.389421	0.615291	-3.774130	24514.365463
HLA B*5101	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.263782	0.489523	-3.774259	18356.164705
HLA B*5801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.288388	0.514013	-3.774375	19426.211031
HLA B*4801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.429411	0.654994	-3.774417	26878.884465
HLA B*5301	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.556596	0.782174	-3.774422	36024.329988
HLA A*0206	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.465579	0.691047	-3.774532	29213.205427
HLA B*4801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.434646	0.659875	-3.774771	27204.822279
HLA A*0201	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.387050	0.612174	-3.774876	24380.916436
HLA A*0301	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.340373	0.565473	-3.774899	21896.404504
HLA B*0801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.394918	0.620011	-3.774907	24826.668838
HLA A*3301	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.635536	0.860615	-3.774921	43205.223767
HLA A*6802	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.377469	0.602429	-3.775040	23848.926005
HLA A*8001	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.447082	0.672009	-3.775072	27995.080281
HLA A*3101	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.409605	0.634444	-3.775161	25680.595012
HLA A*6802	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.265948	0.490659	-3.775289	18447.952470
HLA A*0301	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.364974	0.589436	-3.775538	23172.573315
HLA B*5401	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.544395	0.768800	-3.775595	35026.362382
HLA A*0202	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.375664	0.599894	-3.775771	23750.044169
HLA B*1503	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.435698	0.659875	-3.775824	27270.836677
HLA A*2301	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.543505	0.767455	-3.776050	34954.619724
HLA A*6802	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.391418	0.615291	-3.776127	24627.352043
HLA B*5101	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.463303	0.687090	-3.776213	29060.465167
HLA A*0216	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.413242	0.636799	-3.776443	25896.560410
HLA B*5801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.213308	0.436810	-3.776498	16342.103607
HLA B*5801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.342032	0.565473	-3.776558	21980.195143
HLA B*1801	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.266277	0.489523	-3.776755	18461.929955
HLA A*6801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.111904	0.334728	-3.777176	12939.103501
HLA A*2603	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.637829	0.860615	-3.777214	43433.952906
HLA A*0211	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.127016	0.349724	-3.777292	13397.262733
HLA A*1101	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.462534	0.685107	-3.777427	29009.101668

HLA B*4001	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.377560	0.599894	-3.777667	23853.958318
HLA A*2403	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.432811	0.654994	-3.777817	27090.121031
HLA A*0212	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.365484	0.587655	-3.777829	23199.792637
HLA A*0301	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.365571	0.587655	-3.777916	23204.436909
HLA B*3801	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.546876	0.768800	-3.778076	35227.035149
HLA A*0101	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.378153	0.599894	-3.778259	23886.500407
HLA B*5301	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.447920	0.669638	-3.778283	28049.200276
HLA B*3901	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.059520	0.281226	-3.778294	11468.855191
HLA A*0250	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.552122	0.773810	-3.778312	35655.168462
HLA A*3101	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.370632	0.592259	-3.778373	23476.417524
HLA B*0802	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.446433	0.667908	-3.778525	27953.311195
HLA B*5301	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.563651	0.785097	-3.778555	36614.357331
HLA B*3801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.471479	0.692679	-3.778800	29612.751999
HLA B*1509	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.438769	0.659875	-3.778895	27464.344581
HLA B*1801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.455613	0.676597	-3.779015	28550.432875
HLA A*6801	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.564164	0.785097	-3.779067	36657.564160
HLA B*1502	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.564251	0.785097	-3.779154	36664.902488
HLA B*1501	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.166882	0.387714	-3.779169	14685.276767
HLA B*3901	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.282094	0.502834	-3.779260	19146.695563
HLA A*2301	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.391465	0.612174	-3.779290	24630.016812
HLA B*4402	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.394637	0.615291	-3.779345	24810.556925
HLA B*5401	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.563562	0.784035	-3.779527	36606.831079
HLA A*0101	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.054300	0.274750	-3.779550	11331.815987
HLA B*3501	1:120-128	9	EAYASELPD	0.526970	-0.706526	-3.600323	-0.179556	-3.779879	3984.030215
HLA B*1503	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.459059	0.679020	-3.780039	28777.919393
HLA A*2602	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.551009	0.770901	-3.780108	35563.855488
HLA B*0802	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.471162	0.691047	-3.780114	29591.132665
HLA A*3101	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.338091	0.557970	-3.780122	21781.684216
HLA A*0216	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.400170	0.620011	-3.780159	25128.672730
HLA A*0203	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.392341	0.612174	-3.780167	24679.767622
HLA A*2403	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.440097	0.659875	-3.780222	27548.420176
HLA B*1517	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.320738	0.540487	-3.780251	20928.502835
HLA A*2402	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.448310	0.667908	-3.780402	28074.400939
HLA B*4402	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.397855	0.617415	-3.780440	24995.124683
HLA A*0203	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.440809	0.659875	-3.780934	27593.614479
HLA A*8001	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.440872	0.659875	-3.780997	27597.645290
HLA B*1501	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.369253	0.587655	-3.781597	23401.983946
HLA B*0702	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.272280	0.490659	-3.781621	18718.887452
HLA A*8001	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.384080	0.602429	-3.781651	24214.766019
HLA B*5401	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.265319	0.483430	-3.781888	18421.225080
HLA A*2601	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.381808	0.599894	-3.781915	24088.420560
HLA A*3201	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.265248	0.483198	-3.782050	18418.235619
HLA A*0201	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.377993	0.595896	-3.782097	23877.714838
HLA A*6802	1:122-130	9	YASELPDLS	0.787644	-0.897152	-3.672630	-0.109508	-3.782138	4705.766503
HLA B*4501	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.602383	0.820012	-3.782371	40029.731391
HLA B*1509	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.533442	0.750956	-3.782486	34154.012850
HLA A*0250	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.476126	0.693390	-3.782736	29931.332459
HLA B*4403	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.602904	0.820012	-3.782892	40077.835795
HLA B*5801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.305396	0.522301	-3.783095	20202.077098
HLA A*0219	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.403438	0.620011	-3.783427	25318.483188
HLA A*0201	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.375791	0.592259	-3.783533	23756.983379
HLA A*0250	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.352545	0.568895	-3.783650	22518.812727
HLA A*3201	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.534680	0.750956	-3.783724	34251.525274
HLA A*2403	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.401391	0.617415	-3.783976	25199.462788
HLA B*4403	1:101-109	9	RTPQPDPDA	0.983201	-0.120685	-4.646527	0.862516	-3.784012	44312.591532

HLA B*0803	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.454015	0.669638	-3.784377	28445.596644
HLA A*2402	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.586961	0.802529	-3.784432	38633.197684
HLA A*1101	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.463481	0.679020	-3.784461	29072.415879
HLA A*0202	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.480440	0.695802	-3.784638	30230.108458
HLA B*5401	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.477334	0.692679	-3.784654	30014.677832
HLA B*4001	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.298792	0.514013	-3.784779	19897.184263
HLA B*4601	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.404824	0.620011	-3.784813	25399.424706
HLA A*2402	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.522049	0.737162	-3.784887	33269.715317
HLA A*0101	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.387355	0.602429	-3.784927	24398.069214
HLA B*4001	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.372596	0.587655	-3.784941	23582.834013
HLA A*3201	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.461559	0.676597	-3.784962	28944.046274
HLA B*5101	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.463993	0.679020	-3.784973	29106.722829
HLA A*0301	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.366983	0.581978	-3.785005	23280.005284
HLA B*5401	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.552590	0.767455	-3.785135	35693.574343
HLA A*0202	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.464212	0.679020	-3.785192	29121.370679
HLA B*0802	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.461905	0.676597	-3.785307	28967.073289
HLA B*1502	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.470553	0.685107	-3.785446	29549.699749
HLA A*3301	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.375126	0.589436	-3.785690	23720.639298
HLA B*0801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.385661	0.599894	-3.785768	24303.089168
HLA B*2705	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.457793	0.672009	-3.785784	28694.127213
HLA B*5401	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.559631	0.773810	-3.785821	36277.006832
HLA A*0203	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.299842	0.514013	-3.785829	19945.358265
HLA B*1801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.004378	0.218302	-3.786075	10101.308996
HLA A*3101	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.208985	0.422812	-3.786172	16180.238061
HLA B*1517	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.465208	0.679020	-3.786188	29188.245744
HLA B*5801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.355109	0.568895	-3.786214	22652.116021
HLA A*8001	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.401586	0.615291	-3.786295	25210.780411
HLA B*4402	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.433847	0.647511	-3.786336	27154.828747
HLA A*0101	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.375885	0.589436	-3.786449	23762.124841
HLA B*2705	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.434242	0.647511	-3.786730	27179.519940
HLA A*0301	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.345018	0.557970	-3.787048	22131.851079
HLA A*8001	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.442268	0.654994	-3.787274	27686.472254
HLA A*3201	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.554756	0.767455	-3.787302	35872.055713
HLA B*1509	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.434855	0.647511	-3.787344	27217.924014
HLA B*5701	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.422252	0.634444	-3.787809	26439.446539
HLA B*2705	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.390285	0.602429	-3.787856	24563.218236
HLA A*6901	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.244805	0.456941	-3.787864	17571.351053
HLA B*0802	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.457767	0.669638	-3.788129	28692.419711
HLA A*6802	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.443179	0.654994	-3.788185	27744.648219
HLA B*1801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.475355	0.687090	-3.788266	29878.268091
HLA A*0201	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.390748	0.602429	-3.788319	24589.410395
HLA B*0801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.346336	0.557970	-3.788366	22199.122123
HLA A*2301	1:211-219	9	ALFFVVWMIT	0.834379	-0.166471	-4.456576	0.667908	-3.788668	28613.829575
HLA A*3002	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.423401	0.634444	-3.788958	26509.482994
HLA A*0101	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.376830	0.587655	-3.789174	23813.858360
HLA B*0801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.392085	0.602429	-3.789656	24665.218798
HLA B*1501	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.307041	0.517364	-3.789676	20278.725836
HLA B*1509	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.468859	0.679020	-3.789839	29434.664751
HLA B*4001	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.392524	0.602429	-3.790095	24690.183975
HLA B*4001	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.331320	0.540972	-3.790348	21444.713166
HLA A*2501	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.476554	0.686161	-3.790392	29960.817357
HLA B*1801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.527634	0.737162	-3.790472	33700.303381
HLA B*5101	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.462525	0.672009	-3.790516	29008.473931
HLA A*0206	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.227348	0.436810	-3.790539	16879.068742

HLA B*4601	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.402815	0.612174	-3.790641	25282.212094
HLA A*2402	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.402874	0.612174	-3.790700	25285.631674
HLA A*6801	1:172-180	9	RDARVQLSA	1.088836	-0.228221	-4.651351	0.860615	-3.790736	44807.492659
HLA A*3002	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.475999	0.685107	-3.790892	29922.589776
HLA A*2601	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.383202	0.592259	-3.790943	24165.821849
HLA A*0206	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.427781	0.636799	-3.790982	26778.157892
HLA A*0201	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.391007	0.599894	-3.791113	24604.047609
HLA B*0802	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.484507	0.693390	-3.791116	30514.528505
HLA B*0801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.228053	0.436810	-3.791244	16906.485152
HLA B*4402	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.425885	0.634444	-3.791441	26661.505157
HLA B*1517	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.409032	0.617415	-3.791616	25646.718657
HLA A*2403	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.407007	0.615291	-3.791715	25527.398119
HLA B*2705	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.072123	0.280375	-3.791747	11806.541739
HLA A*2301	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.542753	0.750956	-3.791797	34894.159874
HLA B*4801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.426543	0.634444	-3.792099	26701.921780
HLA B*5301	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.586026	0.793787	-3.792238	38550.104647
HLA B*2705	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.314564	0.522301	-3.792263	20633.063496
HLA B*1501	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.034249	0.241837	-3.792412	10820.541837
HLA A*6901	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.357949	0.565473	-3.792476	22800.759028
HLA A*2403	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.426980	0.634444	-3.792536	26728.803828
HLA B*5401	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.412610	0.620011	-3.792599	25858.901585
HLA B*5701	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.315031	0.522301	-3.792730	20655.288352
HLA A*0101	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.385119	0.592259	-3.792860	24272.736946
HLA B*5801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.333348	0.540487	-3.792861	21545.066915
HLA A*3301	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.560567	0.767455	-3.793112	36355.200307
HLA B*2705	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.430104	0.636799	-3.793306	26921.815190
HLA B*1502	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.587123	0.793787	-3.793335	38647.621466
HLA B*2705	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.472374	0.679020	-3.793354	29673.851796
HLA B*1509	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.465603	0.672009	-3.793593	29214.785872
HLA A*0219	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.448698	0.654994	-3.793704	28099.472227
HLA A*2402	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.562521	0.768800	-3.793721	36519.204891
HLA A*3002	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.578984	0.785097	-3.793887	37930.114591
HLA A*0250	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.577936	0.784035	-3.793901	37838.706730
HLA B*1501	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.277113	0.483198	-3.793915	18928.357232
HLA B*4403	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.596502	0.802529	-3.793973	39491.344064
HLA A*2403	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.386355	0.592259	-3.794096	24341.905855
HLA B*4402	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.431108	0.636799	-3.794309	26984.077079
HLA A*0202	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.578472	0.784035	-3.794437	37885.407857
HLA B*5701	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.394841	0.599894	-3.794947	24822.237019
HLA A*6901	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.340333	0.545171	-3.795162	21894.390825
HLA B*1501	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.336219	0.540972	-3.795247	21687.970705
HLA A*3002	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.391157	0.595896	-3.795261	24612.567814
HLA A*3101	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.391434	0.595896	-3.795538	24628.284679
HLA A*0206	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.395508	0.599894	-3.795615	24860.403428
HLA B*7301	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.488360	0.692679	-3.795681	30786.464615
HLA B*1801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.481859	0.686161	-3.795698	30329.049105
HLA A*2402	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.581895	0.786144	-3.795751	38185.208534
HLA B*0803	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.488487	0.692679	-3.795807	30795.459702
HLA B*0801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.408132	0.612174	-3.795958	25593.633990
HLA B*5301	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.582158	0.786144	-3.796014	38208.352252
HLA A*0301	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.318396	0.522301	-3.796095	20815.925492
HLA B*7301	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.492037	0.695802	-3.796235	31048.224021
HLA B*0803	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.482575	0.686161	-3.796414	30379.133836
HLA A*2403	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.354449	0.557970	-3.796479	22617.706914
HLA A*3101	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.385936	0.589436	-3.796500	24318.476849

HLA B*3901	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.468521	0.672009	-3.796511	29411.743369
HLA A*6802	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.416585	0.620011	-3.796574	26096.688514
HLA B*1502	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.483797	0.687090	-3.796708	30464.714984
HLA B*2705	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.365886	0.568895	-3.796991	23221.264488
HLA A*3002	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.473664	0.676597	-3.797066	29762.115008
HLA A*0216	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.452103	0.654994	-3.797109	28320.607605
HLA A*6801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.386547	0.589436	-3.797111	24352.706585
HLA A*0216	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.483292	0.686161	-3.797131	30429.301276
HLA B*7301	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.534386	0.737162	-3.797224	34228.370985
HLA B*0702	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.412518	0.615291	-3.797227	25853.446303
HLA A*2402	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.579409	0.782174	-3.797235	37967.273568
HLA B*4403	1:269-277	9	LVNIVLMTA	1.071570	-0.223137	-4.645677	0.848433	-3.797244	44225.895564
HLA A*6801	1:56-64	9	AGHRQPPPV	0.805520	0.073702	-4.676514	0.879222	-3.797291	47480.318842
HLA B*5301	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.271133	0.473842	-3.797292	18669.534280
HLA B*4001	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.386730	0.589436	-3.797294	24362.984898
HLA B*1502	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.586406	0.789030	-3.797377	38583.904847
HLA B*3901	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.445247	0.647511	-3.797735	27877.047140
HLA B*5401	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.466376	0.667908	-3.798467	29266.830214
HLA A*0211	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.415888	0.617415	-3.798472	26054.791665
HLA A*8001	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.446031	0.647511	-3.798520	27927.463794
HLA B*1517	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.458575	0.659875	-3.798701	28745.866074
HLA A*0202	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.569715	0.770901	-3.798815	37129.186712
HLA A*6901	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.321227	0.522301	-3.798926	20952.066033
HLA B*3501	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.272968	0.473842	-3.799126	18748.582243
HLA A*0219	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.414555	0.615291	-3.799264	25974.993460
HLA A*6901	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.386989	0.587655	-3.799334	24377.487328
HLA B*1517	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.049525	0.250113	-3.799412	11207.928714
HLA B*0702	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.273373	0.473842	-3.799531	18766.035935
HLA A*3101	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.399533	0.599894	-3.799639	25091.859079
HLA A*8001	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.417166	0.617415	-3.799750	26131.583330
HLA B*4001	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.419816	0.620011	-3.799805	26291.535072
HLA A*6901	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.368778	0.568895	-3.799883	23376.424282
HLA A*2403	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.211193	0.411293	-3.799900	16262.728925
HLA A*0202	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.485054	0.685107	-3.799947	30553.016448
HLA B*1801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.496301	0.695802	-3.800499	31354.586560
HLA B*3901	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.493308	0.692679	-3.800629	31139.227518
HLA B*0801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.390083	0.589436	-3.800647	24551.792845
HLA B*4402	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.392961	0.592259	-3.800703	24715.040714
HLA B*5801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.358870	0.557970	-3.800901	22849.163370
HLA B*4001	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.393199	0.592259	-3.800940	24728.548673
HLA B*1517	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.358950	0.557970	-3.800981	22853.366545
HLA B*4001	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.019518	0.218302	-3.801216	10459.664093
HLA A*8001	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.421291	0.620011	-3.801280	26381.010112
HLA A*0203	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.403800	0.602429	-3.801371	25339.585386
HLA B*5701	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.413559	0.612174	-3.801385	25915.480483
HLA B*1502	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.572340	0.770901	-3.801439	37354.231948
HLA B*5701	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.155525	0.353947	-3.801577	14306.214271
HLA A*2501	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.473751	0.672009	-3.801741	29768.072964
HLA A*0101	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.166238	0.364208	-3.802030	14663.524766
HLA A*3001	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.261456	0.459317	-3.802139	18258.115736
HLA A*6801	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.569692	0.767455	-3.802237	37127.178119
HLA B*1801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.436814	0.634444	-3.802371	27341.004590
HLA B*5301	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.605108	0.802529	-3.802579	40281.726693
HLA A*0212	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.457575	0.654994	-3.802581	28679.694263

HLA B*0802	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.462624	0.659875	-3.802749	29015.065850
HLA A*3001	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.139877	0.337099	-3.802779	13799.938637
HLA A*0202	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.571677	0.768800	-3.802877	37297.288200
HLA A*0202	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.439810	0.636799	-3.803011	27530.244039
HLA B*5701	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.115574	0.312492	-3.803082	13048.905393
HLA A*0301	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.286563	0.483430	-3.803132	19344.724650
HLA B*7301	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.572032	0.768800	-3.803232	37327.768551
HLA B*0803	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.458230	0.654994	-3.803236	28723.014905
HLA B*4601	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.286680	0.483430	-3.803250	19349.957999
HLA B*3901	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.482378	0.679020	-3.803358	30365.331761
HLA A*3101	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.405923	0.602429	-3.803495	25463.813159
HLA A*0211	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.229959	0.426351	-3.803607	16980.823963
HLA A*3001	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.239434	0.435662	-3.803772	17355.384223
HLA B*7301	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.589940	0.786144	-3.803796	38899.122398
HLA B*5801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.344886	0.540972	-3.803914	22125.147167
HLA B*0802	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.483038	0.679020	-3.804018	30411.527601
HLA A*1101	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.459109	0.654994	-3.804115	28781.188971
HLA B*3501	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.416407	0.612174	-3.804233	26085.961025
HLA A*3201	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.490521	0.686161	-3.804360	30940.073814
HLA A*0216	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.392054	0.587655	-3.804399	24663.484190
HLA B*1502	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.556086	0.751562	-3.804524	35982.064186
HLA A*2602	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.578416	0.773810	-3.804605	37880.489236
HLA B*3801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.489730	0.685107	-3.804622	30883.717343
HLA A*0206	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.424787	0.620011	-3.804776	26594.232060
HLA A*3201	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.589973	0.785097	-3.804876	38902.068668
HLA B*1517	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.439390	0.634444	-3.804946	27503.597476
HLA A*2902	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.404930	0.599894	-3.805036	25405.608822
HLA A*6901	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.345530	0.540487	-3.805043	22157.967804
HLA A*2403	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.425072	0.620011	-3.805061	26611.646252
HLA A*0202	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.340331	0.535260	-3.805070	21894.272379
HLA B*4501	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.591265	0.786144	-3.805121	39017.991777
HLA B*4601	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.397463	0.592259	-3.805204	24972.552999
HLA A*0219	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.465145	0.659875	-3.805270	29183.982616
HLA B*1801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.405501	0.599894	-3.805607	25439.029075
HLA B*4601	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.408073	0.602429	-3.805644	25590.172756
HLA A*0101	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.387713	0.581978	-3.805734	24418.140075
HLA A*2402	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.590957	0.785097	-3.805860	38990.349699
HLA A*2301	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.543159	0.737162	-3.805997	34926.832983
HLA A*0250	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.576924	0.770901	-3.806023	37750.582425
HLA B*4402	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.408576	0.602429	-3.806147	25619.816071
HLA B*4601	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.402091	0.595896	-3.806195	25240.120790
HLA A*3201	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.588438	0.782174	-3.806264	38764.883436
HLA B*4403	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.600306	0.793787	-3.806518	39838.752552
HLA B*4601	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.396020	0.589436	-3.806584	24889.739985
HLA A*3101	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.426674	0.620011	-3.806663	26710.012454
HLA A*0212	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.402597	0.595896	-3.806701	25269.495314
HLA B*4501	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.320785	0.514013	-3.806772	20930.767375
HLA B*4801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.424327	0.617415	-3.806912	26566.048123
HLA B*5301	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.596121	0.789030	-3.807092	39456.748931
HLA A*6802	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.372601	0.565473	-3.807127	23583.089175
HLA B*5301	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.575986	0.768800	-3.807186	37669.183948
HLA B*0802	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.443985	0.636799	-3.807186	27796.178761
HLA B*1501	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.403137	0.595896	-3.807241	25300.957073
HLA A*2601	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.372763	0.565473	-3.807289	23591.893969
HLA A*2902	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.467341	0.659875	-3.807467	29331.976368

HLA A*6801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.329819	0.522301	-3.807518	21370.708514
HLA B*4601	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.407420	0.599894	-3.807526	25551.715363
HLA A*2601	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.395207	0.587655	-3.807552	24843.194407
HLA A*3201	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.419753	0.612174	-3.807578	26287.695027
HLA A*0201	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.395257	0.587655	-3.807601	24846.016945
HLA A*1101	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.425408	0.617415	-3.807992	26632.241364
HLA B*5701	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.425502	0.617415	-3.808086	26638.005086
HLA A*0101	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.373609	0.565473	-3.808135	23637.885371
HLA B*1801	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.500847	0.692679	-3.808168	31684.534578
HLA B*4801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.428241	0.620011	-3.808230	26806.566857
HLA A*8001	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.445310	0.636799	-3.808511	27881.119354
HLA B*0803	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.476424	0.667908	-3.808516	29951.904025
HLA A*2601	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.390534	0.581978	-3.808556	24577.308010
HLA A*0101	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.377513	0.568895	-3.808618	23851.377512
HLA B*7301	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.502053	0.693390	-3.808662	31772.589947
HLA B*3801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.559662	0.750956	-3.808706	36279.558231
HLA A*2902	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.426296	0.617415	-3.808881	26686.758372
HLA A*6901	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.330305	0.521317	-3.808988	21394.653844
HLA A*0212	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.401387	0.592259	-3.809128	25199.190137
HLA A*2403	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.411760	0.602429	-3.809331	25808.309588
HLA A*8001	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.443865	0.634444	-3.809422	27788.510732
HLA B*1801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.421653	0.612174	-3.809479	26402.997894
HLA B*5701	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.375093	0.565473	-3.809620	23718.842802
HLA A*2402	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.064313	0.254408	-3.809905	11596.128484
HLA A*0301	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.351082	0.540972	-3.810110	22443.043957
HLA A*0250	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.457800	0.647511	-3.810289	28694.592913
HLA B*4002	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.604208	0.793787	-3.810421	40198.349865
HLA A*0219	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.406384	0.595896	-3.810488	25490.827734
HLA B*3801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.487206	0.676597	-3.810609	30704.796411
HLA B*1501	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.368672	0.557970	-3.810703	23370.734101
HLA A*0212	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.410815	0.599894	-3.810921	25752.243298
HLA B*7301	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-3.972100	0.161134	-3.810966	9377.788447
HLA B*0803	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.487570	0.676597	-3.810973	30730.554188
HLA A*2403	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.400449	0.589436	-3.811013	25144.855195
HLA A*3002	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.237449	0.426351	-3.811097	17276.227642
HLA B*0801	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.300638	0.489523	-3.811116	19981.970665
HLA B*4402	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.029602	0.218302	-3.811300	10705.371114
HLA A*0201	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.393314	0.581978	-3.811335	24735.104698
HLA A*3002	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.426752	0.615291	-3.811460	26714.781321
HLA B*4601	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.399554	0.587655	-3.811899	25093.080806
HLA A*0211	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.491203	0.679020	-3.812183	30988.652798
HLA A*0219	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.424684	0.612174	-3.812510	26587.902452
HLA A*1101	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.472428	0.659875	-3.812553	29677.544267
HLA B*3801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.491762	0.679020	-3.812742	31028.578047
HLA A*2501	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.412678	0.599894	-3.812785	25862.958823
HLA B*0702	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.447241	0.634444	-3.812798	28005.380795
HLA A*3101	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.123125	0.310085	-3.813041	13277.775680
HLA B*0801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.409351	0.595896	-3.813455	25665.595043
HLA B*5401	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.564556	0.750956	-3.813600	36690.697455
HLA A*2501	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.461153	0.647511	-3.813641	28916.969900
HLA B*3501	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.468735	0.654994	-3.813741	29426.226332
HLA A*6801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.509592	0.695802	-3.813790	32328.988387
HLA B*5701	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.406093	0.592259	-3.813834	25473.733552
HLA A*3301	1:256-264	9	SSGTIFGGA	1.035439	-0.241652	-4.607730	0.793787	-3.813943	40525.660679
HLA B*5701	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.416691	0.602429	-3.814262	26103.042396

HLA B*4801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.426535	0.612174	-3.814361	26701.488421
HLA B*1517	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.250075	0.435662	-3.814413	17785.867407
HLA B*0803	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.474303	0.659875	-3.814428	29805.941895
HLA A*6802	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.426785	0.612174	-3.814610	26716.804734
HLA B*0803	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.494156	0.679020	-3.815136	31200.100918
HLA B*2705	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.329382	0.514013	-3.815369	21349.215281
HLA B*7301	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.597592	0.782174	-3.815418	39590.599307
HLA B*5801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.350788	0.535260	-3.815528	22427.872289
HLA A*0216	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.384534	0.568895	-3.815638	24240.062068
HLA A*2603	1:268-276	9	GLVNIVLMT	1.158521	-0.338509	-4.635710	0.820012	-3.815698	43222.523655
HLA B*2705	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.333125	0.517364	-3.815760	21533.996900
HLA A*0206	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.251438	0.435662	-3.815776	17841.762404
HLA A*2602	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.604857	0.789030	-3.815827	40258.416036
HLA B*1509	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.483767	0.667908	-3.815858	30462.572519
HLA B*3501	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.252775	0.436810	-3.815965	17896.768014
HLA A*6901	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.251760	0.435662	-3.816098	17854.990814
HLA A*0212	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.436460	0.620011	-3.816449	27318.679027
HLA B*4501	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.431930	0.615291	-3.816639	27035.218784
HLA B*3801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.502877	0.686161	-3.816716	31832.979318
HLA B*3901	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.476601	0.659875	-3.816726	29964.059227
HLA A*0203	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.382302	0.565473	-3.816828	24115.802405
HLA A*3001	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.306373	0.489523	-3.816851	20247.593352
HLA B*0803	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.502046	0.685107	-3.816938	31772.074293
HLA A*0202	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.554103	0.737162	-3.816941	35818.146513
HLA A*2603	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.606055	0.789030	-3.817025	40369.644126
HLA B*5801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.362207	0.545171	-3.817036	23025.367553
HLA B*4601	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.399037	0.581978	-3.817059	25063.233399
HLA B*4002	1:50-58	9	ATRQSQAGH	0.892588	-0.090059	-4.619682	0.802529	-3.817153	41656.419090
HLA A*3001	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.214158	0.397004	-3.817155	16374.139012
HLA B*2705	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.434822	0.617415	-3.817407	27215.862649
HLA B*5401	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.465004	0.647511	-3.817492	29174.511226
HLA B*2705	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.452088	0.634444	-3.817645	28319.688352
HLA B*1502	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.586477	0.768800	-3.817676	38590.167394
HLA B*1501	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.363015	0.545171	-3.817844	23068.257702
HLA A*0212	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.420471	0.602429	-3.818043	26331.248402
HLA A*0101	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.340413	0.522301	-3.818112	21898.418367
HLA A*0211	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.410392	0.592259	-3.818134	25727.178483
HLA A*0206	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.405811	0.587655	-3.818155	25457.201710
HLA A*0301	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.358809	0.540487	-3.818322	22845.949698
HLA A*0203	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.254006	0.435662	-3.818344	17947.573425
HLA B*5101	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.340934	0.522301	-3.818633	21924.734066
HLA B*4801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.414530	0.595896	-3.818634	25973.447766
HLA A*2402	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.589874	0.770901	-3.818973	38893.230525
HLA B*1509	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.190884	0.371790	-3.819095	15519.741192
HLA A*2602	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.603184	0.784035	-3.819148	40103.645283
HLA B*4601	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.359643	0.540487	-3.819156	22889.867747
HLA A*0201	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.388107	0.568895	-3.819212	24440.342867
HLA B*0803	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.510306	0.691047	-3.819259	32382.200589
HLA A*6801	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.605648	0.786144	-3.819504	40331.879414
HLA B*1502	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.506004	0.686161	-3.819843	32063.021897
HLA B*1801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.499167	0.679020	-3.820147	31562.213283
HLA A*8001	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.416083	0.595896	-3.820187	26066.493435
HLA A*0101	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.360795	0.540487	-3.820307	22950.625748
HLA B*5401	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.516161	0.695802	-3.820360	32821.715395
HLA A*3001	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.257337	0.436810	-3.820528	18085.782699
HLA B*0702	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.155327	0.334728	-3.820599	14299.714565

HLA A*3002	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.420735	0.599894	-3.820841	26347.207540
HLA A*0201	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.386477	0.565473	-3.821003	24348.754543
HLA A*0202	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.433243	0.612174	-3.821069	27117.100495
HLA B*0801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.302854	0.481784	-3.821070	20084.169661
HLA B*5301	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.594916	0.773810	-3.821106	39347.397486
HLA B*7301	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.605172	0.784035	-3.821136	40287.610954
HLA A*0201	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.335453	0.514013	-3.821440	21649.754991
HLA A*0301	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.366960	0.545171	-3.821789	23278.745896
HLA A*3002	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.592703	0.770901	-3.821802	39147.388668
HLA B*4801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.424242	0.602429	-3.821814	26560.874729
HLA A*0216	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.335836	0.514013	-3.821823	21668.854423
HLA A*0203	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.403823	0.581978	-3.821845	25340.956266
HLA A*3002	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.508133	0.686161	-3.821972	32220.560056
HLA A*2501	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.481885	0.659875	-3.822010	30330.854003
HLA B*5301	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.606078	0.784035	-3.822043	40371.828138
HLA A*0212	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.336087	0.514013	-3.822074	21681.401247
HLA B*0802	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.477308	0.654994	-3.822314	30012.891748
HLA A*6801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.492072	0.669638	-3.822434	31050.743635
HLA A*2601	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.391397	0.568895	-3.822501	24626.152991
HLA B*4601	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.344945	0.522301	-3.822644	22128.139734
HLA A*0219	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.410324	0.587655	-3.822669	25723.142546
HLA B*3901	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.367996	0.545171	-3.822825	23334.349725
HLA A*3201	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.611865	0.789030	-3.822836	40913.364717
HLA B*0802	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.470370	0.647511	-3.822858	29537.233253
HLA B*0803	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.518776	0.695802	-3.822975	33019.937895
HLA A*2902	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.345401	0.522301	-3.823100	22151.375817
HLA B*4001	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.392019	0.568895	-3.823124	24661.482871
HLA A*3001	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.297521	0.473842	-3.823679	19839.035314
HLA A*8001	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.405740	0.581978	-3.823762	25453.070426
HLA A*0219	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.341230	0.517364	-3.823866	21939.684069
HLA B*0801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.405928	0.581978	-3.823950	25464.088673
HLA A*0206	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.221898	0.397920	-3.823978	16668.544419
HLA B*4801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.423972	0.599894	-3.824079	26544.355359
HLA B*5701	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.413559	0.589436	-3.824123	25915.480483
HLA A*3002	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.471815	0.647511	-3.824303	29635.669707
HLA A*2402	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.591815	0.767455	-3.824360	39067.416479
HLA B*0801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.369697	0.545171	-3.824526	23425.923987
HLA B*1509	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.442115	0.617415	-3.824700	27676.738218
HLA A*3001	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.212443	0.387714	-3.824730	16309.601470
HLA B*1502	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.609377	0.784035	-3.825342	40679.639235
HLA A*2403	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.394244	0.568895	-3.825349	24788.151913
HLA A*2403	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.425248	0.599894	-3.825354	26622.445897
HLA A*2402	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.521199	0.695802	-3.825397	33204.624333
HLA A*0203	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.308596	0.483198	-3.825398	20351.481186
HLA B*1509	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.462205	0.636799	-3.825407	28987.138943
HLA B*0802	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.445501	0.620011	-3.825490	27893.339566
HLA B*1801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.485367	0.659875	-3.825492	30575.007720
HLA B*5101	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.473020	0.647511	-3.825509	29718.031019
HLA B*0803	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.512738	0.687090	-3.825649	32564.024712
HLA B*5101	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.511873	0.686161	-3.825712	32499.259464
HLA B*5401	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.040452	0.214699	-3.825752	10976.190829
HLA B*1503	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.383791	0.557970	-3.825822	24198.658477
HLA B*4402	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.446017	0.620011	-3.826006	27926.557302
HLA B*7301	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.611334	0.785097	-3.826238	40863.373174

HLA A*3002	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.100993	0.274750	-3.826243	12618.077151
HLA A*2602	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.611344	0.785097	-3.826247	40864.257449
HLA A*2501	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.422403	0.595896	-3.826507	26448.602330
HLA B*7301	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.513718	0.687090	-3.826628	32637.569594
HLA B*3801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.520026	0.693390	-3.826636	33115.108179
HLA A*1101	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.310342	0.483430	-3.826911	20433.449561
HLA B*1501	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.329967	0.502834	-3.827133	21377.993385
HLA B*0702	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.427144	0.599894	-3.827250	26738.927736
HLA B*1503	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.311188	0.483430	-3.827757	20473.283709
HLA B*0802	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.396836	0.568895	-3.827940	24936.507673
HLA A*0250	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.523910	0.695802	-3.828108	33412.569631
HLA A*0216	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.488066	0.659875	-3.828192	30765.652732
HLA B*3901	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.445921	0.617415	-3.828506	27920.363726
HLA A*1101	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.431164	0.602429	-3.828735	26987.580847
HLA A*0219	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.431187	0.602429	-3.828759	26989.040885
HLA A*2902	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.397787	0.568895	-3.828892	24991.203586
HLA A*0101	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.386961	0.557970	-3.828991	24375.904825
HLA B*5701	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.416656	0.587655	-3.829001	26100.924264
HLA A*0203	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.398149	0.568895	-3.829254	25012.033006
HLA B*1509	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.525228	0.695802	-3.829426	33514.129072
HLA A*0206	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.320104	0.490659	-3.829445	20897.955512
HLA A*3101	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.266348	0.436810	-3.829538	18464.926508
HLA B*3501	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.170049	0.340384	-3.829665	14792.761036
HLA A*0206	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.441852	0.612174	-3.829678	27659.973751
HLA A*1101	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.422055	0.592259	-3.829796	26427.434372
HLA A*3201	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.613836	0.784035	-3.829801	41099.488343
HLA A*0250	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.567016	0.737162	-3.829854	36899.108894
HLA A*3101	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.417720	0.587655	-3.830065	26164.967714
HLA A*0203	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.119756	0.289672	-3.830084	13175.168121
HLA B*5401	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.445385	0.615291	-3.830094	27885.946452
HLA B*2705	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.485103	0.654994	-3.830110	30556.487702
HLA B*4002	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.604175	0.773810	-3.830365	40195.305420
HLA B*3801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.521629	0.691047	-3.830581	33237.513512
HLA B*3501	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.314080	0.483430	-3.830649	20610.082051
HLA B*5101	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.485688	0.654994	-3.830695	30597.676934
HLA A*0301	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.365956	0.535260	-3.830696	23225.033528
HLA B*1503	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.465173	0.634444	-3.830729	29185.877263
HLA B*1503	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.442989	0.612174	-3.830815	27732.493149
HLA A*2403	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.426857	0.595896	-3.830961	26721.285693
HLA A*2501	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.468046	0.636799	-3.831247	29379.619842
HLA A*3101	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.396824	0.565473	-3.831350	24935.833163
HLA B*5701	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.371870	0.540487	-3.831383	23543.444565
HLA B*1502	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.491268	0.659875	-3.831394	30993.347218
HLA B*3501	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.046236	0.214699	-3.831537	11123.362252
HLA A*0206	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.517759	0.686161	-3.831598	32942.679808
HLA A*8001	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.443844	0.612174	-3.831670	27787.157770
HLA B*3901	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.121448	0.289672	-3.831776	13226.587061
HLA B*4601	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.397329	0.565473	-3.831856	24964.853557
HLA B*4002	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.614067	0.782174	-3.831892	41121.283801
HLA A*0211	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.523139	0.691047	-3.832092	33353.333480
HLA B*0802	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.466658	0.634444	-3.832214	29285.836019
HLA B*0801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.306136	0.473842	-3.832294	20236.533113
HLA B*2705	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.492300	0.659875	-3.832425	31067.042075
HLA A*2601	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.373463	0.540972	-3.832491	23629.958244
HLA B*5101	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.377680	0.545171	-3.832509	23860.540637

HLA A*2603	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.421975	0.589436	-3.832539	26422.573857
HLA A*3301	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.616715	0.784035	-3.832679	41372.763860
HLA A*3001	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.289654	0.456941	-3.832714	19482.939175
HLA A*3301	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.603734	0.770901	-3.832833	40154.445199
HLA B*4801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.390837	0.557970	-3.832868	24594.465902
HLA A*3002	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.230823	0.397920	-3.832903	17014.663726
HLA A*0216	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.445306	0.612174	-3.833131	27880.817688
HLA A*2601	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.378373	0.545171	-3.833202	23898.650488
HLA B*0803	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.505231	0.672009	-3.833222	32006.005170
HLA B*3501	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.151413	0.318175	-3.833238	14171.412077
HLA A*0211	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.505347	0.672009	-3.833337	32014.490593
HLA B*1801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.450827	0.617415	-3.833411	28237.535918
HLA B*5101	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.350880	0.517364	-3.833515	22432.604748
HLA A*2602	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.615850	0.782174	-3.833676	41290.479275
HLA A*2501	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.488757	0.654994	-3.833763	30814.624666
HLA B*7301	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.584787	0.750956	-3.833831	38440.354376
HLA A*0203	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.421493	0.587655	-3.833838	26393.286745
HLA A*8001	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.426122	0.592259	-3.833863	26676.076952
HLA B*1509	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.433788	0.599894	-3.833895	27151.156380
HLA A*3201	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.604833	0.770901	-3.833932	40256.238159
HLA A*2902	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.430121	0.595896	-3.834225	26922.834718
HLA B*4801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.421989	0.587655	-3.834334	26423.431530
HLA B*0702	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.403297	0.568895	-3.834401	25310.266310
HLA A*2603	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.527855	0.693390	-3.834464	33717.445341
HLA B*0803	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.314481	0.480013	-3.834468	20629.157075
HLA A*0206	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.317738	0.483198	-3.834540	20784.418043
HLA A*0250	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.519902	0.685107	-3.834794	33105.614639
HLA B*2705	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.318231	0.483430	-3.834801	20808.044155
HLA A*6901	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.375869	0.540972	-3.834897	23761.225004
HLA A*2301	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.530763	0.695802	-3.834962	33944.023902
HLA A*1101	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.469674	0.634444	-3.835231	29489.972328
HLA B*4402	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.435130	0.599894	-3.835236	27235.157244
HLA B*4002	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.624282	0.789030	-3.835253	42100.012579
HLA A*2301	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.528026	0.692679	-3.835347	33730.763728
HLA A*3002	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.507391	0.672009	-3.835381	32165.525259
HLA A*2403	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.338364	0.502834	-3.835530	21795.357540
HLA A*2402	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.586488	0.750956	-3.835532	38591.211251
HLA B*4402	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.423213	0.587655	-3.835558	26498.012408
HLA B*4501	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.512402	0.676597	-3.835805	32538.842463
HLA B*5801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.353462	0.517364	-3.836097	22566.374353
HLA A*6901	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.394148	0.557970	-3.836178	24782.654375
HLA B*0802	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.451506	0.615291	-3.836215	28281.718648
HLA A*2902	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.456299	0.620011	-3.836288	28595.569282
HLA B*5701	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.432341	0.595896	-3.836445	27060.825972
HLA A*3101	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.418470	0.581978	-3.836491	26210.161013
HLA B*4001	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.394486	0.557970	-3.836516	24801.968181
HLA B*0802	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.454090	0.617415	-3.836675	28450.521471
HLA A*0250	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.515952	0.679020	-3.836932	32805.916195
HLA A*2403	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.224679	0.387714	-3.836966	16775.654262
HLA B*4801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.418947	0.581978	-3.836968	26238.961020
HLA A*8001	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.402519	0.565473	-3.837046	25264.984447

HLA A*2403	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.372342	0.535260	-3.837082	23569.059341
HLA B*4501	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.533045	0.695802	-3.837243	34122.801087
HLA A*0211	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.523529	0.686161	-3.837368	33383.299615
HLA B*5101	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.433321	0.595896	-3.837425	27121.942044
HLA B*3901	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.492483	0.654994	-3.837489	31080.154243
HLA A*0201	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.395764	0.557970	-3.837795	24875.067382
HLA A*0202	1:122-130	9	YASELPDLS	0.787644	-0.897152	-3.728886	-0.109508	-3.838394	5356.565784
HLA B*4402	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.407303	0.568895	-3.838407	25544.804700
HLA B*4501	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.627482	0.789030	-3.838453	42411.362444
HLA A*0219	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.430743	0.592259	-3.838485	26961.459529
HLA A*0216	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.430767	0.592259	-3.838508	26962.918153
HLA B*5101	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.458918	0.620011	-3.838907	28768.579788
HLA B*4501	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.531717	0.692679	-3.839038	34018.661002
HLA B*5301	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.606642	0.767455	-3.839188	40424.279889
HLA B*1517	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.431488	0.592259	-3.839230	27007.736345
HLA B*2705	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.276239	0.436810	-3.839429	18890.302620
HLA B*4501	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.624534	0.785097	-3.839437	42124.389569
HLA A*2501	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.441882	0.602429	-3.839453	27661.919106
HLA B*2705	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.397752	0.557970	-3.839782	24989.175674
HLA A*6901	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.375065	0.535260	-3.839805	23717.303056
HLA A*0219	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.421855	0.581978	-3.839877	26415.284759
HLA A*3101	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.323233	0.483198	-3.840035	21049.089481
HLA A*6802	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.408980	0.568895	-3.840085	25643.666429
HLA B*3501	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.432355	0.592259	-3.840097	27061.704363
HLA B*5301	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.611113	0.770901	-3.840212	40842.598223
HLA A*2402	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.510081	0.669638	-3.840443	32365.387280
HLA B*1517	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.442909	0.602429	-3.840480	27727.392608
HLA B*1509	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.455812	0.615291	-3.840521	28563.564541
HLA B*4002	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.611658	0.770901	-3.840758	40893.891717
HLA A*2603	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.591749	0.750956	-3.840793	39061.499116
HLA B*0702	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.422772	0.581978	-3.840793	26471.076062
HLA B*4001	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.406328	0.565473	-3.840854	25487.518288
HLA B*1503	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.461007	0.620011	-3.840996	28907.272395
HLA B*4601	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.409929	0.568895	-3.841034	25699.774396
HLA B*4403	1:85-93	9	FISGASAPV	0.612670	0.205652	-4.659416	0.818322	-3.841095	45647.439777
HLA A*3101	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.317860	0.476646	-3.841214	20790.265819
HLA A*0101	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.376520	0.535260	-3.841260	23796.858826
HLA B*5801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.324970	0.483430	-3.841539	21133.410247
HLA B*4601	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.399592	0.557970	-3.841622	25095.252913
HLA A*3001	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.213430	0.371790	-3.841641	16346.701520
HLA A*2602	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.518304	0.676597	-3.841707	32984.051935
HLA A*6801	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.623972	0.782174	-3.841798	42069.959466
HLA A*3301	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.623993	0.782174	-3.841819	42072.007861
HLA A*8001	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.431535	0.589436	-3.842099	27010.658680
HLA A*3201	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.434420	0.592259	-3.842162	27190.697140
HLA A*0211	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.438313	0.595896	-3.842417	27435.535364
HLA B*4002	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.627534	0.785097	-3.842437	42416.410441
HLA B*0801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.382992	0.540487	-3.842505	24154.189286
HLA A*3201	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.611381	0.768800	-3.842581	40867.794740
HLA A*0101	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.356603	0.514013	-3.842590	22730.189154
HLA A*3201	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.538484	0.695802	-3.842682	34552.838661
HLA B*3801	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.529777	0.687090	-3.842687	33866.985426
HLA B*5801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.364157	0.521317	-3.842840	23128.988709

HLA A*2601	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.400978	0.557970	-3.843008	25175.480778
HLA A*2603	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.629172	0.786144	-3.843027	42576.651612
HLA B*1509	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.512665	0.669638	-3.843027	32558.563969
HLA B*5701	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.425011	0.581978	-3.843032	26607.903398
HLA A*3301	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.632085	0.789030	-3.843055	42863.227106
HLA A*0301	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.364542	0.521317	-3.843225	23149.518358
HLA A*3201	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.594970	0.751562	-3.843408	39352.293687
HLA B*0801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.431105	0.587655	-3.843450	26983.931098
HLA A*2602	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.445935	0.602429	-3.843506	27921.270017
HLA B*5301	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.503648	0.659875	-3.843773	31889.515290
HLA A*0203	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.384813	0.540972	-3.843841	24255.672282
HLA A*0101	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.389045	0.545171	-3.843874	24493.155444
HLA A*2603	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.617833	0.773810	-3.844022	41479.440456
HLA B*0702	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.446461	0.602429	-3.844033	27955.125945
HLA A*6801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.459445	0.615291	-3.844154	28803.463121
HLA A*2301	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.537657	0.693390	-3.844267	34487.102957
HLA B*3501	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.365884	0.521317	-3.844567	23221.138864
HLA A*0216	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.447246	0.602429	-3.844817	28005.683808
HLA A*3301	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.630967	0.786144	-3.844822	42752.991695
HLA B*5701	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.413764	0.568895	-3.844868	25927.680743
HLA A*3301	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.630006	0.785097	-3.844909	42658.499094
HLA A*3101	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.242839	0.397920	-3.844919	17491.966484
HLA B*3901	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.479909	0.634444	-3.845465	30193.170656
HLA A*2602	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.582663	0.737162	-3.845502	38252.819242
HLA A*6801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.479986	0.634444	-3.845543	30198.561413
HLA B*4801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.435125	0.589436	-3.845689	27234.862567
HLA B*1503	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.325714	0.480013	-3.845701	21169.683763
HLA A*0202	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.834209	-0.011592	-3.845801	6826.673880
HLA B*5301	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.583023	0.737162	-3.845861	38284.494706
HLA B*4601	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.325940	0.480013	-3.845926	21180.681080
HLA A*2602	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.597275	0.750956	-3.846319	39561.695461
HLA A*8001	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.446386	0.599894	-3.846493	27950.286872
HLA A*2902	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.210850	0.364208	-3.846642	16249.888981
HLA B*5701	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.330247	0.483430	-3.846816	21391.760472
HLA A*0301	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.364213	0.517364	-3.846849	23131.991910
HLA A*0101	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.364387	0.517364	-3.847023	23141.254236
HLA A*0201	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.392463	0.545171	-3.847292	24686.711369
HLA B*4801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.416376	0.568895	-3.847481	26084.126501
HLA A*2402	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.540359	0.692679	-3.847679	34702.328878
HLA A*2403	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.327787	0.480013	-3.847773	21270.936753
HLA B*1503	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.495295	0.647511	-3.847784	31282.071114
HLA B*1801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.495528	0.647511	-3.848017	31298.829623
HLA B*4402	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.413883	0.565473	-3.848410	25934.835290
HLA A*0201	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.383838	0.535260	-3.848578	24201.276860
HLA A*3101	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.365949	0.517364	-3.848585	23224.656596
HLA A*2501	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.468814	0.620011	-3.848803	29431.639379
HLA B*7301	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.616278	0.767455	-3.848823	41331.153894
HLA A*2403	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.390013	0.540972	-3.849041	24547.808494
HLA B*1509	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.389604	0.540487	-3.849117	24524.712006
HLA A*2301	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.535335	0.686161	-3.849174	34303.262160

HLA B*4001	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.394601	0.545171	-3.849430	24808.543671
HLA A*2602	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.461634	0.612174	-3.849460	28949.057398
HLA A*6801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.449687	0.599894	-3.849794	28163.543490
HLA B*7301	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.504846	0.654994	-3.849852	31977.621337
HLA B*3501	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.452417	0.602429	-3.849989	28341.145369
HLA B*7301	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.535126	0.685107	-3.850019	34286.749796
HLA A*0212	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.395269	0.545171	-3.850098	24846.689025
HLA B*3801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.522211	0.672009	-3.850202	33282.136633
HLA A*3301	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.519909	0.669638	-3.850271	33106.151937
HLA A*0250	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.467727	0.617415	-3.850311	29358.011886
HLA B*4402	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.446248	0.595896	-3.850352	27941.367026
HLA B*1509	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.439824	0.589436	-3.850388	27531.137667
HLA B*0702	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.415993	0.565473	-3.850520	26061.135346
HLA A*0203	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.408562	0.557970	-3.850592	25618.984483
HLA A*0212	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.416104	0.565473	-3.850630	26067.762618
HLA A*2601	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.385894	0.535260	-3.850634	24316.108879
HLA B*0801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.187816	0.337099	-3.850717	15410.475781
HLA B*1501	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.248788	0.398058	-3.850730	17733.217164
HLA B*4002	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.636906	0.786144	-3.850762	43341.706665
HLA A*0101	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.391780	0.540972	-3.850807	24647.878204
HLA A*2603	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.633027	0.782174	-3.850853	42956.314047
HLA B*5701	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.396030	0.545171	-3.850859	24890.278594
HLA A*2603	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.520661	0.669638	-3.851023	33163.513770
HLA B*5301	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.544454	0.693390	-3.851064	35031.099920
HLA A*2501	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.466380	0.615291	-3.851089	29267.146876
HLA B*4403	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.519086	0.667908	-3.851178	33043.526031
HLA A*3201	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.440656	0.589436	-3.851220	27583.913089
HLA A*2301	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.538446	0.687090	-3.851357	34549.847958
HLA B*1801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.506392	0.654994	-3.851398	32091.655145
HLA B*3801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.511615	0.659875	-3.851740	32479.925305
HLA B*3901	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.441264	0.589436	-3.851828	27622.589690
HLA A*2301	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.530897	0.679020	-3.851877	33954.492621
HLA B*1801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.447801	0.595896	-3.851905	28041.462448
HLA A*2301	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.521861	0.669638	-3.852223	33255.319595
HLA B*5801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.355095	0.502834	-3.852261	22651.380760
HLA A*0216	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.374678	0.522301	-3.852377	23696.141685
HLA B*7301	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.604091	0.751562	-3.852529	40187.477905
HLA B*5301	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.548476	0.695802	-3.852674	35357.055644
HLA B*1502	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.590107	0.737162	-3.852945	38914.066503
HLA A*0101	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.374309	0.521317	-3.852992	23676.023851
HLA A*0212	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.355870	0.502834	-3.853036	22691.855560
HLA B*7301	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.532058	0.679020	-3.853038	34045.356863
HLA A*3201	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.546030	0.692679	-3.853351	35158.495146
HLA B*5101	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.490221	0.636799	-3.853422	30918.656287
HLA B*5101	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.487871	0.634444	-3.853428	30751.841415
HLA B*1509	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.508523	0.654994	-3.853529	32249.508456
HLA A*2403	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.375133	0.521317	-3.853817	23721.024279
HLA A*2301	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.544879	0.691047	-3.853832	35065.418821
HLA B*0702	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.466063	0.612174	-3.853889	29245.779857
HLA A*3101	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.394897	0.540487	-3.854410	24825.460082
HLA B*3801	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.550264	0.695802	-3.854462	35502.918059
HLA A*0201	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.394961	0.540487	-3.854473	24829.086527
HLA B*1801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.526739	0.672009	-3.854729	33630.912940
HLA A*2301	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.539837	0.685107	-3.854730	34660.676558

HLA A*0201	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.395729	0.540972	-3.854757	24873.048893
HLA B*0802	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.444448	0.589436	-3.855012	27825.818279
HLA B*4402	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.444516	0.589436	-3.855080	27830.184124
HLA A*6801	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.644333	0.789030	-3.855303	44089.251978
HLA B*0803	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.503075	0.647511	-3.855563	31847.448488
HLA A*6802	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.437597	0.581978	-3.855619	27390.303613
HLA A*3201	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.470931	0.615291	-3.855640	29575.448517
HLA B*5301	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.400813	0.545171	-3.855642	25165.948824
HLA B*1517	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.443330	0.587655	-3.855674	27754.255993
HLA A*0206	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.358671	0.502834	-3.855837	22838.658813
HLA B*3901	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.448212	0.592259	-3.855953	28068.022729
HLA A*2403	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.373517	0.517364	-3.856153	23632.898642
HLA B*5701	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.414227	0.557970	-3.856257	25955.327851
HLA A*0211	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.456191	0.599894	-3.856297	28588.454019
HLA A*6801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.174494	0.318175	-3.856320	14944.950031
HLA B*0802	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.456590	0.599894	-3.856696	28614.758376
HLA A*1101	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.469209	0.612174	-3.857035	29458.400819
HLA A*3002	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.333874	0.476646	-3.857228	21571.191380
HLA B*2705	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.453155	0.595896	-3.857259	28389.329534
HLA A*0211	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.374631	0.517364	-3.857266	23693.577954
HLA A*0212	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.397759	0.540487	-3.857272	24989.581243
HLA B*5301	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.608390	0.750956	-3.857434	40587.313781
HLA A*8001	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.445110	0.587655	-3.857455	27868.301431
HLA B*4801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.379769	0.522301	-3.857468	23975.571710
HLA B*0801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.340681	0.483198	-3.857482	21911.927887
HLA B*0702	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.446936	0.589436	-3.857500	27985.691938
HLA B*1517	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.398694	0.540972	-3.857722	25043.445174
HLA B*5701	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.398739	0.540972	-3.857767	25046.019470
HLA A*0212	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.255855	0.397920	-3.857935	18024.149603
HLA A*3001	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.256200	0.398058	-3.858142	18038.489076
HLA A*0203	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.341583	0.483430	-3.858153	21957.494983
HLA A*2902	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.445860	0.587655	-3.858205	27916.436805
HLA A*6802	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.446050	0.587655	-3.858395	27928.672496
HLA A*2301	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.535530	0.676597	-3.858933	34318.668496
HLA A*0203	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.394261	0.535260	-3.859001	24789.090639
HLA A*2402	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.546190	0.687090	-3.859101	35171.431367
HLA B*1801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.495972	0.636799	-3.859173	31330.848073
HLA B*1502	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.451466	0.592259	-3.859207	28279.117751
HLA B*1517	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.471436	0.612174	-3.859262	29609.868509
HLA A*6901	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.285728	0.426351	-3.859377	19307.608553
HLA A*2603	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.494022	0.634444	-3.859578	31190.481423
HLA A*2603	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.644713	0.785097	-3.859617	44127.908825
HLA B*3801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.514644	0.654994	-3.859650	32707.210647
HLA B*0802	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.425631	0.565473	-3.860157	26645.932242
HLA B*4001	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.400827	0.540487	-3.860340	25166.765707
HLA B*0802	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.377765	0.517364	-3.860401	23865.188073
HLA B*5401	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.546686	0.686161	-3.860525	35211.602008
HLA A*2501	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.477961	0.617415	-3.860546	30058.063572
HLA A*0211	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.442571	0.581978	-3.860592	27705.800714
HLA A*2403	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.426153	0.565473	-3.860679	26677.953108
HLA A*3201	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.258604	0.397920	-3.860684	18138.596543
HLA A*0211	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.497528	0.636799	-3.860729	31443.255866
HLA B*7301	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.495173	0.634444	-3.860730	31273.272260

HLA B*5401	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-3.853700	-0.007282	-3.860982	7140.037358
HLA B*5101	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.478530	0.617415	-3.861114	30097.441154
HLA A*6901	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.179400	0.318175	-3.861225	15114.722983
HLA A*3301	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.375267	0.514013	-3.861254	23728.340110
HLA B*4601	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.402338	0.540972	-3.861366	25254.462219
HLA B*5801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.352064	0.490659	-3.861405	22493.852593
HLA B*4501	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.635271	0.773810	-3.861460	43178.819730
HLA A*6802	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.379139	0.517364	-3.861775	23940.835907
HLA A*0211	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.430694	0.568895	-3.861799	26958.396674
HLA B*1517	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.461696	0.599894	-3.861802	28953.129575
HLA A*2501	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.443811	0.581978	-3.861833	27785.053294
HLA A*0203	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.383157	0.521317	-3.861840	24163.338023
HLA A*2402	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.541016	0.679020	-3.861997	34754.934721
HLA B*7301	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.548326	0.686161	-3.862165	35344.815987
HLA A*2501	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.474394	0.612174	-3.862220	29812.231186
HLA B*7301	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.531992	0.669638	-3.862354	34040.200169
HLA A*0250	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.539428	0.676597	-3.862831	34628.065096
HLA A*3301	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.636706	0.773810	-3.862896	43321.780971
HLA A*2603	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.647072	0.784035	-3.863037	44368.242928
HLA B*2705	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.428603	0.565473	-3.863130	26828.909328
HLA A*0301	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.366187	0.502834	-3.863353	23237.349988
HLA B*2705	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.483471	0.620011	-3.863460	30441.814903
HLA B*2705	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.475785	0.612174	-3.863611	29907.862513
HLA A*2601	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.404154	0.540487	-3.863667	25360.293579
HLA B*1501	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.340453	0.476646	-3.863806	21900.432416
HLA B*4402	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.409072	0.545171	-3.863901	25649.077446
HLA B*2705	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.453442	0.589436	-3.864006	28408.072860
HLA B*0702	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.460027	0.595896	-3.864131	28842.133294
HLA B*4601	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.409337	0.545171	-3.864166	25664.761969
HLA A*0202	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.347602	0.483430	-3.864172	22263.947682
HLA B*3501	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.433166	0.568895	-3.864270	27112.259810
HLA B*1501	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.204723	0.340384	-3.864339	16022.229246
HLA B*5801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.347581	0.483198	-3.864383	22262.863699
HLA B*2705	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.234392	0.369909	-3.864484	17155.059866
HLA A*6901	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.367338	0.502834	-3.864504	23299.030333
HLA A*0211	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.484568	0.620011	-3.864557	30518.820893
HLA A*2602	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.616202	0.751562	-3.864641	41323.999411
HLA B*5801	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.354338	0.489523	-3.864816	22611.956759
HLA A*0201	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.382196	0.517364	-3.864832	24109.932248
HLA A*0101	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.367697	0.502834	-3.864863	23318.323228
HLA B*4002	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.649008	0.784035	-3.864973	44566.466892
HLA A*2601	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.386543	0.521317	-3.865226	24352.443096
HLA A*3001	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.205691	0.340384	-3.865307	16057.980610
HLA B*1502	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.558410	0.692679	-3.865730	36175.097857
HLA B*0801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.406788	0.540972	-3.865816	25514.558012
HLA A*3002	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.545048	0.679020	-3.866028	35079.079883
HLA A*0203	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.411231	0.545171	-3.866060	25776.914178
HLA B*5401	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.545086	0.679020	-3.866066	35082.116397
HLA B*4601	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.383650	0.517364	-3.866286	24190.805028
HLA A*3001	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.298879	0.432524	-3.866355	19901.167399
HLA B*4801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.431831	0.565473	-3.866358	27029.076665
HLA A*2601	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.388666	0.522301	-3.866366	24471.831386
HLA B*1502	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.562326	0.695802	-3.866525	36502.810689
HLA A*2902	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.459055	0.592259	-3.866796	28777.608024
HLA A*0211	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.521880	0.654994	-3.866886	33256.758886

HLA B*4403	1:150-158	9	GAGSRGDSA	1.152566	-0.370392	-4.649074	0.782174	-3.866900	44573.218193
HLA B*1502	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.545950	0.679020	-3.866930	35152.028819
HLA B*7301	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.075623	0.208647	-3.866976	11902.095741
HLA B*3501	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.407512	0.540487	-3.867024	25557.106977
HLA B*3501	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.449349	0.581978	-3.867371	28141.611957
HLA A*0301	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.350598	0.483198	-3.867400	22418.046526
HLA A*0216	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.326870	0.459317	-3.867553	21226.105434
HLA B*3801	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.537394	0.669638	-3.867756	34466.213289
HLA A*0212	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.304684	0.436810	-3.867874	20168.989052
HLA B*0802	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.480130	0.612174	-3.867955	30208.528681
HLA A*2501	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.084833	0.216823	-3.868010	12157.196060
HLA B*4403	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.638934	0.770901	-3.868033	43544.530676
HLA B*3501	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.097408	0.229292	-3.868116	12514.337531
HLA A*2301	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.540232	0.672009	-3.868222	34692.192628
HLA A*2902	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.450310	0.581978	-3.868332	28203.948283
HLA B*5701	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.294849	0.426351	-3.868498	19717.379075
HLA A*0203	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.359249	0.490659	-3.868590	22869.073481
HLA B*4402	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.351885	0.483198	-3.868687	22484.606111
HLA A*3301	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.503190	0.634444	-3.868746	31855.891874
HLA B*1502	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-3.884563	0.015810	-3.868753	7665.902990
HLA A*0250	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.540934	0.672009	-3.868925	34748.354632
HLA A*3101	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.404460	0.535260	-3.869200	25378.135382
HLA A*0250	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.524309	0.654994	-3.869315	33443.312676
HLA A*0216	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.410329	0.540972	-3.869357	25723.420866
HLA A*3001	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.280823	0.411293	-3.869530	19090.739895
HLA A*0201	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.390908	0.521317	-3.869591	24598.457826
HLA A*2602	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.555785	0.686161	-3.869624	35957.156461
HLA A*6802	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.326657	0.456941	-3.869716	21215.658396
HLA B*3501	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.457478	0.587655	-3.869823	28673.333656
HLA A*1101	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.457800	0.587655	-3.870145	28694.592913
HLA B*4501	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.621869	0.751562	-3.870308	41866.755339
HLA B*1801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.485691	0.615291	-3.870400	30597.842464
HLA B*4002	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.622172	0.751562	-3.870611	41895.983328
HLA A*0219	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.385046	0.514013	-3.871033	24268.666590
HLA A*3101	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.416256	0.545171	-3.871086	26076.930770
HLA A*0206	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.531069	0.659875	-3.871194	33967.904642
HLA A*2602	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.567009	0.695802	-3.871207	36898.510038
HLA A*6901	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.345053	0.473842	-3.871211	22133.647115
HLA B*4501	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.655340	0.784035	-3.871305	45220.990203
HLA B*4001	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.374382	0.502834	-3.871548	23679.994808
HLA B*0702	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.429526	0.557970	-3.871557	26886.010587
HLA A*0206	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.526626	0.654994	-3.871632	33622.180977
HLA B*4001	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.393967	0.522301	-3.871666	24772.333027
HLA B*4402	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.412260	0.540487	-3.871773	25838.065809
HLA A*2602	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.541482	0.669638	-3.871844	34792.182695
HLA A*2603	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.609015	0.737162	-3.871853	40645.762208
HLA A*0212	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.298235	0.426351	-3.871883	19871.689560
HLA B*5701	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.181994	0.310085	-3.871909	15205.266048
HLA A*6901	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.352059	0.480013	-3.872046	22493.609216
HLA A*3101	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.413040	0.540972	-3.872068	25884.514825
HLA B*1503	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.459764	0.587655	-3.872109	28824.662920
HLA B*4402	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.374990	0.502834	-3.872156	23713.197556

HLA A*6901	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.355367	0.483198	-3.872169	22665.600031
HLA B*4403	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.641065	0.768800	-3.872264	43758.718705
HLA B*0802	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.454349	0.581978	-3.872370	28467.457068
HLA B*4403	1:32-40	9	TGPGRIPDA	1.084963	-0.295933	-4.661449	0.789030	-3.872419	45861.550021
HLA A*1101	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.472369	0.599894	-3.872476	29673.530733
HLA B*4801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.309301	0.436810	-3.872491	20384.537781
HLA B*4403	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.646504	0.773810	-3.872693	44310.194334
HLA A*0201	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.355894	0.483198	-3.872695	22693.083198
HLA A*6802	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.407970	0.535260	-3.872710	25584.082121
HLA B*5101	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.472776	0.599894	-3.872882	29701.315512
HLA A*0212	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.395189	0.522301	-3.872888	24842.119239
HLA B*0702	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.386980	0.514013	-3.872966	24376.959816
HLA A*2402	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.559263	0.686161	-3.873101	36246.207943
HLA A*2601	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.390772	0.517364	-3.873407	24590.740691
HLA B*7301	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.550182	0.676597	-3.873585	35496.196356
HLA B*3901	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.455585	0.581978	-3.873606	28548.579479
HLA B*2705	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.461273	0.587655	-3.873617	28924.949319
HLA B*1501	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.332948	0.459317	-3.873631	21525.261432
HLA A*0203	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.414158	0.540487	-3.873671	25951.256123
HLA B*4402	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.431643	0.557970	-3.873674	27017.381251
HLA B*1502	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.510473	0.636799	-3.873674	32394.641050
HLA A*6802	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.414283	0.540487	-3.873796	25958.698041
HLA B*4402	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.414906	0.540972	-3.873933	25995.939654
HLA B*1801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.409361	0.535260	-3.874101	25666.150441
HLA B*4402	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.388258	0.514013	-3.874245	24448.806383
HLA B*7301	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.546279	0.672009	-3.874270	35178.662505
HLA A*8001	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.443370	0.568895	-3.874474	27756.808617
HLA A*0201	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.311361	0.436810	-3.874552	20481.481457
HLA B*1503	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.474705	0.599894	-3.874811	29833.527863
HLA B*4403	1:166-174	9	SITAESRDA	0.897252	-0.111108	-4.661070	0.786144	-3.874926	45821.622361
HLA A*2402	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.546965	0.672009	-3.874956	35234.277719
HLA B*0803	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.509550	0.634444	-3.875106	32325.840408
HLA A*3101	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.378242	0.502834	-3.875408	23891.411398
HLA B*4001	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.392806	0.517364	-3.875442	24706.217718
HLA A*0202	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.552158	0.676597	-3.875560	35658.061938
HLA B*1509	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.510008	0.634444	-3.875564	32359.959848
HLA B*4002	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.643055	0.767455	-3.875600	43959.688949
HLA B*4801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.410881	0.535260	-3.875621	25756.144464
HLA A*2403	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.420899	0.545171	-3.875728	26357.186912
HLA B*0803	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.512534	0.636799	-3.875735	32548.701722
HLA B*7301	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.512684	0.636799	-3.875885	32559.973105
HLA B*0803	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.495956	0.620011	-3.875945	31329.661621
HLA A*0301	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.366748	0.490659	-3.876089	23267.414466
HLA A*0212	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.417192	0.540972	-3.876219	26133.138435
HLA B*1503	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.417199	0.540972	-3.876226	26133.562571
HLA A*8001	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.416726	0.540487	-3.876239	26105.160701
HLA B*1509	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.393878	0.517364	-3.876513	24767.240958
HLA A*8001	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.434568	0.557970	-3.876599	27199.965935
HLA A*0203	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.264799	0.387714	-3.877086	18399.214091
HLA A*2601	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.357172	0.480013	-3.877158	22759.966851
HLA A*0101	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.367827	0.490659	-3.877168	23325.262485
HLA A*6801	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.661230	0.784035	-3.877195	45838.481975
HLA A*3002	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.446097	0.568895	-3.877202	27931.694480

HLA B*4601	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.412464	0.535260	-3.877204	25850.229624
HLA A*0212	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.446144	0.568895	-3.877249	27934.716791
HLA A*2301	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.524779	0.647511	-3.877268	33479.517182
HLA B*4601	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.391509	0.514013	-3.877496	24632.548610
HLA B*4501	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.646327	0.768800	-3.877527	44292.219488
HLA A*3201	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.512003	0.634444	-3.877559	32508.930860
HLA B*1517	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.368400	0.490659	-3.877741	23356.072464
HLA B*4801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.418787	0.540972	-3.877815	26229.310204
HLA B*1509	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.359686	0.481784	-3.877901	22892.096825
HLA A*0206	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.413442	0.535260	-3.878182	25908.471437
HLA A*6801	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.550318	0.672009	-3.878309	35507.335871
HLA B*1801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.159665	0.281226	-3.878439	14443.236345
HLA B*5701	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.399812	0.521317	-3.878495	25108.017836
HLA B*1517	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.468345	0.589436	-3.878909	29399.812219
HLA B*4403	1:45-53	9	PWQRAATRQ	1.010040	-0.226005	-4.662952	0.784035	-3.878917	46020.613003
HLA A*6802	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.213646	0.334728	-3.878918	16354.839458
HLA A*0301	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.368468	0.489523	-3.878945	23359.737011
HLA B*4403	1:88-96	9	GASAPVTGP	0.774850	0.010247	-4.664151	0.785097	-3.879054	46147.761197
HLA A*3101	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.400409	0.521317	-3.879092	25142.542776
HLA B*4601	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.400543	0.521317	-3.879226	25150.297019
HLA B*5801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.359256	0.480013	-3.879242	22869.444642
HLA A*6901	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.355966	0.476646	-3.879320	22696.889296
HLA B*5801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.356117	0.476646	-3.879470	22704.749066
HLA A*0206	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.481913	0.602429	-3.879484	30332.823106
HLA A*3301	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.630454	0.750956	-3.879498	42702.600425
HLA A*3001	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.082536	0.203022	-3.879513	12093.043757
HLA B*0702	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.467170	0.587655	-3.879514	29320.394815
HLA B*1801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.482009	0.602429	-3.879580	30339.551838
HLA B*1503	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.482369	0.602429	-3.879940	30364.674676
HLA B*5101	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.492610	0.612174	-3.880436	31089.235140
HLA B*5401	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.497929	0.617415	-3.880514	31472.357199
HLA A*0211	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.468218	0.587655	-3.880562	29391.224789
HLA A*0201	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.339882	0.459317	-3.880565	21871.660956
HLA B*4002	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.576423	0.695802	-3.880622	37707.107241
HLA B*4801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.425802	0.545171	-3.880631	26656.457382
HLA A*2501	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.370268	0.489523	-3.880745	23456.740029
HLA B*5801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.362611	0.481784	-3.880826	23046.802650
HLA B*3901	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.493021	0.612174	-3.880847	31118.682207
HLA A*0101	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.360933	0.480013	-3.880920	22957.952378
HLA B*4801	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.303829	0.422812	-3.881017	20129.311366
HLA B*1509	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.370571	0.489523	-3.881048	23473.115631
HLA A*0219	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.449960	0.568895	-3.881065	28181.222988
HLA B*0801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.364542	0.483430	-3.881112	23149.518358
HLA B*1502	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.477028	0.595896	-3.881132	29993.576363
HLA A*0250	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.501174	0.620011	-3.881163	31708.369503
HLA A*6901	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.364617	0.483430	-3.881187	23153.526267
HLA B*3501	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.215953	0.334728	-3.881226	16441.955924
HLA A*1101	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.477216	0.595896	-3.881320	30006.560126
HLA A*3001	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-3.897138	0.015810	-3.881328	7891.103921
HLA A*0250	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.518229	0.636799	-3.881430	32978.342347
HLA B*5801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.355402	0.473842	-3.881560	22667.439381
HLA A*6802	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.423009	0.540972	-3.882037	26485.543778
HLA A*2403	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.404401	0.522301	-3.882100	25374.703291
HLA B*1501	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.403440	0.521317	-3.882123	25318.620158

HLA B*3501	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.447629	0.565473	-3.882156	28030.390446
HLA A*1101	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.464139	0.581978	-3.882161	29116.487243
HLA B*4002	1:39-47	9	DAGDPPPWQ	1.064157	-0.295357	-4.651069	0.768800	-3.882269	44778.413671
HLA A*6802	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.440332	0.557970	-3.882362	27563.327598
HLA B*5401	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.099433	0.217020	-3.882413	12572.832231
HLA A*0211	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.065305	0.182878	-3.882427	11622.632377
HLA A*1101	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.502466	0.620011	-3.882455	31802.856323
HLA A*0202	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.568964	0.686161	-3.882802	37064.965586
HLA B*4501	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.650357	0.767455	-3.882902	44705.073182
HLA A*8001	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.396984	0.514013	-3.882971	24945.008057
HLA B*2705	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.482928	0.599894	-3.883034	30403.796003
HLA A*0250	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.498444	0.615291	-3.883153	31509.666666
HLA B*4002	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.620476	0.737162	-3.883314	41732.659307
HLA B*3901	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.486008	0.602429	-3.883579	30620.197303
HLA B*5701	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.418862	0.535260	-3.883602	26233.851322
HLA A*0101	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.366859	0.483198	-3.883660	23273.331302
HLA B*4001	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.405024	0.521317	-3.883707	25411.107077
HLA A*0101	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.373360	0.489523	-3.883837	23624.334153
HLA A*0212	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.419102	0.535260	-3.883842	26248.331384
HLA A*0101	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.367408	0.483430	-3.883978	23302.811995
HLA B*2705	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.035297	0.151290	-3.884007	10846.681277
HLA B*0802	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.480115	0.595896	-3.884219	30207.548148
HLA A*2603	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.576928	0.692679	-3.884249	37750.990880
HLA A*3001	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.248477	0.364208	-3.884269	17720.558299
HLA A*3002	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.575389	0.691047	-3.884342	37617.457823
HLA A*0301	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.361011	0.476646	-3.884364	22962.051343
HLA B*1501	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.196871	0.312492	-3.884379	15735.152723
HLA B*0801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.282517	0.398058	-3.884459	19165.349314
HLA B*5101	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.472289	0.587655	-3.884634	29668.073198
HLA B*0803	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.502238	0.617415	-3.884823	31786.171858
HLA A*2902	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.442860	0.557970	-3.884890	27724.242743
HLA B*4601	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.375613	0.490659	-3.884954	23747.217665
HLA A*2601	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.374483	0.489523	-3.884960	23685.504013
HLA A*0219	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.450481	0.565473	-3.885008	28215.088840
HLA B*4001	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.375862	0.490659	-3.885203	23760.839371
HLA A*0301	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.322176	0.436810	-3.885366	20997.908846
HLA A*2501	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.477721	0.592259	-3.885463	30041.481847
HLA A*2301	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.545405	0.659875	-3.885531	35107.937384
HLA A*0301	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.367446	0.481784	-3.885662	23304.829133
HLA B*7301	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.576717	0.691047	-3.885670	37732.614773
HLA B*4403	1:20-28	9	GLVDRGGAH	1.094785	-0.327330	-4.653162	0.767455	-3.885708	44994.776121
HLA B*0801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.407072	0.521317	-3.885755	25531.265222
HLA A*0101	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.345271	0.459317	-3.885954	22144.785791
HLA A*0206	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.451597	0.565473	-3.886124	28287.686315
HLA B*4801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.426705	0.540487	-3.886217	26711.890997
HLA A*0212	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.369492	0.483198	-3.886294	23414.900927
HLA B*5301	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.554329	0.667908	-3.886420	35836.753475
HLA A*0202	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.274282	0.387714	-3.886568	18805.366173
HLA A*2902	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.284526	0.397920	-3.886606	19254.203115
HLA A*0212	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.444988	0.557970	-3.887019	27860.462784
HLA A*0219	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.409368	0.522301	-3.887067	25666.566998
HLA A*0201	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.389985	0.502834	-3.887151	24546.214935

HLA A*2402	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.580683	0.693390	-3.887293	38078.763058
HLA B*5401	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.475022	0.587655	-3.887366	29855.324292
HLA A*6802	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.432590	0.545171	-3.887419	27076.348406
HLA B*1517	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.367521	0.480013	-3.887508	23308.863931
HLA A*0301	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.367780	0.480013	-3.887766	23322.738880
HLA A*3201	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.456785	0.568895	-3.887890	28627.609882
HLA A*3002	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.508345	0.620011	-3.888334	32236.251745
HLA B*1801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.433542	0.545171	-3.888371	27135.737861
HLA B*5701	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.406013	0.517364	-3.888648	25469.048441
HLA A*8001	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.423951	0.535260	-3.888691	26543.062972
HLA A*0203	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.370585	0.481784	-3.888801	23473.877565
HLA B*5801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.348267	0.459317	-3.888950	22298.059861
HLA B*1517	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.471373	0.581978	-3.889395	29605.543800
HLA A*3301	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.626596	0.737162	-3.889435	42324.951422
HLA B*2705	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.430429	0.540972	-3.889456	26941.921571
HLA A*2601	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.373190	0.483430	-3.889760	23615.133983
HLA B*4402	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.407148	0.517364	-3.889783	25535.685487
HLA B*0702	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.392834	0.502834	-3.890001	24707.821665
HLA A*2403	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.430508	0.540487	-3.890021	26946.877623
HLA B*1502	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.581329	0.691047	-3.890282	38135.455738
HLA A*0211	1:283-291	9	AFVVYNLITD	1.244680	-0.632506	-4.502499	0.612174	-3.890325	31805.265114
HLA A*2902	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.430953	0.540487	-3.890465	26974.444061
HLA A*0216	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.411950	0.521317	-3.890633	25819.621294
HLA A*0206	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.408207	0.517364	-3.890843	25598.065053
HLA B*5101	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.493489	0.602429	-3.891060	31152.201623
HLA A*0216	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.374386	0.483198	-3.891188	23680.251022
HLA B*3501	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.449192	0.557970	-3.891222	28131.413524
HLA A*2601	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.381909	0.490659	-3.891250	24094.024786
HLA B*4001	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.374685	0.483430	-3.891254	23696.526269
HLA A*0203	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.108089	0.216823	-3.891265	12825.922849
HLA B*5401	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.526031	0.634444	-3.891588	33576.193711
HLA A*0211	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.289563	0.397920	-3.891643	19478.828988
HLA A*1101	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.318027	0.426351	-3.891675	20798.252938
HLA B*0802	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.494179	0.602429	-3.891751	31201.788854
HLA B*3501	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.289941	0.398058	-3.891883	19495.802286
HLA B*3801	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.559810	0.667908	-3.891902	36291.925247
HLA A*2902	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.146385	0.254408	-3.891978	14008.293380
HLA A*6802	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.328858	0.436810	-3.892048	21323.475005
HLA A*2301	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.547127	0.654994	-3.892134	35247.432508
HLA A*6801	1:59-67	9	RQPPPVSHP	0.607496	0.166314	-4.666011	0.773810	-3.892201	46345.911579
HLA A*3201	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.564279	0.672009	-3.892269	36667.282802
HLA A*6801	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.585692	0.693390	-3.892302	38520.501664
HLA A*2402	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.583368	0.691047	-3.892321	38314.952702
HLA A*0250	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.492312	0.599894	-3.892418	31067.882433
HLA A*0301	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.366396	0.473842	-3.892554	23248.541005
HLA A*0202	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.488599	0.595896	-3.892703	30803.457542
HLA B*1503	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.482554	0.589436	-3.893118	30377.654742
HLA B*0801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.407394	0.514013	-3.893381	25550.194857
HLA B*4501	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.644337	0.750956	-3.893381	44089.729016
HLA A*2601	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.396363	0.502834	-3.893529	24909.406758
HLA B*5401	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.459205	0.565473	-3.893732	28787.573504
HLA B*4002	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.580913	0.687090	-3.893824	38098.956595

HLA A*2602	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.587243	0.693390	-3.893852	38658.285984
HLA A*2902	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.459391	0.565473	-3.893917	28799.879402
HLA B*3501	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.434961	0.540972	-3.893989	27224.550889
HLA B*3901	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.514155	0.620011	-3.894144	32670.427330
HLA B*5401	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.549226	0.654994	-3.894232	35418.125928
HLA A*0211	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.554108	0.659875	-3.894233	35818.534059
HLA A*8001	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.411600	0.517364	-3.894235	25798.817168
HLA B*4002	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.645282	0.750956	-3.894326	44185.718616
HLA A*3101	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.320684	0.426351	-3.894333	20925.898916
HLA B*0801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.291344	0.397004	-3.894340	19558.869743
HLA B*7301	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.554246	0.659875	-3.894372	35829.968567
HLA A*2603	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.581508	0.687090	-3.894418	38151.138414
HLA A*0216	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.452486	0.557970	-3.894516	28345.592069
HLA B*4601	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.397432	0.502834	-3.894598	24970.796777
HLA A*3201	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.579752	0.685107	-3.894645	37997.273630
HLA A*3001	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.229482	0.334728	-3.894754	16962.185731
HLA A*2403	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.385532	0.490659	-3.894873	24295.859008
HLA A*2902	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.430323	0.535260	-3.895063	26935.363493
HLA B*5301	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.567234	0.672009	-3.895225	36917.678233
HLA B*0801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.371945	0.476646	-3.895299	23547.520675
HLA A*0201	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.378782	0.483430	-3.895352	23921.157374
HLA B*0802	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.483097	0.587655	-3.895442	30415.640954
HLA B*5101	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.487829	0.592259	-3.895570	30748.847008
HLA B*3501	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.318560	0.422812	-3.895748	20823.809814
HLA A*6801	1:23-31	9	DRGGAHRAA	1.100473	-0.329572	-4.666801	0.770901	-3.895900	46430.232209
HLA B*3801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.488181	0.592259	-3.895923	30773.809313
HLA A*3002	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.377725	0.481784	-3.895941	23862.993338
HLA B*0803	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.488372	0.592259	-3.896113	30787.297383
HLA B*1517	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.465119	0.568895	-3.896223	29182.245964
HLA B*4601	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.378042	0.481784	-3.896258	23880.427683
HLA A*6801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.379809	0.483430	-3.896379	23977.776799
HLA B*1509	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.370453	0.473842	-3.896611	23466.767142
HLA B*1503	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.441788	0.545171	-3.896617	27655.933837
HLA B*3801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.514063	0.617415	-3.896648	32663.535065
HLA A*0219	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.437197	0.540487	-3.896710	27365.124847
HLA B*5801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.353810	0.456941	-3.896869	22584.449663
HLA B*3901	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.308194	0.411293	-3.896901	20332.662918
HLA A*6801	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.647892	0.750956	-3.896936	44452.091578
HLA B*7301	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.512379	0.615291	-3.897087	32537.082196
HLA A*2402	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.582440	0.685107	-3.897333	38233.164659
HLA A*0219	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-3.723638	-0.173733	-3.897371	5292.217607
HLA A*0301	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.356880	0.459317	-3.897563	22744.703988
HLA B*0801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.354740	0.456941	-3.897799	22632.884556
HLA A*0301	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.216109	0.318175	-3.897934	16447.827616
HLA B*5301	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.590703	0.692679	-3.898024	38967.575538
HLA B*2705	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.480024	0.581978	-3.898046	30201.175460
HLA A*2402	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.574706	0.676597	-3.898108	37558.284086
HLA A*1101	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.463636	0.565473	-3.898163	29082.798117
HLA B*4402	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.420565	0.522301	-3.898265	26336.946984
HLA B*4801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.401128	0.502834	-3.898294	25184.198867
HLA B*4501	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.401222	0.502834	-3.898388	25189.649206
HLA B*4801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.382090	0.483430	-3.898660	24104.063519
HLA A*0219	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.439697	0.540972	-3.898725	27523.096060
HLA A*0202	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.589804	0.691047	-3.898756	38886.918796
HLA A*6801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.535610	0.636799	-3.898812	34324.981523

HLA B*1509	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.501390	0.602429	-3.898961	31724.154997
HLA A*6901	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.358318	0.459317	-3.899001	22820.133138
HLA A*0219	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.401864	0.502834	-3.899030	25226.879278
HLA A*2603	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.584181	0.685107	-3.899074	38386.738624
HLA A*0202	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.297076	0.397920	-3.899156	19818.760881
HLA A*0216	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.887759	-0.011592	-3.899350	7722.512477
HLA A*0216	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.465196	0.565473	-3.899723	29187.456229
HLA B*0702	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.440280	0.540487	-3.899793	27560.047273
HLA B*1801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.519841	0.620011	-3.899830	33100.958427
HLA A*0219	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.390727	0.490659	-3.900068	24588.213191
HLA A*3002	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.489556	0.589436	-3.900120	30871.356084
HLA B*0801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.435480	0.535260	-3.900220	27257.119633
HLA B*3901	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.500500	0.599894	-3.900606	31659.176077
HLA A*0203	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.327054	0.426351	-3.900702	21235.064132
HLA A*0219	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.384010	0.483198	-3.900812	24210.836361
HLA B*0802	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.493176	0.592259	-3.900918	31129.795200
HLA A*0219	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.446203	0.545171	-3.901032	27938.495140
HLA B*5301	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.537918	0.636799	-3.901119	34507.818602
HLA B*4403	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.415338	0.514013	-3.901325	26021.829406
HLA B*1502	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.516885	0.615291	-3.901594	32876.450030
HLA A*0250	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.592700	0.691047	-3.901653	39147.176886
HLA A*2501	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.470555	0.568895	-3.901660	29549.859610
HLA A*3301	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.594378	0.692679	-3.901699	39298.681570
HLA A*2402	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.459710	0.557970	-3.901741	28821.076564
HLA A*0101	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.328280	0.426351	-3.901929	21295.115901
HLA B*3901	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.489589	0.587655	-3.901933	30873.694321
HLA A*3002	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.514340	0.612174	-3.902166	32684.393042
HLA A*3001	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.191909	0.289672	-3.902237	15556.390993
HLA A*0211	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.361748	0.459317	-3.902431	23001.090247
HLA A*0211	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.505036	0.602429	-3.902608	31991.637034
HLA B*4501	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.588861	0.686161	-3.902700	38802.650292
HLA B*0802	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.416921	0.514013	-3.902908	26116.885093
HLA B*3801	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.539724	0.636799	-3.902926	34651.677226
HLA B*5101	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.492394	0.589436	-3.902958	31073.765573
HLA A*3002	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.257192	0.353947	-3.903244	18079.717507
HLA B*5401	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.540114	0.636799	-3.903316	34682.809851
HLA B*1509	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.485331	0.581978	-3.903353	30572.526710
HLA A*0206	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.424712	0.521317	-3.903395	26589.628559
HLA B*5301	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.590508	0.687090	-3.903419	38950.082214
HLA A*0101	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.385260	0.481784	-3.903475	24280.616994
HLA B*0702	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.385264	0.481784	-3.903480	24280.879707
HLA A*2301	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.518847	0.615291	-3.903556	33025.297356
HLA B*1509	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.469169	0.565473	-3.903696	29455.691710
HLA A*2301	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.540577	0.636799	-3.903778	34719.792695
HLA B*3501	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.417939	0.514013	-3.903926	26178.135136
HLA B*4501	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.516112	0.612174	-3.903938	32817.986808
HLA A*0206	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.472952	0.568895	-3.904057	29713.369019
HLA A*0201	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.393650	0.489523	-3.904127	24754.247529
HLA A*6901	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.385934	0.481784	-3.904150	24318.345289
HLA A*3101	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.394923	0.490659	-3.904264	24826.937458
HLA A*0201	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.395019	0.490659	-3.904361	24832.444819
HLA B*5701	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.386183	0.481784	-3.904399	24332.294601
HLA B*1509	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.496724	0.592259	-3.904465	31385.133902
HLA A*1101	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.462440	0.557970	-3.904471	29002.824907

HLA B*0702	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.426888	0.522301	-3.904587	26723.165028
HLA B*4501	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.641873	0.737162	-3.904711	43840.229584
HLA B*4801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.418904	0.514013	-3.904891	26236.406047
HLA B*3901	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.473889	0.568895	-3.904994	29777.575957
HLA B*3901	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.378871	0.473842	-3.905029	23926.075491
HLA A*0250	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.501082	0.595896	-3.905186	31701.680197
HLA B*0803	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.520574	0.615291	-3.905282	33156.876230
HLA B*3801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.552799	0.647511	-3.905288	35710.764228
HLA B*5401	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.497551	0.592259	-3.905292	31444.956957
HLA A*3101	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.275245	0.369909	-3.905336	18847.123795
HLA A*2603	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.601191	0.695802	-3.905390	39920.087726
HLA B*1503	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.302485	0.397004	-3.905481	20067.118362
HLA A*0203	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.385560	0.480013	-3.905547	24297.436314
HLA A*2403	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.388988	0.483430	-3.905558	24489.975525
HLA B*1509	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.396326	0.490659	-3.905667	24907.250737
HLA B*0803	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.487725	0.581978	-3.905747	30741.528574
HLA B*0801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.195612	0.289672	-3.905940	15689.591580
HLA A*2301	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.540396	0.634444	-3.905953	34705.332780
HLA A*0219	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.441450	0.535260	-3.906190	27634.397589
HLA B*1502	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.195908	0.289672	-3.906236	15700.289974
HLA A*0250	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.592658	0.686161	-3.906497	39143.364997
HLA A*0201	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.388711	0.481784	-3.906927	24474.346923
HLA A*0216	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.424386	0.517364	-3.907021	26569.641350
HLA B*3901	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.503053	0.595896	-3.907158	31845.897905
HLA A*0219	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.333533	0.426351	-3.907182	21554.276841
HLA B*4403	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.594451	0.687090	-3.907361	39305.272770
HLA B*3901	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.465941	0.557970	-3.907971	29237.553760
HLA B*0801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.279782	0.371790	-3.907992	19045.042174
HLA B*0803	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.508018	0.599894	-3.908124	32212.020015
HLA A*2601	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.391441	0.483198	-3.908243	24628.684392
HLA A*2501	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.473786	0.565473	-3.908313	29770.488692
HLA B*4801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.429855	0.521317	-3.908538	26906.381348
HLA B*5101	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.474035	0.565473	-3.908562	29787.565423
HLA A*6801	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.587842	0.679020	-3.908822	38711.652732
HLA A*8001	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.454118	0.545171	-3.908947	28452.368501
HLA B*4403	1:227-235	9	LGGMGVWAK	0.713360	0.038202	-4.660579	0.751562	-3.909018	45769.842651
HLA A*6802	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.389197	0.480013	-3.909184	24501.769800
HLA B*4001	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.389303	0.480013	-3.909290	24507.735360
HLA A*3201	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.602749	0.693390	-3.909359	40063.528450
HLA B*0803	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.511838	0.602429	-3.909409	32496.622311
HLA B*4002	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.526837	0.617415	-3.909422	33638.555267
HLA A*0202	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.501724	0.592259	-3.909465	31748.534991
HLA A*0301	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.366469	0.456941	-3.909528	23252.440264
HLA A*3101	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.391380	0.481784	-3.909596	24625.220435
HLA B*0803	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.522183	0.612174	-3.910009	33279.976071
HLA A*2501	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.497680	0.587655	-3.910025	31454.314604
HLA A*8001	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.451128	0.540972	-3.910155	28257.096218
HLA A*0101	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.386832	0.476646	-3.910185	24368.653002
HLA B*4001	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.393535	0.483198	-3.910336	24747.686430
HLA A*2501	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.401187	0.490659	-3.910528	25187.605190
HLA B*1517	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.506449	0.595896	-3.910553	32095.822110

HLA A*3001	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.244920	0.334139	-3.910781	17576.009564
HLA B*5101	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.492760	0.581978	-3.910782	31100.001120
HLA A*0202	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.513269	0.602429	-3.910840	32603.862975
HLA B*5701	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.390976	0.480013	-3.910963	24602.317302
HLA A*3201	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.566017	0.654994	-3.911024	36814.367812
HLA B*4501	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.548065	0.636799	-3.911266	35323.597878
HLA B*5401	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.523442	0.612174	-3.911268	33376.618085
HLA B*0702	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.387933	0.476646	-3.911287	24430.560579
HLA A*3002	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.153128	0.241837	-3.911291	14227.488744
HLA A*3301	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-3.930383	0.019002	-3.911381	8518.889316
HLA B*4402	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.394813	0.483430	-3.911382	24820.625645
HLA B*4001	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.201241	0.289672	-3.911569	15894.285311
HLA A*1101	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.501056	0.589436	-3.911620	31699.793725
HLA A*2601	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.388439	0.476646	-3.911792	24458.992935
HLA B*4501	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.583982	0.672009	-3.911972	38369.090902
HLA A*3301	1:89-97	9	ASAPVTGPA	0.844183	-0.157093	-4.599082	0.687090	-3.911992	39726.623043
HLA A*0203	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.334814	0.422812	-3.912002	21617.921024
HLA B*1517	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.457267	0.545171	-3.912096	28659.376294
HLA B*1801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.504402	0.592259	-3.912143	31944.941919
HLA A*0101	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.347823	0.435662	-3.912161	22275.272437
HLA B*5401	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-3.765501	-0.146721	-3.912222	5827.748712
HLA B*7301	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.434669	0.522301	-3.912368	27206.294070
HLA A*1101	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.457687	0.545171	-3.912516	28687.142621
HLA A*0203	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.415425	0.502834	-3.912591	26027.038610
HLA A*2902	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.231028	0.318175	-3.912853	17022.673739
HLA B*4403	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.525087	0.612174	-3.912913	33503.252374
HLA B*0802	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.448473	0.535260	-3.913213	28084.882573
HLA B*1509	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.533284	0.620011	-3.913273	34141.635542
HLA A*0101	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.350083	0.436810	-3.913274	22391.502120
HLA B*4501	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.404065	0.490659	-3.913406	25355.080653
HLA B*7301	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.530857	0.617415	-3.913442	33951.370033
HLA B*4601	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.396775	0.483198	-3.913576	24933.000422
HLA A*0201	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.393753	0.480013	-3.913740	24760.140611
HLA B*4001	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.390412	0.476646	-3.913766	24570.395036
HLA B*2705	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.454447	0.540487	-3.913960	28473.926046
HLA B*4801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.431401	0.517364	-3.914037	27002.330858
HLA A*8001	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.436518	0.522301	-3.914218	27322.374053
HLA A*2902	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.459464	0.545171	-3.914293	28804.709736
HLA A*0216	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.417509	0.502834	-3.914675	26152.231353
HLA B*1509	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.483623	0.568895	-3.914728	30452.521430
HLA B*1503	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.086539	0.171766	-3.914773	12205.038305
HLA B*5101	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.455307	0.540487	-3.914820	28530.360826
HLA A*3101	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.395151	0.480013	-3.915138	24839.969042
HLA A*0301	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.338162	0.422812	-3.915350	21785.219598
HLA B*1501	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.313347	0.397920	-3.915427	20575.323937
HLA A*0301	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.341909	0.426351	-3.915558	21974.012671
HLA B*3501	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.279801	0.364208	-3.915592	19045.866444
HLA B*5701	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.418742	0.502834	-3.915908	26226.614287
HLA B*3801	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.550384	0.634444	-3.915940	35512.714820
HLA B*5301	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.563456	0.647511	-3.915945	36597.920413
HLA A*2403	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.352778	0.436810	-3.915968	22530.876562
HLA B*4001	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.405616	0.489523	-3.916093	25445.773463

HLA A*0301	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.314087	0.397920	-3.916167	20610.416549
HLA B*5701	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.407148	0.490659	-3.916489	25535.685487
HLA B*1517	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.433920	0.517364	-3.916556	27159.383172
HLA A*0216	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.457044	0.540487	-3.916556	28644.650894
HLA A*6801	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.653839	0.737162	-3.916677	45064.934786
HLA B*1502	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.571788	0.654994	-3.916794	37306.772793
HLA B*5301	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.434199	0.517364	-3.916835	27176.873382
HLA A*3101	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.390781	0.473842	-3.916939	24591.272830
HLA B*4403	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.610350	0.693390	-3.916960	40770.851288
HLA A*3101	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.406485	0.489523	-3.916962	25496.758234
HLA B*5301	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.603142	0.686161	-3.916980	40099.740260
HLA B*4801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.393941	0.476646	-3.917295	24770.858899
HLA B*4002	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.587111	0.669638	-3.917473	38646.576084
HLA A*0101	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.391411	0.473842	-3.917569	24626.952353
HLA B*1517	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.439025	0.521317	-3.917708	27480.544474
HLA A*6802	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.399570	0.481784	-3.917786	25094.031079
HLA B*2705	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.207500	0.289672	-3.917828	16125.011484
HLA A*8001	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.401236	0.483198	-3.918038	25190.466858
HLA A*0101	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.375086	0.456941	-3.918146	23718.457856
HLA B*5401	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.432285	0.514013	-3.918272	27057.312695
HLA A*2603	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.597524	0.679020	-3.918504	39584.388552
HLA A*1101	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.421364	0.502834	-3.918530	26385.434751
HLA B*1801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.432668	0.514013	-3.918655	27081.182679
HLA B*5401	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.459203	0.540487	-3.918715	28787.417767
HLA A*0202	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.316079	0.397004	-3.919076	20705.185822
HLA A*2501	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.477193	0.557970	-3.919223	30004.936848
HLA A*0212	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.440632	0.521317	-3.919315	27582.420870
HLA A*6802	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.378768	0.459317	-3.919451	23920.380922
HLA B*0702	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.440860	0.521317	-3.919543	27596.898799
HLA B*2705	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.269329	0.349724	-3.919605	18592.127112
HLA A*2902	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.460629	0.540972	-3.919657	28882.105350
HLA A*2602	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.579647	0.659875	-3.919772	37988.024509
HLA B*4001	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.393697	0.473842	-3.919855	24756.926029
HLA B*5801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.352416	0.432524	-3.919892	22512.113389
HLA A*8001	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.401786	0.481784	-3.920002	25222.376017
HLA B*5301	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.599115	0.679020	-3.920095	39729.631989
HLA A*2902	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.357181	0.436810	-3.920371	22760.459372
HLA B*2705	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.465840	0.545171	-3.920669	29230.753158
HLA A*2602	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.592745	0.672009	-3.920736	39151.200948
HLA A*0219	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.478861	0.557970	-3.920891	30120.408071
HLA B*0702	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.290902	0.369909	-3.920993	19538.987327
HLA B*4403	1:110-118	9	SLGCGDGSP	0.679170	0.071786	-4.672000	0.750956	-3.921044	46989.439641
HLA B*0801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.380474	0.459317	-3.921157	24014.514859
HLA B*5301	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.062429	0.141159	-3.921270	11545.924989
HLA B*0702	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.293383	0.371790	-3.921594	19650.929944
HLA B*4601	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.398600	0.476646	-3.921954	25038.026470
HLA A*0201	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.398631	0.476646	-3.921984	25039.787421
HLA B*1509	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.518022	0.595896	-3.922126	32962.646076
HLA B*4402	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.443454	0.521317	-3.922137	27762.214948
HLA A*0216	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.412798	0.490659	-3.922139	25870.095510
HLA B*0802	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.480170	0.557970	-3.922200	30211.307030
HLA A*3201	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.359232	0.436810	-3.922422	22868.207463

HLA B*5701	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.405693	0.483198	-3.922495	25450.316609
HLA A*0203	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.412063	0.489523	-3.922540	25826.326866
HLA B*3501	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.235052	0.312492	-3.922561	17181.158457
HLA B*3501	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.458152	0.535260	-3.922892	28717.887548
HLA A*2601	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.404739	0.481784	-3.922955	25394.478497
HLA A*0206	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.382290	0.459317	-3.922973	24115.150095
HLA B*1801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.413681	0.490659	-3.923023	25922.771902
HLA A*0201	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.396880	0.473842	-3.923038	24939.070976
HLA B*1801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.440959	0.517364	-3.923595	27603.169950
HLA A*0301	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.359314	0.435662	-3.923652	22872.537880
HLA B*0702	1:3-11	9	APNEPGALS	0.822079	-1.082447	-3.663420	-0.260368	-3.923789	4607.023130
HLA B*1509	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.536033	0.612174	-3.923859	34358.422785
HLA A*2301	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.544174	0.620011	-3.924163	35008.554969
HLA A*2601	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.398039	0.473842	-3.924197	25005.674136
HLA B*1801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.446675	0.522301	-3.924374	27968.891640
HLA A*0301	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.274355	0.349724	-3.924630	18808.520221
HLA B*2705	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.407841	0.483198	-3.924643	25576.470866
HLA B*0803	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.483055	0.557970	-3.925085	30412.679283
HLA B*0802	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.466080	0.540972	-3.925107	29246.887393
HLA B*3901	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.447575	0.522301	-3.925274	28026.902913
HLA A*0203	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.323226	0.397920	-3.925306	21048.747864
HLA A*3301	1:86-94	9	ISGASAPVT	1.091631	-0.395829	-4.621108	0.695802	-3.925306	41793.435396
HLA A*3101	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.243513	0.318175	-3.925338	17519.146274
HLA B*0802	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.470577	0.545171	-3.925406	29551.298398
HLA A*2902	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.442796	0.517364	-3.925432	27720.193441
HLA A*2301	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.542851	0.617415	-3.925436	34902.089264
HLA B*4402	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.415044	0.489523	-3.925522	26004.238453
HLA A*2602	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.604742	0.679020	-3.925722	40247.745565
HLA A*0212	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.407512	0.481784	-3.925727	25557.106977
HLA A*6802	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.408954	0.483198	-3.925756	25642.140451
HLA B*1501	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.295723	0.369909	-3.925815	19757.099837
HLA A*0212	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.416475	0.490659	-3.925816	26090.053889
HLA A*0219	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.447277	0.521317	-3.925960	28007.653477
HLA B*4002	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.562846	0.636799	-3.926047	36546.479020
HLA A*1101	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.467109	0.540972	-3.926137	29316.270983
HLA A*3001	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.292316	0.365931	-3.926386	19602.724720
HLA B*1501	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.408285	0.481784	-3.926500	25602.635389
HLA B*3801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.546613	0.620011	-3.926602	35205.697286
HLA A*0219	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.408632	0.481784	-3.926848	25623.142696
HLA A*6802	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.429792	0.502834	-3.926958	26902.451500
HLA A*0216	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.276711	0.349724	-3.926987	18910.854875
HLA A*2301	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.529417	0.602429	-3.926988	33838.964879
HLA B*0803	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.516443	0.589436	-3.927007	32843.029734
HLA A*0202	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.582083	0.654994	-3.927089	38201.738330
HLA B*0803	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.514773	0.587655	-3.927117	32716.943926
HLA B*1502	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.599239	0.672009	-3.927230	39741.025067
HLA B*4601	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.386662	0.459317	-3.927345	24359.162968
HLA B*4601	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.364161	0.436810	-3.927352	23129.238960
HLA A*2501	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.467919	0.540487	-3.927432	29371.038309
HLA B*1503	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.410808	0.483198	-3.927610	25751.825351
HLA A*2602	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.595534	0.667908	-3.927626	39403.420842
HLA A*8001	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.449112	0.521317	-3.927795	28126.239614

HLA A*1101	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.445545	0.517364	-3.928181	27896.206811
HLA B*0702	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.469195	0.540972	-3.928223	29457.444634
HLA A*0212	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.408421	0.480013	-3.928408	25610.670080
HLA B*5801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.364107	0.435662	-3.928445	23126.361227
HLA B*0803	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.493999	0.565473	-3.928525	31188.794098
HLA B*1501	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.418169	0.489523	-3.928646	26192.017655
HLA B*5801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.292927	0.364208	-3.928719	19630.316748
HLA B*1509	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.516394	0.587655	-3.928739	32839.298725
HLA B*7301	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.521107	0.592259	-3.928848	33197.619372
HLA A*0301	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.361485	0.432524	-3.928961	22987.157933
HLA A*0216	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.474190	0.545171	-3.929019	29798.203052
HLA A*2601	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.364728	0.435662	-3.929066	23159.414142
HLA A*3201	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.565909	0.636799	-3.929111	36805.207516
HLA A*8001	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.412556	0.483430	-3.929126	25855.684228
HLA B*1801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.412603	0.483430	-3.929173	25858.481907
HLA A*0211	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.326365	0.397004	-3.929362	21201.431148
HLA A*3301	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.615770	0.686161	-3.929609	41282.885158
HLA B*1509	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.464881	0.535260	-3.929621	29166.305175
HLA A*0212	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.419285	0.489523	-3.929762	26259.409765
HLA B*3801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.498683	0.568895	-3.929788	31527.058772
HLA B*2705	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.451193	0.521317	-3.929876	28261.376839
HLA A*2902	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.328076	0.398058	-3.930018	21285.095493
HLA A*3001	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.184433	0.254408	-3.930025	15290.890872
HLA A*0250	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.444424	0.514013	-3.930411	27824.312973
HLA A*3001	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.269033	0.338222	-3.930811	18579.458180
HLA A*1101	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.466075	0.535260	-3.930815	29246.570950
HLA B*2705	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.421562	0.490659	-3.930903	26397.427828
HLA B*4001	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.412706	0.481784	-3.930922	25864.637867
HLA B*0802	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.471439	0.540487	-3.930952	29610.028696
HLA A*0201	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.387908	0.456941	-3.930967	24429.106789
HLA A*2301	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.526889	0.595896	-3.930993	33642.559084
HLA A*2501	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.466305	0.535260	-3.931045	29262.080690
HLA A*2603	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.591044	0.659875	-3.931169	38998.155018
HLA A*2301	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.520675	0.589436	-3.931239	33164.590253
HLA A*2602	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.568073	0.636799	-3.931274	36989.047365
HLA A*3301	1:244-252	9	LNNASGSSA	1.008650	-0.315260	-4.624820	0.693390	-3.931430	42152.201116
HLA B*3901	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.413219	0.481784	-3.931434	25895.159473
HLA A*3201	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.622501	0.691047	-3.931454	41927.726715
HLA B*1501	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.367192	0.435662	-3.931530	23291.216843
HLA B*4501	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.610665	0.679020	-3.931645	40800.417819
HLA B*4402	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.413536	0.481784	-3.931751	25914.078522
HLA A*1101	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.472404	0.540487	-3.931917	29675.938789
HLA B*1801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.500854	0.568895	-3.931959	31685.048811
HLA A*2402	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.587142	0.654994	-3.932148	38649.294137
HLA B*4801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.422859	0.490659	-3.932200	26476.375199
HLA B*1503	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.528174	0.595896	-3.932278	33742.261908
HLA B*7301	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.415810	0.483430	-3.932380	26050.140613
HLA B*4403	1:135-143	9	RAPQRNPAP	0.633630	0.103532	-4.669759	0.737162	-3.932597	46747.550270
HLA B*2705	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.412636	0.480013	-3.932622	25860.440463
HLA B*4002	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.625563	0.692679	-3.932883	42224.322986
HLA A*1101	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.454269	0.521317	-3.932952	28462.221353
HLA A*6901	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.149820	0.216823	-3.932997	14119.527897
HLA B*2705	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.468340	0.535260	-3.933080	29399.494122
HLA A*1101	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.331015	0.397920	-3.933095	

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21429.636711
HLA B*0702	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.468380	0.535260	-3.933120	29402.198062
HLA A*2601	1:19-27 9	DGLVDRGGA	0.866546	-0.409605	-4.390114	0.456941	-3.933173	24553.519598
HLA B*5701	1:42-50 9	DPPPWQRAA	1.009754	-0.520231	-4.422833	0.489523	-3.933310	26474.799669
HLA A*2602	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.624402	0.691047	-3.933355	42111.629758
HLA A*2402	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.570366	0.636799	-3.933568	37184.867967
HLA A*0216	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.417060	0.483430	-3.933630	26125.222501
HLA A*2402	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.581376	0.647511	-3.933864	38139.582133
HLA B*0702	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.414067	0.480013	-3.934053
25945.781357
HLA A*3201	1:72-80 9	TNPPAAADA	1.055160	-0.376140	-4.613087	0.679020	-3.934067	41028.621878
HLA A*6802	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.331135	0.397004	-3.934131	21435.550056
HLA B*4601	1:42-50 9	DPPPWQRAA	1.009754	-0.520231	-4.423742	0.489523	-3.934219	26530.286091
HLA B*0803	1:14-22 9	DGPNADGLV	0.733182	-0.137286	-4.530232	0.595896	-3.934336	33902.548113
HLA B*1501	1:55-63 9	QAGHRQPPP	0.312125	0.024974	-4.271455	0.337099	-3.934357	18683.376424
HLA A*2403	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.411024	0.476646	-3.934378	25764.645477
HLA B*4002	1:70-78 9	RPTNPPAAA	0.962707	-0.286110	-4.611059	0.676597	-3.934462	40837.516599
HLA B*3901	1:26-34 9	GAHRAATGP	0.552469	-0.011497	-4.475522	0.540972	-3.934550	29889.746602
HLA B*4001	1:19-27 9	DGLVDRGGA	0.866546	-0.409605	-4.391540	0.456941	-3.934599	24634.281042
HLA B*5801	1:24-32 9	RGGAHRAAT	0.870371	-0.447559	-4.357451	0.422812	-3.934639	22774.623907
HLA A*0206	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.418557	0.483430	-3.935126	26215.407919
HLA A*2603	1:53-61 9	QSQAGHRQP	0.575848	0.110313	-4.621310	0.686161	-3.935149	41812.884335
HLA A*0203	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.411837	0.476646	-3.935191	25812.917462
HLA A*2402	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.569701	0.634444	-3.935258	37127.981543
HLA B*1503	1:11-19 9	SKGDGPNAD	1.160358	-0.794427	-4.301261	0.365931	-3.935330	20010.637775
HLA A*2902	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.456863	0.521317	-3.935546	28632.721121
HLA A*0202	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-3.948714	0.013159	-3.935555	8886.150360
HLA B*7301	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.537997	0.602429	-3.935569	34514.166424
HLA B*3901	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.456891	0.521317	-3.935574	28634.579980
HLA B*1509	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.480809	0.545171	-3.935638	30255.795386
HLA B*5101	1:66-74 9	HPEGRPTNP	0.640941	-0.167099	-4.409504	0.473842	-3.935662	25674.621752
HLA A*6802	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.419179	0.483430	-3.935749	26253.017821
HLA B*4002	1:53-61 9	QSQAGHRQP	0.575848	0.110313	-4.622003	0.686161	-3.935842	41879.667517
HLA B*4601	1:66-74 9	HPEGRPTNP	0.640941	-0.167099	-4.409725	0.473842	-3.935883	25687.681377
HLA B*2705	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.334001	0.398058	-3.935943	21577.493979
HLA A*2603	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.591004	0.654994	-3.936010	38994.568597
HLA B*4002	1:91-99 9	APVTGPAAA	0.928870	-0.243763	-4.621517	0.685107	-3.936410	41832.794944
HLA B*1502	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.583939	0.647511	-3.936428	38365.354778
HLA B*3801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.494478	0.557970	-3.936508
31223.233594
HLA B*1517	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-3.858672	-0.077944	-3.936616	7222.241299
HLA A*2601	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.396248	0.459317	-3.936931	24902.804534
HLA A*3002	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.596840	0.659875	-3.936966	39522.120756
HLA A*0219	1:42-50 9	DPPPWQRAA	1.009754	-0.520231	-4.426559	0.489523	-3.937036	26702.932981
HLA B*4801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.418843	0.481784	-3.937059	26232.715969
HLA A*2402	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.597059	0.659875	-3.937184	39542.010117
HLA B*4801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.417271	0.480013	-3.937258
26137.945708
HLA B*4403	1:86-94 9	ISGASAPVT	1.091631	-0.395829	-4.633144	0.695802	-3.937343	42967.935064
HLA B*3901	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.472639	0.535260	-3.937379	29691.997486
HLA B*3501	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.414055	0.476646	-3.937409	25945.079548
HLA A*2501	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.454776	0.517364	-3.937412	28495.499925
HLA A*0216	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.472839	0.535260	-3.937579	29705.654211
HLA A*6901	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.374527	0.436810	-3.937718	23687.938721
HLA A*0202	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.558426	0.620011	-3.938415	36176.467806
HLA B*4801	1:42-50 9	DPPPWQRAA	1.009754	-0.520231	-4.428058	0.489523	-3.938535	26795.257639
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HLA A*0212	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.422140	0.483430	-3.938709	26432.581775
HLA B*4001	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.375538	0.436810	-3.938728	23743.106987
HLA B*5101	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.496738	0.557970	-3.938768	31386.152659
HLA A*0201	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.365367	0.426351	-3.939015	23193.518071
HLA A*3001	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.288804	0.349724	-3.939079	19444.821516
HLA A*6801	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.625250	0.686161	-3.939089	42193.952868
HLA A*0211	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.422316	0.483198	-3.939118	26443.308752
HLA B*5701	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.398497	0.459317	-3.939180	25032.067250
HLA B*4501	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.609027	0.669638	-3.939389	40646.861668
HLA A*0250	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.599324	0.659875	-3.939449	39748.765624
HLA A*3001	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-3.958459	0.019002	-3.939457	9087.811731
HLA A*3301	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.616059	0.676597	-3.939462	41310.364607
HLA A*0203	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.396413	0.456941	-3.939472	24912.236819
HLA B*5801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.337532	0.398058	-3.939474	21753.657177
HLA A*2902	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.442331	0.502834	-3.939497	27690.516630
HLA B*1517	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.398880	0.459317	-3.939563	25054.150561
HLA A*0201	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.337570	0.397920	-3.939650	21755.540216
HLA A*2301	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.539548	0.599894	-3.939654	34637.620448
HLA B*3501	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.423049	0.483198	-3.939851	26487.979716
HLA B*4402	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.264106	0.324195	-3.939912	18369.873886
HLA A*0216	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.366346	0.426351	-3.939995	23245.899942
HLA A*0216	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.421827	0.481784	-3.940043	26413.569970
HLA A*2403	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.413928	0.473842	-3.940086	25937.501214
HLA B*7301	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.522171	0.581978	-3.940193	33279.075878
HLA A*6901	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.363106	0.422812	-3.940294	23073.125287
HLA B*5301	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.595315	0.654994	-3.940322	39383.601192
HLA B*4403	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.555687	0.615291	-3.940396	35948.987372
HLA B*0801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.376186	0.435662	-3.940524	23778.584998
HLA B*5101	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.461898	0.521317	-3.940581	28966.603167
HLA A*0201	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.376346	0.435662	-3.940684	23787.334094
HLA A*1101	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.258883	0.318175	-3.940708	18150.277510
HLA B*4501	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.588246	0.647511	-3.940734	38747.690725
HLA B*5401	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.540662	0.599894	-3.940768	34726.555242
HLA A*2601	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.378009	0.436810	-3.941200	23878.619085
HLA A*2403	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.430950	0.489523	-3.941428	26974.298133
HLA B*5401	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.482660	0.540972	-3.941688	30385.050931
HLA B*4403	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.627219	0.685107	-3.942112	42385.672861
HLA A*3301	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.627539	0.685107	-3.942431	42416.869380
HLA B*1517	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.379294	0.436810	-3.942485	23949.385573
HLA B*1517	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.477954	0.535260	-3.942694	30057.575744
HLA B*5801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.354063	0.411293	-3.942770	22597.648890
HLA A*0211	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.483480	0.540487	-3.942993	30442.473658
HLA A*3301	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.615014	0.672009	-3.943004	41211.033620
HLA B*4402	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.434073	0.490659	-3.943414	27168.935252
HLA A*0101	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.366234	0.422812	-3.943421	23239.864354
HLA B*3901	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.509045	0.565473	-3.943571	32288.263234
HLA B*1801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-3.932930	-0.010665	-3.943595	8568.993577
HLA B*5401	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.539557	0.595896	-3.943661	34638.369999
HLA B*4001	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.379426	0.435662	-3.943764	23956.642229
HLA A*2402	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.559216	0.615291	-3.943924	36242.286396
HLA A*2603	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.620753	0.676597	-3.944156	41759.308561
HLA A*6901	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.376795	0.432524	-3.944271	23811.925983
HLA B*4002	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.635393	0.691047	-3.944346	43190.968256

HLA B*5101	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.485390	0.540972	-3.944418	30576.661839
HLA A*3101	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.403748	0.459317	-3.944431	25336.569710
HLA A*8001	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.435118	0.490659	-3.944459	27234.420558
HLA A*3101	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.380204	0.435662	-3.944542	23999.579181
HLA A*2902	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.426380	0.481784	-3.944596	26691.956284
HLA B*0803	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.462046	0.517364	-3.944681	28976.477334
HLA B*1503	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.421369	0.476646	-3.944723	26385.720238
HLA B*0802	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.424809	0.480013	-3.944795	26595.526938
HLA B*4801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.234580	0.289672	-3.944908	17162.486030
HLA B*5401	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.547525	0.602429	-3.945096	35279.672958
HLA B*1501	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.402176	0.456941	-3.945235	25245.036934
HLA A*0202	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.605207	0.659875	-3.945332	40290.880360
HLA B*3501	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.402406	0.456941	-3.945465	25258.424622
HLA B*0802	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.467901	0.522301	-3.945600	29369.767184
HLA A*3101	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.299781	0.353947	-3.945833	19942.553006
HLA A*2403	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.200405	0.254408	-3.945997	15863.703639
HLA B*5701	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.382938	0.436810	-3.946129	24151.184029
HLA A*2603	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.637195	0.691047	-3.946148	43370.556543
HLA B*1503	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.300288	0.353947	-3.946341	19965.870219
HLA B*1517	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.369161	0.422812	-3.946349	23397.046983
HLA A*6901	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.344595	0.398058	-3.946537	22110.310014
HLA A*0206	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.436190	0.489523	-3.946667	27301.688345
HLA A*2402	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.542579	0.595896	-3.946683	34880.193428
HLA B*3801	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.546801	0.599894	-3.946907	35220.937297
HLA B*3501	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-3.785006	-0.162047	-3.947053	6095.456574
HLA B*7301	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.594582	0.647511	-3.947071	39317.182255
HLA B*5701	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.423721	0.476646	-3.947074	26528.994389
HLA A*2602	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.564610	0.617415	-3.947195	36695.263069
HLA A*1101	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.423937	0.476646	-3.947291	26542.201416
HLA B*0801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.228927	0.281226	-3.947701	16940.543353
HLA B*5101	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.516615	0.568895	-3.947719	32856.002727
HLA B*5701	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.421562	0.473842	-3.947720	26397.427828
HLA A*2403	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.370893	0.422812	-3.948080	23490.519293
HLA A*8001	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.424811	0.476646	-3.948165	26595.670817
HLA B*4001	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.407514	0.459317	-3.948197	25557.245239
HLA A*0203	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.261000	0.312492	-3.948508	18238.963558
HLA B*5801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.345518	0.397004	-3.948515	22157.368452
HLA A*0206	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.489145	0.540487	-3.948657	30842.143057
HLA B*3501	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.375014	0.426351	-3.948662	23714.480448
HLA A*0206	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.506674	0.557970	-3.948704	32112.495384
HLA A*3301	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.639859	0.691047	-3.948812	43637.444671
HLA A*0202	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.536552	0.587655	-3.948897	34399.525783
HLA B*1801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.536649	0.587655	-3.948993	34407.156632
HLA B*4001	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.375357	0.426351	-3.949005	23733.218583
HLA A*2601	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.381580	0.432524	-3.949057	24075.783255
HLA B*1501	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.422931	0.473842	-3.949089	26480.815833
HLA A*0212	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.423117	0.473842	-3.949275	26492.135656
HLA A*0206	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.490399	0.540972	-3.949427	30931.371155
HLA B*4002	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.628617	0.679020	-3.949597	42522.327246
HLA A*0202	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.515236	0.565473	-3.949762	32751.830535
HLA A*6802	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.423718	0.473842	-3.949876	26528.850870
HLA A*0206	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.372749	0.422812	-3.949936	23591.128204
HLA A*6802	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.321911	0.371790	-3.950121	20985.076381
HLA B*5401	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.539607	0.589436	-3.950171	34642.305407
HLA A*3002	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.532227	0.581978	-3.950249	34058.620522

HLA B*1517	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.314590	0.364208	-3.950381	20634.291381
HLA B*5401	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.285155	0.334728	-3.950427	19282.139073
HLA B*4601	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.347496	0.397004	-3.950493	22258.528295
HLA B*2705	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.377095	0.426351	-3.950744	23828.420638
HLA A*3001	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.167587	0.216823	-3.950763	14709.129834
HLA A*3002	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.553379	0.602429	-3.950951	35758.514369
HLA B*3801	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.566273	0.615291	-3.950982	36836.082833
HLA A*2501	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.496221	0.545171	-3.951050	31348.819846
HLA B*1502	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.520108	0.568895	-3.951213	33121.378990
HLA A*2603	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.553647	0.602429	-3.951218	35780.574425
HLA A*0202	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.533261	0.581978	-3.951283	34139.788567
HLA B*1502	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.571447	0.620011	-3.951436	37277.519570
HLA A*0202	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.520357	0.568895	-3.951462	33140.377833
HLA B*3801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.533442	0.581978	-3.951463	34154.012850
HLA A*2902	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.441227	0.489523	-3.951704	27620.198831
HLA A*8001	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.454558	0.502834	-3.951724	28481.166884
HLA B*1503	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.411308	0.459317	-3.951991	25781.516447
HLA B*5101	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.466214	0.514013	-3.952200	29255.907461
HLA B*4801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.435421	0.483198	-3.952223	27253.433432
HLA B*3801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.564460	0.612174	-3.952285	36682.560161
HLA B*5401	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.389205	0.436810	-3.952395	24502.167459
HLA B*4403	1:1-9	9	VTAPNEPGA	0.903317	-0.210638	-4.645388	0.692679	-3.952708	44196.476718
HLA B*0702	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.349891	0.397004	-3.952887	22381.571209
HLA B*0802	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.474289	0.521317	-3.952972	29804.974430
HLA A*3301	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.552928	0.599894	-3.953035	35721.391329
HLA A*2601	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.351148	0.397920	-3.953227	22446.443817
HLA A*0211	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.435306	0.481784	-3.953522	27246.209925
HLA B*3501	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.456374	0.502834	-3.953540	28600.520074
HLA B*5301	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.475889	0.522301	-3.953588	29914.982482
HLA B*3801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.556067	0.602429	-3.953638	35980.506948
HLA B*3901	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.494245	0.540487	-3.953758	31206.515562
HLA A*3001	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.203938	0.250113	-3.953825	15993.304772
HLA B*7301	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.573942	0.620011	-3.953931	37492.306605
HLA A*0219	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.437681	0.483430	-3.954251	27395.638559
HLA A*8001	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.444088	0.489523	-3.954566	27802.796015
HLA B*0803	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.436370	0.481784	-3.954586	27313.063546
HLA A*0219	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.391444	0.436810	-3.954634	24628.817630
HLA B*4001	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.377584	0.422812	-3.954772	23855.248826
HLA A*3002	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.547123	0.592259	-3.954864	35247.051140
HLA A*2301	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.547139	0.592259	-3.954881	35248.385944
HLA A*2501	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.436763	0.481784	-3.954978	27337.750724
HLA A*3101	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.411983	0.456941	-3.955042	25821.576906
HLA B*4402	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.435240	0.480013	-3.955227	27242.083066
HLA B*1501	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.184531	0.229292	-3.955240	15294.365592
HLA B*7301	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.567490	0.612174	-3.955316	36939.454192
HLA B*4801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.429907	0.473842	-3.956065	26909.583870
HLA A*0301	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.367401	0.411293	-3.956108	23302.433802
HLA B*3501	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.055249	0.099112	-3.956136	11356.609834
HLA A*6901	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.354103	0.397920	-3.956183	22599.727249
HLA A*0101	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.353220	0.397004	-3.956216	22553.803453
HLA A*2301	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.543909	0.587655	-3.956253	34987.160167
HLA A*0203	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.430170	0.473842	-3.956328	26925.893532

HLA A*3002	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.544014	0.587655	-3.956359	34995.678654
HLA B*0801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.354329	0.397920	-3.956409	22611.467451
HLA A*3101	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.320670	0.364208	-3.956462	20925.219687
HLA A*3301	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.635708	0.679020	-3.956688	43222.289826
HLA A*3002	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.368179	0.411293	-3.956886	23344.198230
HLA B*5801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.354867	0.397920	-3.956947	22639.497357
HLA A*2301	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.525865	0.568895	-3.956969	33563.299500
HLA B*5301	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.574475	0.617415	-3.957060	37538.377121
HLA B*5101	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.492370	0.535260	-3.957110	31072.084562
HLA A*8001	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.414490	0.456941	-3.957549	25971.059147
HLA B*5101	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.448219	0.490659	-3.957560	28068.478267
HLA B*4601	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.393370	0.435662	-3.957708	24738.316447
HLA A*2301	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.539818	0.581978	-3.957840	34659.176507
HLA A*0216	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.393511	0.435662	-3.957849	24746.347643
HLA A*0301	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.327892	0.369909	-3.957984	21276.115687
HLA B*4601	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.415021	0.456941	-3.958080	26002.831690
HLA A*3301	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.573512	0.615291	-3.958221	37455.207225
HLA B*1502	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.540316	0.581978	-3.958338	34698.949799
HLA B*1509	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.516424	0.557970	-3.958455	32841.608347
HLA B*4403	1:72-80	9	TNPPAAADA	1.055160	-0.376140	-4.637613	0.679020	-3.958593	43412.340781
HLA B*3501	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.440656	0.481784	-3.958872	27583.913089
HLA B*0702	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.442319	0.483430	-3.958889	27689.767627
HLA A*3301	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.618991	0.659875	-3.959117	41590.216908
HLA B*4002	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.631354	0.672009	-3.959345	42791.171408
HLA B*1501	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.392012	0.432524	-3.959488	24661.082626
HLA A*0211	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.347224	0.387714	-3.959510	22244.564401
HLA B*1517	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.442738	0.483198	-3.959539	27716.444615
HLA B*0802	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.441464	0.481784	-3.959680	27635.294598
HLA B*2705	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.433605	0.473842	-3.959763	27139.701786
HLA B*1801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.525273	0.565473	-3.959799	33517.574096
HLA B*1503	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.358027	0.398058	-3.959969	22804.829927
HLA B*0803	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.501033	0.540972	-3.960061	31698.078847
HLA B*3801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.525552	0.565473	-3.960079	33539.158880
HLA B*4402	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.437108	0.476646	-3.960462	27359.499818
HLA A*0219	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.417560	0.456941	-3.960620	26155.344113
HLA A*0250	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.572829	0.612174	-3.960654	37396.288715
HLA A*2403	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.420070	0.459317	-3.960753	26306.900864
HLA B*1501	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.310520	0.349724	-3.960796	20441.852534
HLA B*1517	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.442669	0.481784	-3.960885	27712.096613
HLA B*1801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.519204	0.557970	-3.961234	33052.465331
HLA A*0203	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.333052	0.371790	-3.961262	21530.385810
HLA A*0211	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.482763	0.521317	-3.961446	30392.284501
HLA B*3901	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.451109	0.489523	-3.961586	28255.873302
HLA B*4501	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.616583	0.654994	-3.961589	41360.231723
HLA B*3901	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.445183	0.483430	-3.961753	27872.975520
HLA A*3101	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.296588	0.334728	-3.961860	19796.472225
HLA B*0702	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.418827	0.456941	-3.961886	26231.722575
HLA A*0212	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.397555	0.435662	-3.961893	24977.822405
HLA A*0211	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.519930	0.557970	-3.961960	33107.763882
HLA B*4501	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.653312	0.691047	-3.962265	45010.357490
HLA B*1801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.419299	0.456941	-3.962358	26260.262142

HLA A*0211	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.527965	0.565473	-3.962492	33726.019590
HLA B*5801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.350205	0.387714	-3.962492	22397.802055
HLA A*0212	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.439343	0.476646	-3.962696	27500.621809
HLA A*2902	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.389136	0.426351	-3.962785	24498.323695
HLA A*2501	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.485160	0.522301	-3.962859	30560.455333
HLA A*0101	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.361093	0.398058	-3.963035	22966.399530
HLA A*2403	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.420002	0.456941	-3.963061	26302.773982
HLA B*0803	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.465941	0.502834	-3.963107	29237.553760
HLA A*6901	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.374877	0.411293	-3.963584	23707.040638
HLA A*2501	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.437580	0.473842	-3.963738	27389.266383
HLA A*2902	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.454436	0.490659	-3.963777	28473.155853
HLA B*5301	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.598278	0.634444	-3.963835	39653.189510
HLA A*0219	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.423176	0.459317	-3.963859	26495.718886
HLA A*0201	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.386735	0.422812	-3.963923	24363.248502
HLA A*2902	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.440698	0.476646	-3.964052	27586.599286
HLA B*4601	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.390642	0.426351	-3.964291	24583.424955
HLA A*2403	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.361304	0.397004	-3.964301	22977.584363
HLA A*2501	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.362265	0.397920	-3.964345	23028.481881
HLA A*0202	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.146724	0.182285	-3.964439	14019.210429
HLA B*5801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.282808	0.318175	-3.964633	19178.210246
HLA A*0216	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.361746	0.397004	-3.964742	23000.965814
HLA A*0216	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.454306	0.489523	-3.964784	28464.685099
HLA A*3201	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.352677	0.387714	-3.964964	22525.635921
HLA A*3301	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.601894	0.636799	-3.965095	39984.712991
HLA A*2501	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.445303	0.480013	-3.965290	27880.666856
HLA B*1801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.505831	0.540487	-3.965343	32050.188619
HLA B*5301	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.585433	0.620011	-3.965423	38497.585403
HLA A*3001	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.289854	0.324195	-3.965660	19491.900281
HLA A*0216	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.363656	0.397920	-3.965736	23102.352377
HLA A*0216	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.284065	0.318175	-3.965890	19233.797966
HLA A*0202	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.401614	0.435662	-3.965953	25212.417115
HLA B*0802	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.468833	0.502834	-3.965999	29432.913182
HLA A*0201	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.363019	0.397004	-3.966016	23068.507297
HLA A*3201	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.613564	0.647511	-3.966052	41073.704568
HLA A*0202	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.364126	0.398058	-3.966068	23127.362137
HLA A*0211	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.468960	0.502834	-3.966126	29441.512793
HLA A*6901	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.363320	0.397004	-3.966317	23084.486981
HLA A*2402	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.558614	0.592259	-3.966356	36192.128049
HLA A*0212	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.354070	0.387714	-3.966357	22598.015646
HLA B*1517	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.469207	0.502834	-3.966373	29458.241453
HLA B*1501	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.330590	0.364208	-3.966381	21408.663296
HLA A*2603	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.613944	0.647511	-3.966433	41109.717425
HLA A*0219	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.440287	0.473842	-3.966445	27560.494567
HLA B*0801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.336466	0.369909	-3.966557	21700.293804
HLA A*1101	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.449758	0.483198	-3.966560	28168.114711
HLA B*7301	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.480597	0.514013	-3.966584	30241.067727
HLA B*7301	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.556213	0.589436	-3.966777	35992.577306
HLA A*0301	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.363783	0.397004	-3.966779	23109.102345
HLA A*2501	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.488174	0.521317	-3.966857	30773.309869
HLA B*3901	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.480945	0.514013	-3.966932	30265.290344
HLA A*2902	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.426458	0.459317	-3.967141	26696.721927
HLA B*0803	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.502414	0.535260	-3.967154	31799.071450
HLA A*0212	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.426585	0.459317	-3.967268	26704.522087

HLA A*3201	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.627165	0.659875	-3.967290	42380.399248
HLA B*1502	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.484782	0.517364	-3.967417	30533.849005
HLA A*2501	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.508511	0.540972	-3.967539	32248.636136
HLA A*0101	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.400228	0.432524	-3.967704	25132.071543
HLA A*0216	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.444399	0.476646	-3.967752	27822.657232
HLA A*3201	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.490230	0.522301	-3.967929	30919.325360
HLA A*0211	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.509005	0.540972	-3.968033	32285.293880
HLA B*5101	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.451600	0.483430	-3.968170	28287.839349
HLA B*7301	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.458925	0.490659	-3.968267	28769.046696
HLA A*2601	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-3.956697	-0.011592	-3.968289	9051.013394
HLA B*4402	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.427753	0.459317	-3.968435	26776.419546
HLA A*6802	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.333052	0.364208	-3.968843	21530.385810
HLA B*1502	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.365867	0.397004	-3.968863	23220.259514
HLA B*0801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.198323	0.229292	-3.969031	15787.848280
HLA B*0803	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.514265	0.545171	-3.969094	32678.735326
HLA A*2402	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.558553	0.589436	-3.969117	36187.037726
HLA A*8001	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.404897	0.435662	-3.969235	25403.684713
HLA A*0250	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.571717	0.602429	-3.969288	37300.718519
HLA A*2403	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.451238	0.481784	-3.969454	28264.281916
HLA A*8001	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.428810	0.459317	-3.969493	26841.684814
HLA A*0206	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.514759	0.545171	-3.969588	32715.881973
HLA B*3801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.557324	0.587655	-3.969669	36084.795842
HLA B*3801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.514869	0.545171	-3.969698	32724.201527
HLA A*2402	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.535216	0.565473	-3.969742	34293.799046
HLA B*1509	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.453181	0.483430	-3.969751	28391.018998
HLA A*2403	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.405458	0.435662	-3.969796	25436.551994
HLA A*0301	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.367869	0.398058	-3.969811	23327.533963
HLA B*7301	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.569828	0.599894	-3.969935	37138.829474
HLA B*4001	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.402792	0.432524	-3.970268	25280.844391
HLA B*5401	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.552252	0.581978	-3.970273	35665.779019
HLA A*2402	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.590304	0.620011	-3.970293	38931.754268
HLA A*2402	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.492685	0.522301	-3.970384	31094.617664
HLA A*2301	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.528543	0.557970	-3.970573	33770.933160
HLA B*1517	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.152968	0.182285	-3.970684	14222.255805
HLA B*5701	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.427912	0.456941	-3.970971	26786.271665
HLA B*4801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.428081	0.456941	-3.971141	26796.707272
HLA B*4402	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.406870	0.435662	-3.971208	25519.389552
HLA B*4402	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.445263	0.473842	-3.971421	27878.102842
HLA A*2603	1:211-219	9	ALFFVWMIT	0.834379	-0.166471	-4.639357	0.667908	-3.971448	43586.954123
HLA A*0206	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.448108	0.476646	-3.971462	28061.342349
HLA A*0201	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.404161	0.432524	-3.971637	25360.705172
HLA A*2601	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.382971	0.411293	-3.971678	24153.013272
HLA A*0201	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.289936	0.318175	-3.971761	19495.591347
HLA A*2501	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.474611	0.502834	-3.971777	29827.072718
HLA A*3301	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.626789	0.654994	-3.971795	42343.731398
HLA B*4501	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.564103	0.592259	-3.971844	36652.408375
HLA A*2403	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.370077	0.398058	-3.972019	23446.463513
HLA B*5101	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.453900	0.481784	-3.972116	28438.057155
HLA B*1503	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.252631	0.280375	-3.972256	17890.862997
HLA A*6901	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.307062	0.334728	-3.972334	20279.713211
HLA A*2603	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.568287	0.595896	-3.972391	37007.261552
HLA B*5101	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.475337	0.502834	-3.972503	29876.975014
HLA A*0250	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.554512	0.581978	-3.972534	35851.878750
HLA A*2601	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.399021	0.426351	-3.972669	25062.284291
HLA A*6802	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.313187	0.340384	-3.972803	20567.756234

HLA B*5301	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.562401	0.589436	-3.972965	36509.130473
HLA A*3002	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.495556	0.522301	-3.973255	31300.861567
HLA A*0212	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.430243	0.456941	-3.973302	26930.409560
HLA A*2902	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.453343	0.480013	-3.973330	28401.618843
HLA B*3501	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.432691	0.459317	-3.973374	27082.647780
HLA A*6801	1:91-99	9	APVTGPAAA	0.928870	-0.243763	-4.658486	0.685107	-3.973379	45549.753207
HLA B*4403	1:53-61	9	QSQAGHRQP	0.575848	0.110313	-4.659604	0.686161	-3.973443	45667.199860
HLA A*2403	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.399829	0.426351	-3.973477	25108.968676
HLA A*0212	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.323330	0.349724	-3.973605	21053.758802
HLA A*6901	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.254896	0.281226	-3.973670	17984.409947
HLA B*1502	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.576137	0.602429	-3.973708	37682.228517
HLA B*3801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.514376	0.540487	-3.973888	32687.045434
HLA A*0216	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.430929	0.456941	-3.973988	26972.984813
HLA A*0301	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.361906	0.387714	-3.974192	23009.428792
HLA B*3901	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.465215	0.490659	-3.974556	29188.719464
HLA B*1502	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.586770	0.612174	-3.974596	38616.272286
HLA B*3901	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.454884	0.480013	-3.974871	28502.592052
HLA B*0801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.401224	0.426351	-3.974873	25189.785479
HLA B*5301	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.587163	0.612174	-3.974988	38651.175979
HLA B*4002	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.567270	0.592259	-3.975011	36920.674163
HLA A*0203	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.285101	0.310085	-3.975017	19279.739995
HLA B*1501	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.329206	0.353947	-3.975258	21340.554772
HLA A*2603	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.612194	0.636799	-3.975395	40944.363602
HLA B*4501	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.458599	0.483198	-3.975401	28747.421236
HLA B*4601	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.373707	0.398058	-3.975649	23643.256872
HLA A*2402	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.593100	0.617415	-3.975685	39183.196367
HLA A*3201	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.578124	0.602429	-3.975695	37855.086531
HLA B*4002	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.635628	0.659875	-3.975753	43214.340412
HLA A*3002	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.398577	0.422812	-3.975764	25036.671977
HLA A*3101	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.325665	0.349724	-3.975941	21167.278861
HLA B*2705	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.286093	0.310085	-3.976008	19323.805406
HLA B*5301	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.465605	0.489523	-3.976083	29214.943921
HLA A*2301	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.490150	0.514013	-3.976137	30913.638699
HLA B*0702	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.411851	0.435662	-3.976189	25813.755346
HLA B*7301	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.127618	0.151290	-3.976328	13415.829880
HLA B*4801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.435710	0.459317	-3.976393	27271.574348
HLA B*2705	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.465967	0.489523	-3.976444	29239.293703
HLA B*0702	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.193610	0.217020	-3.976590	15617.441120
HLA A*3301	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.588873	0.612174	-3.976699	38803.699896
HLA A*0219	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.456787	0.480013	-3.976774	28627.764755
HLA B*5701	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.412610	0.435662	-3.976948	25858.901585
HLA B*0802	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.467656	0.490659	-3.976997	29353.247565
HLA B*4601	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.400076	0.422812	-3.977263	25123.235585
HLA B*5801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.347205	0.369909	-3.977296	22243.601697
HLA B*1517	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.454114	0.476646	-3.977467	28452.060655
HLA A*0219	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.374525	0.397004	-3.977521	23687.810573
HLA B*0803	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.414438	0.436810	-3.977628	25967.968318
HLA B*4403	1:272-280	9	IVLMTALAT	0.837199	-0.167561	-4.647338	0.669638	-3.977700	44395.374303
HLA A*0206	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.434674	0.456941	-3.977733	27206.588437
HLA B*4402	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.311925	0.334139	-3.977786	20508.091338
HLA B*2705	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.312473	0.334139	-3.978333	20533.958172

HLA B*4403	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.669411	0.691047	-3.978364	46710.136189
HLA A*2902	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.410937	0.432524	-3.978413	25759.488790
HLA A*2402	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.580885	0.602429	-3.978456	38096.483342
HLA A*3002	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.543979	0.565473	-3.978506	34992.838928
HLA B*1801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.461954	0.483198	-3.978756	28970.364357
HLA B*0702	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.462125	0.483198	-3.978927	28981.807648
HLA B*5301	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.161572	0.182632	-3.978941	14506.822586
HLA A*2602	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.626507	0.647511	-3.978996	42316.251332
HLA B*5801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.350971	0.371790	-3.979182	22437.338206
HLA B*4002	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.634249	0.654994	-3.979255	43077.326406
HLA A*0211	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.469994	0.490659	-3.979335	29511.677409
HLA A*6801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.343671	0.364208	-3.979463	22063.351521
HLA A*2402	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.462823	0.483198	-3.979625	29028.411223
HLA A*0101	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.390920	0.411293	-3.979626	24599.123210
HLA B*1801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.459663	0.480013	-3.979650	28817.958356
HLA A*0250	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.572067	0.592259	-3.979809	37330.797760
HLA A*0219	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.415498	0.435662	-3.979836	26031.403881
HLA A*2301	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.545452	0.565473	-3.979979	35111.736191
HLA A*0211	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.298160	0.318175	-3.979985	19868.249742
HLA B*3801	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.569473	0.589436	-3.980037	37108.503403
HLA B*0802	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.463303	0.483198	-3.980104	29060.465167
HLA A*3101	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.378749	0.398058	-3.980691	23919.345692
HLA A*6901	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.321114	0.340384	-3.980730	20946.626018
HLA B*5301	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.583197	0.602429	-3.980768	38299.824275
HLA A*1101	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.440242	0.459317	-3.980925	27557.661828
HLA A*0211	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.526123	0.545171	-3.980952	33583.278554
HLA B*5101	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.461103	0.480013	-3.981090	28913.684897
HLA B*0803	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.495117	0.514013	-3.981104	31269.212085
HLA B*2705	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.379027	0.397920	-3.981106	23934.619885
HLA A*2602	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.601126	0.620011	-3.981115	39914.041213
HLA A*2501	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.464548	0.483430	-3.981118	29143.908099
HLA B*4403	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.653228	0.672009	-3.981219	45001.592306
HLA A*3201	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.598725	0.617415	-3.981309	39693.969143
HLA A*2601	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.404147	0.422812	-3.981335	25359.881994
HLA B*1502	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.539344	0.557970	-3.981374	34621.321729
HLA B*1801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.463338	0.481784	-3.981554	29062.823471
HLA A*0101	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.379482	0.397920	-3.981562	23959.752898
HLA A*2902	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.455514	0.473842	-3.981672	28543.946515
HLA A*3101	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.393079	0.411293	-3.981786	24721.726900
HLA A*3201	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.522345	0.540487	-3.981858	33292.401217
HLA A*2603	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.601870	0.620011	-3.981860	39982.549921
HLA B*3801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.578075	0.595896	-3.982179	37850.786147
HLA A*2902	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.320546	0.338222	-3.982324	20919.220781
HLA B*0802	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.456240	0.473842	-3.982398	28591.702072
HLA B*4001	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.393784	0.411293	-3.982491	24761.882017
HLA A*6801	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.659181	0.676597	-3.982584	45622.751697
HLA A*8001	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.405400	0.422812	-3.982587	25433.112003
HLA A*6802	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.415223	0.432524	-3.982699	26014.932335
HLA B*1503	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.317437	0.334728	-3.982709	20770.030526
HLA A*3301	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.551610	0.568895	-3.982715	35613.143118
HLA A*6901	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.346980	0.364208	-3.982771	22232.052496

HLA B*0802	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.472320	0.489523	-3.982797	29670.159784
HLA A*0301	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.347123	0.364208	-3.982914	22239.390356
HLA A*6801	1:126-134	9	LPDLSGPTP	0.926231	-0.235184	-4.674277	0.691047	-3.983230	47236.413638
HLA B*4001	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.371064	0.387714	-3.983351	23499.798045
HLA A*2402	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.552524	0.568895	-3.983629	35688.168001
HLA B*0802	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.467186	0.483430	-3.983756	29321.505177
HLA A*2301	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.506073	0.522301	-3.983772	32068.052556
HLA B*4501	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.618613	0.634444	-3.984169	41554.007927
HLA A*2601	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.371950	0.387714	-3.984236	23547.775455
HLA B*4402	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.441189	0.456941	-3.984248	27617.808179
HLA B*0803	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.506561	0.522301	-3.984260	32104.157665
HLA B*4601	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.416827	0.432524	-3.984304	26111.234126
HLA B*4402	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.421139	0.436810	-3.984329	26371.735051
HLA B*3501	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.150563	0.166065	-3.984497	14143.686226
HLA B*3801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.501952	0.517364	-3.984587	31765.199701
HLA B*1801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.525663	0.540972	-3.984690	33547.687791
HLA B*1509	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.507118	0.522301	-3.984817	32145.346208
HLA B*7301	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.520195	0.535260	-3.984935	33128.009424
HLA B*4403	1:70-78	9	RPTNPPAAA	0.962707	-0.286110	-4.661576	0.676597	-3.984978	45874.949697
HLA A*8001	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.465001	0.480013	-3.984988	29174.353396
HLA B*3901	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.461660	0.476646	-3.985014	28950.780173
HLA B*5701	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.407888	0.422812	-3.985075	25579.238333
HLA A*6901	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.354996	0.369909	-3.985087	22646.234604
HLA A*2602	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.339092	0.353947	-3.985145	21831.940452
HLA B*4801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.372927	0.387714	-3.985214	23600.829728
HLA A*2603	1:97-105	9	AAAVRTPQP	0.598271	0.073738	-4.657262	0.672009	-3.985253	45421.549607
HLA A*3001	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.169993	0.184583	-3.985410	14790.840508
HLA A*3301	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.632992	0.647511	-3.985480	42952.828355
HLA A*3002	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.526020	0.540487	-3.985532	33575.285506
HLA B*1502	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.585499	0.599894	-3.985606	38503.417339
HLA A*0201	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.396920	0.411293	-3.985627	24941.364681
HLA A*0216	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.373353	0.387714	-3.985639	23623.950741
HLA B*1502	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.476706	0.490659	-3.986048	29971.354715
HLA A*2402	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.500229	0.514013	-3.986216	31639.485850
HLA B*4403	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.588897	0.602429	-3.986468	38805.799190
HLA A*3002	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.477148	0.490659	-3.986489	30001.852863
HLA B*4501	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.646389	0.659875	-3.986514	44298.449942
HLA A*0101	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.374302	0.387714	-3.986588	23675.639600
HLA A*0202	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.508370	0.521317	-3.987053	32238.170142
HLA B*4002	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.634634	0.647511	-3.987123	43115.562510
HLA B*2705	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.446476	0.459317	-3.987158	27956.033365
HLA A*0201	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.385323	0.398058	-3.987265	24284.163850
HLA B*3501	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.375122	0.387714	-3.987408	23720.382647
HLA A*2402	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.587334	0.599894	-3.987441	38666.443189
HLA B*0803	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.528064	0.540487	-3.987576	33733.683530
HLA B*5701	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.385504	0.397920	-3.987584	24294.281804
HLA B*1502	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.575274	0.587655	-3.987619	37607.487337
HLA A*2603	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.580093	0.592259	-3.987835	38027.091674
HLA B*0801	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.328508	0.340384	-3.988124	21306.293643
HLA B*5101	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.447441	0.459317	-3.988124	28018.261767
HLA A*2301	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.528879	0.540487	-3.988392	33797.068940
HLA B*1509	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.468464	0.480013	-3.988451	29407.924874
HLA B*0801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.421179	0.432524	-3.988655	26374.160521

HLA B*4402	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.415279	0.426351	-3.988928	26018.310263
HLA B*0802	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.424668	0.435662	-3.989006	26586.895608
HLA B*5801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.355177	0.365931	-3.989246	22655.670118
HLA B*5701	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.359249	0.369909	-3.989340	22869.073481
HLA A*0202	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.529835	0.540487	-3.989348	33871.566152
HLA A*2501	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.400710	0.411293	-3.989417	25159.959157
HLA A*8001	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.463272	0.473842	-3.989430	29058.421458
HLA B*3901	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.426385	0.436810	-3.989575	26692.245087
HLA B*3901	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.355802	0.365931	-3.989871	22688.295787
HLA A*3001	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.231808	0.241837	-3.989970	17053.275350
HLA A*6802	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.412859	0.422812	-3.990047	25873.734579
HLA B*5301	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.589970	0.599894	-3.990077	38901.858213
HLA A*0212	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.387121	0.397004	-3.990117	24384.873699
HLA A*0212	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.413099	0.422812	-3.990286	25888.015871
HLA A*1101	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.481145	0.490659	-3.990486	30279.210753
HLA B*4501	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.593147	0.602429	-3.990718	39187.436132
HLA A*0203	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.232628	0.241837	-3.990790	17085.503224
HLA A*0101	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.309197	0.318175	-3.991023	20379.686122
HLA A*1101	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.360971	0.369909	-3.991062	22959.939663
HLA B*4402	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.402439	0.411293	-3.991146	25260.337728
HLA A*0202	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.532370	0.540972	-3.991398	34069.861832
HLA A*6801	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.638920	0.647511	-3.991408	43543.117272
HLA A*0250	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.579170	0.587655	-3.991514	37946.328675
HLA A*8001	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.428328	0.436810	-3.991518	26811.933154
HLA B*0802	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.468227	0.476646	-3.991581	29391.860809
HLA B*1509	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.532570	0.540972	-3.991598	34085.532139
HLA B*1801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.513039	0.521317	-3.991722	32586.581994
HLA B*0702	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.389790	0.398058	-3.991732	24535.195648
HLA A*0211	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.427398	0.435662	-3.991736	26754.555001
HLA A*0203	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.361687	0.369909	-3.991779	22997.855207
HLA B*3801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.482766	0.490659	-3.992107	30392.448920
HLA A*1101	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.429021	0.436810	-3.992212	26854.756945
HLA A*1101	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.472430	0.480013	-3.992417	29677.704820
HLA B*1517	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.267193	0.274750	-3.992443	18500.923103
HLA B*1503	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.415390	0.422812	-3.992577	26024.926645
HLA B*1517	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.390699	0.398058	-3.992641	24586.617008
HLA A*8001	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.390821	0.398058	-3.992763	24593.534547
HLA A*2602	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.585022	0.592259	-3.992764	38461.155808
HLA B*4001	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.390781	0.397920	-3.992861	24591.272830
HLA B*4002	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.605082	0.612174	-3.992908	40279.329648
HLA B*4601	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.390849	0.397920	-3.992929	24595.131178
HLA A*0212	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.391009	0.398058	-3.992951	24604.180714
HLA A*0211	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.476422	0.483430	-3.992992	29951.741989
HLA B*5701	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.425603	0.432524	-3.993079	26644.202479
HLA B*1501	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.327824	0.334728	-3.993096	21272.778007
HLA B*5401	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.562218	0.568895	-3.993323	36493.727916
HLA B*0702	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.425983	0.432524	-3.993459	26667.563748
HLA A*0301	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.347428	0.353947	-3.993481	22255.036500
HLA A*2501	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.470163	0.476646	-3.993517	29523.174801
HLA B*1501	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.404864	0.411293	-3.993571	25401.760750
HLA A*3201	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.496437	0.502834	-3.993603	31364.426344
HLA A*3001	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.175895	0.182285	-3.993610	14993.214711
HLA B*5301	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.581352	0.587655	-3.993697	38137.518879

HLA B*4001	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.391937	0.398058	-3.993879	24656.813757
HLA B*4002	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.477322	0.483430	-3.993892	30013.865963
HLA B*1503	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.331031	0.337099	-3.993933	21430.448250
HLA B*4601	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.381703	0.387714	-3.993989	24082.557068
HLA A*1101	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.476392	0.481784	-3.994607	29949.635600
HLA B*1503	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.211433	0.216823	-3.994610	16271.705317
HLA A*3301	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.614663	0.620011	-3.994652	41177.827884
HLA B*2705	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.417755	0.422812	-3.994943	26167.091044
HLA A*0219	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.392881	0.397920	-3.994961	24710.495141
HLA A*0219	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.313166	0.318175	-3.994991	20566.754835
HLA A*6901	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.382706	0.387714	-3.994992	24138.252625
HLA A*0201	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.382725	0.387714	-3.995011	24139.297330
HLA B*0702	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.421663	0.426351	-3.995311	26403.569250
HLA B*4801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.427901	0.432524	-3.995377	26785.547121
HLA A*2601	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.392393	0.397004	-3.995389	24682.705123
HLA B*7301	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.564998	0.568895	-3.996102	36728.033048
HLA A*0101	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.368163	0.371790	-3.996373	23343.314220
HLA A*6801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.432115	0.435662	-3.996454	27046.775599
HLA A*0250	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.513842	0.517364	-3.996478	32646.928914
HLA B*5301	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.592564	0.595896	-3.996668	39134.895463
HLA B*2705	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.473333	0.476646	-3.996686	29739.421290
HLA A*0301	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.368621	0.371790	-3.996831	23367.952738
HLA A*2603	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.473520	0.476646	-3.996874	29752.295034
HLA B*1509	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.511025	0.514013	-3.997012	32435.851324
HLA A*6802	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.180077	0.182878	-3.997199	15138.290803
HLA B*3901	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.432891	0.435662	-3.997229	27095.104345
HLA A*2301	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.542400	0.545171	-3.997229	34865.855330
HLA A*3002	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.361605	0.364208	-3.997397	22993.501065
HLA B*4801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.433135	0.435662	-3.997473	27110.353111
HLA B*4001	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.394505	0.397004	-3.997501	24803.041611
HLA B*1801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.500622	0.502834	-3.997788	31668.083507
HLA A*6901	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.334978	0.337099	-3.997880	21626.109113
HLA B*0702	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.395886	0.397920	-3.997966	24882.066077
HLA B*5801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.347729	0.349724	-3.998005	22270.452688
HLA A*2301	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.515548	0.517364	-3.998184	32775.404457
HLA B*4403	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.481394	0.483198	-3.998195	30296.579293
HLA A*0206	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.479991	0.481784	-3.998207	30198.888157
HLA B*4601	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.310701	0.312492	-3.998209	20450.369595
HLA B*1517	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.472073	0.473842	-3.998231	29653.310781
HLA B*5401	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.091280	0.092742	-3.998539	12339.012594
HLA B*0801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.333388	0.334728	-3.998660	21547.048466
HLA A*6801	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.601288	0.602429	-3.998859	39928.943202
HLA A*2601	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.397136	0.398058	-3.999078	24953.781332
HLA B*1502	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.475764	0.476646	-3.999118	29906.406365
HLA B*4601	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.410519	0.411293	-3.999226	25734.695365
HLA B*4801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.397268	0.397920	-3.999348	24961.342320
HLA B*4501	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.619442	0.620011	-3.999431	41633.439057
HLA A*0206	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.312101	0.312492	-3.999610	20516.414014
HLA A*0301	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.309696	0.310085	-3.999611	20403.072921
HLA A*0216	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.473492	0.473842	-3.999650	29750.363617
HLA B*0803	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.521004	0.521317	-3.999687	33189.718113
HLA A*2602	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.517193	0.517364	-3.999828	32899.757680

HLA B*0803	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.490524	0.490659	-3.999865	30940.241196
HLA B*0702	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.437099	0.436810	-4.000289	27358.907777
HLA B*3801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.412326	0.411293	-4.001033	25841.979975
HLA A*2301	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.536362	0.535260	-4.001102	34384.455178
HLA B*5801	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.341750	0.340384	-4.001366	21965.930524
HLA A*6802	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.399441	0.398058	-4.001383	25086.565614
HLA A*0101	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.251499	0.250113	-4.001386	17844.272151
HLA A*0211	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-3.827673	-0.173733	-4.001406	6724.699608
HLA A*1101	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.424245	0.422812	-4.001432	26561.018421
HLA A*1101	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.490961	0.489523	-4.001438	30971.390155
HLA B*0803	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.490998	0.489523	-4.001476	30974.071099
HLA A*8001	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.428060	0.426351	-4.001709	26795.402599
HLA A*1101	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.475673	0.473842	-4.001831	29900.097207
HLA A*0219	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.478551	0.476646	-4.001904	30098.906604
HLA B*7301	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.567483	0.565473	-4.002010	36938.854682
HLA B*1503	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.389726	0.387714	-4.002013	24531.612127
HLA A*0301	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.368141	0.365931	-4.002211	23342.177685
HLA B*1801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.479213	0.476646	-4.002567	30144.860202
HLA A*3201	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.568468	0.565473	-4.002994	37022.680563
HLA B*5101	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.486480	0.483198	-4.003282	30653.511439
HLA A*2602	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.585685	0.581978	-4.003707	38519.876495
HLA A*2402	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.591533	0.587655	-4.003877	39042.062662
HLA B*1801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.477789	0.473842	-4.003948	30046.195328
HLA A*2402	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.586009	0.581978	-4.004031	38548.644812
HLA B*1517	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.402002	0.397920	-4.004082	25234.932565
HLA A*0203	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.436993	0.432524	-4.004469	27352.248198
HLA A*6801	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.659482	0.654994	-4.004488	45654.354833
HLA B*4002	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.639028	0.634444	-4.004584	43553.954539
HLA A*3201	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.488047	0.483430	-4.004617	30764.321251
HLA B*7301	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.600517	0.595896	-4.004621	39858.154366
HLA A*0216	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.416106	0.411293	-4.004813	26067.903642
HLA A*6802	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.392738	0.387714	-4.005025	24702.341943
HLA B*5401	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-3.772018	-0.233064	-4.005082	5915.865458
HLA B*0702	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.464444	0.459317	-4.005127	29136.971651
HLA B*4801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.402310	0.397004	-4.005306	25252.822787
HLA A*2301	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.526828	0.521317	-4.005511	33637.827352
HLA A*0250	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.527876	0.522301	-4.005575	33719.087049
HLA A*3201	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.432238	0.426351	-4.005886	27054.385312
HLA A*2402	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.546427	0.540487	-4.005940	35190.654246
HLA A*2601	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.370355	0.364208	-4.006146	23461.435738
HLA B*1509	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.295918	0.289672	-4.006246	19765.973178
HLA B*5701	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.403348	0.397004	-4.006345	25313.278856
HLA A*2902	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.463382	0.456941	-4.006442	29065.810931
HLA B*1503	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.495965	0.489523	-4.006443	31330.339588
HLA A*2301	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.547456	0.540972	-4.006484	35274.138478
HLA B*1501	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.256729	0.250113	-4.006616	18060.459346
HLA A*0211	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.496186	0.489523	-4.006663	31346.276045
HLA B*0803	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.480527	0.473842	-4.006685	30236.160100
HLA B*7301	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.594373	0.587655	-4.006718	39298.256370
HLA A*6901	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.378552	0.371790	-4.006762	23908.478476
HLA B*5401	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.564817	0.557970	-4.006847	36712.736751
HLA B*5701	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.404953	0.398058	-4.006895	25406.983274
HLA B*2705	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.442587	0.435662	-4.006925	27706.849931
HLA A*3001	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.281744	0.274750	-4.006994	19131.268138

HLA A*2902	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.442719	0.435662	-4.007057	27715.245098
HLA B*1503	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.528437	0.521317	-4.007120	33762.712796
HLA A*3201	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.210169	0.203022	-4.007147	16224.415040
HLA A*0211	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.542429	0.535260	-4.007168	34868.118848
HLA A*3101	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.394937	0.387714	-4.007224	24827.743337
HLA A*2603	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.619513	0.612174	-4.007339	41640.196574
HLA A*2602	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.622795	0.615291	-4.007504	41956.089348
HLA B*1509	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.510619	0.502834	-4.007785	32405.508461
HLA B*5701	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.419123	0.411293	-4.007830	26249.609420
HLA A*1101	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.443515	0.435662	-4.007853	27766.120176
HLA B*5801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.342586	0.334728	-4.007858	22008.275924
HLA A*2403	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.362054	0.353947	-4.008107	23017.272272
HLA B*1503	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.419442	0.411293	-4.008149	26268.929544
HLA B*4403	1:160-168	9	GSSGGRSIT	0.939195	-0.302396	-4.645298	0.636799	-4.008500	44187.391927
HLA B*4402	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.406635	0.398058	-4.008577	25505.587579
HLA A*6901	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.362679	0.353947	-4.008731	23050.418673
HLA A*3002	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.492211	0.483430	-4.008780	31060.656100
HLA A*6901	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.374743	0.365931	-4.008813	23699.731375
HLA B*4801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.319126	0.310085	-4.009042	20850.977256
HLA A*6801	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.668960	0.659875	-4.009085	46661.643619
HLA B*4002	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.611560	0.602429	-4.009131	40884.601053
HLA A*0216	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.489354	0.480013	-4.009340	30856.996512
HLA A*8001	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.373609	0.364208	-4.009400	23637.885371
HLA B*1502	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.574962	0.565473	-4.009488	37580.437908
HLA A*3002	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.445273	0.435662	-4.009611	27878.706118
HLA A*3201	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.629860	0.620011	-4.009849	42644.193273
HLA A*0219	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.432820	0.422812	-4.010008	27090.707256
HLA B*2705	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.397771	0.387714	-4.010057	24990.257207
HLA B*5101	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.446917	0.436810	-4.010108	27984.480769
HLA B*3901	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.493526	0.483198	-4.010328	31154.898219
HLA B*1501	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.382149	0.371790	-4.010359	24107.323748
HLA B*1502	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.555555	0.545171	-4.010384	35938.098139
HLA B*4801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.026665	0.015810	-4.010855	10633.221751
HLA B*0702	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.364998	0.353947	-4.011050	23173.826959
HLA B*5401	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.546338	0.535260	-4.011078	35183.420643
HLA A*0101	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.381143	0.369909	-4.011235	24051.569438
HLA A*2602	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.611198	0.599894	-4.011304	40850.553339
HLA B*4801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.422640	0.411293	-4.011347	26463.057764
HLA A*2403	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.409828	0.397920	-4.011908	25693.796675
HLA B*4403	1:113-121	9	CGDGSPAEA	1.102209	-0.454698	-4.659478	0.647511	-4.011966	45653.860866
HLA B*4002	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.632075	0.620011	-4.012065	42862.299575
HLA B*5801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.349268	0.337099	-4.012169	22349.507516
HLA B*1501	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.266592	0.254408	-4.012184	18475.318324
HLA B*4801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.410256	0.398058	-4.012198	25719.107241
HLA B*1503	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.410143	0.397920	-4.012223	25712.429507
HLA B*3801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.553243	0.540972	-4.012271	35747.296052
HLA A*6801	1:283-291	9	AFVYNLITD	1.244680	-0.632506	-4.624649	0.612174	-4.012474	42135.557575
HLA B*0801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.423946	0.411293	-4.012653	26542.775783
HLA B*4402	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.378594	0.365931	-4.012664	23910.806750
HLA A*2403	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.445320	0.432524	-4.012796	27881.722696
HLA A*0301	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.347546	0.334728	-4.012818	22261.057178
HLA A*8001	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.287683	0.274750	-4.012933	19394.708508
HLA A*0202	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.570935	0.557970	-4.012965	

37233.582024

HLA B*5801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.351347	0.338222	-4.013125	22456.767976
HLA B*5401	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.516041	0.502834	-4.013207	32812.660990
HLA A*2601	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.347987	0.334728	-4.013260	22283.709507
HLA B*4403	1:99-107	9	AVRTPQPDP	0.400112	0.254882	-4.668429	0.654994	-4.013435	46604.628325
HLA B*0803	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.496679	0.483198	-4.013481	31381.908056
HLA B*4601	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.379602	0.365931	-4.013671	23966.364410
HLA A*3002	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.531221	0.517364	-4.013857	33979.851311
HLA B*4801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.440313	0.426351	-4.013961	27562.134707
HLA A*3201	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.601626	0.587655	-4.013971	39960.060927
HLA B*4402	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.437155	0.422812	-4.014343	27362.460215
HLA A*0203	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.364370	0.349724	-4.014646	23140.377911
HLA A*0219	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.412706	0.398058	-4.014648	25864.637867
HLA A*0250	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.572826	0.557970	-4.014856	37396.086406
HLA A*2601	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.384921	0.369909	-4.015013	24261.709176
HLA B*4403	1:133-141	9	TPRAPQRNP	0.799325	-0.139450	-4.674892	0.659875	-4.015018	47303.413575
HLA A*0212	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.381024	0.365931	-4.015093	24044.934421
HLA B*4402	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.224430	0.209282	-4.015148	16766.037050
HLA B*1503	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.441525	0.426351	-4.015174	27639.181972
HLA B*0802	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.472357	0.456941	-4.015417	29672.728091
HLA A*0201	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.385563	0.369909	-4.015654	24297.567761
HLA B*4801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.349876	0.334139	-4.015737	22380.844730
HLA A*2501	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.472729	0.456941	-4.015788	29698.102069
HLA A*0202	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.561041	0.545171	-4.015870	36394.950899
HLA B*1801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.412951	0.397004	-4.015947	25879.194143
HLA B*0802	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.442364	0.426351	-4.016012	27692.613946
HLA A*3101	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.448588	0.432524	-4.016064	28092.328429
HLA A*0101	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.382191	0.365931	-4.016261	24109.671385
HLA B*1502	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.453096	0.436810	-4.016287	28385.490215
HLA A*2403	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.388133	0.371790	-4.016344	24441.797325
HLA A*0201	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.380575	0.364208	-4.016366	24020.101890
HLA A*3001	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.285303	0.268910	-4.016393	19288.711990
HLA A*0212	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.427713	0.411293	-4.016419	26773.957082
HLA B*3801	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.506324	0.489523	-4.016801	32086.620783
HLA B*5301	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.609271	0.592259	-4.017013	40669.737185
HLA A*2402	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.552411	0.535260	-4.017151	35678.901890
HLA A*0203	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.415368	0.398058	-4.017310	26023.659548
HLA B*5801	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.330108	0.312492	-4.017616	21384.933666
HLA A*3201	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.575725	0.557970	-4.017756	37646.570480
HLA B*5801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.351921	0.334139	-4.017781	22486.430774
HLA B*4001	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.371879	0.353947	-4.017932	23543.954040
HLA B*0803	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.494819	0.476646	-4.018172	31247.735766
HLA A*3201	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.600360	0.581978	-4.018381	39843.709895
HLA B*2705	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-3.910036	-0.108442	-4.018478	8128.987120
HLA A*2602	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.614464	0.595896	-4.018568	41158.897001
HLA A*3201	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.388509	0.369909	-4.018600	24462.962870
HLA B*4403	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.636218	0.617415	-4.018802	43273.060253
HLA A*0250	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.509658	0.490659	-4.018999	32333.885852
HLA B*3901	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.441911	0.422812	-4.019098	27663.714939
HLA A*6801	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.584621	0.565473	-4.019147	38425.592190
HLA A*0203	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.430647	0.411293	-4.019354	26955.479993
HLA A*2402	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.536764	0.517364	-4.019400	34416.278647
HLA A*2603	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.636852	0.617415	-4.019437	43336.314102

HLA A*0301	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.356711	0.337099	-4.019612	22735.846377
HLA B*5401	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.478974	0.459317	-4.019657	30128.230594
HLA A*3001	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.301202	0.281226	-4.019976	20007.931574
HLA A*3301	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.616315	0.595896	-4.020419	41334.731600
HLA B*4001	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.390365	0.369909	-4.020457	24567.736717
HLA A*3301	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.637947	0.617415	-4.020532	43445.703139
HLA A*0216	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.418606	0.398058	-4.020548	26218.386360
HLA B*4002	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.523783	0.502834	-4.020949	33402.810109
HLA A*6901	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.359227	0.338222	-4.021005	22867.960036
HLA B*1801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.480402	0.459317	-4.021085	30227.491906
HLA A*2902	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.444314	0.422812	-4.021502	27817.239130
HLA A*0212	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.454074	0.432524	-4.021550	28449.444093
HLA A*0101	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.371308	0.349724	-4.021584	23513.023421
HLA A*0201	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.204629	0.182878	-4.021751	16018.762482
HLA A*8001	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.418972	0.397004	-4.021969	26240.522515
HLA B*5301	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.604016	0.581978	-4.022037	40180.521393
HLA A*0301	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.362723	0.340384	-4.022340	23052.788098
HLA A*2403	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.362827	0.340384	-4.022443	23058.276125
HLA A*2501	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.505643	0.483198	-4.022445	32036.320583
HLA A*2403	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.386796	0.364208	-4.022588	24366.675607
HLA A*0216	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.445489	0.422812	-4.022676	27892.585077
HLA A*8001	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.455249	0.432524	-4.022725	28526.502434
HLA B*4402	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.455317	0.432524	-4.022793	28530.978217
HLA A*3101	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.312473	0.289672	-4.022801	20533.958172
HLA A*2601	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.394803	0.371790	-4.023014	24820.088543
HLA A*0201	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.394817	0.371790	-4.023028	24820.894200
HLA A*6802	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.420967	0.397920	-4.023047	26361.322331
HLA A*2301	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.278081	0.254408	-4.023673	18970.593214
HLA A*3002	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.373458	0.349724	-4.023734	23629.702574
HLA A*2301	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.505753	0.481784	-4.023969	32044.467327
HLA B*5801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.240896	0.216823	-4.024072	17413.882608
HLA A*2603	1:282-290	9	GAFVYNLIT	0.924708	-0.309417	-4.639486	0.615291	-4.024195	43599.925085
HLA A*2902	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.435630	0.411293	-4.024337	27266.558578
HLA A*0202	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.541726	0.517364	-4.024362	34811.763275
HLA A*6802	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.436020	0.411293	-4.024727	27291.056080
HLA B*1517	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.514315	0.489523	-4.024792	32682.448091
HLA A*2501	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.484159	0.459317	-4.024842	30490.106412
HLA B*2705	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.481915	0.456941	-4.024974	30332.987204
HLA B*5301	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.508443	0.483430	-4.025013	32243.577148
HLA A*8001	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.436624	0.411293	-4.025331	27329.026358
HLA B*0803	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.461200	0.435662	-4.025538	28920.098821
HLA A*0101	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.379738	0.353947	-4.025791	23973.885602
HLA A*0301	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.364093	0.338222	-4.025871	23125.610573
HLA A*0101	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.366518	0.340384	-4.026134	23255.082070
HLA B*5101	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.461804	0.435662	-4.026142	28960.335600
HLA A*3101	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.423171	0.397004	-4.026167	26495.432210
HLA A*2601	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.380154	0.353947	-4.026207	23996.852799
HLA A*3101	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.392318	0.365931	-4.026387	24678.432510
HLA B*5401	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.547950	0.521317	-4.026633	35314.235378
HLA A*0250	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.567728	0.540972	-4.026756	36959.643381
HLA A*0250	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.548140	0.521317	-4.026823	35329.713503
HLA A*3201	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.622781	0.595896	-4.026885	41954.727503
HLA A*0212	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.365205	0.338222	-4.026983	23184.861955

HLA A*0250	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.592529	0.565473	-4.027056	39131.719860
HLA A*6801	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.623014	0.595896	-4.027118	41977.203594
HLA B*1801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.425410	0.398058	-4.027352	26632.385442
HLA A*1101	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.424487	0.397004	-4.027483	26575.822838
HLA A*2902	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.424654	0.397004	-4.027650	26586.032629
HLA A*2403	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.393605	0.365931	-4.027674	24751.703223
HLA A*3201	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.563010	0.535260	-4.027750	36560.321509
HLA B*5801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.351968	0.324195	-4.027773	22488.863887
HLA B*0702	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.340500	0.312492	-4.028008	21902.802123
HLA A*2501	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.415772	0.387714	-4.028059	26047.885857
HLA B*1501	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.366476	0.338222	-4.028254	23252.817647
HLA A*1101	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.392534	0.364208	-4.028325	24690.718265
HLA A*2601	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.346519	0.318175	-4.028344	22208.491493
HLA B*5101	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.505029	0.476646	-4.028383	31991.117825
HLA A*2403	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.346676	0.318175	-4.028502	22216.542699
HLA B*0803	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.511996	0.483430	-4.028565	32508.403255
HLA A*0203	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.382619	0.353947	-4.028672	24133.421453
HLA B*3501	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.427066	0.397920	-4.029146	26734.154559
HLA A*0203	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.363905	0.334728	-4.029177	23115.604179
HLA B*4501	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.629265	0.599894	-4.029372	42585.866007
HLA B*3801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.503335	0.473842	-4.029493	31866.578550
HLA A*2301	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.532410	0.502834	-4.029576	34072.995317
HLA A*0219	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.417466	0.387714	-4.029753	26149.684825
HLA B*3501	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.366929	0.337099	-4.029830	23277.108793
HLA A*0219	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.462377	0.432524	-4.029853	28998.588860
HLA B*5701	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.417617	0.387714	-4.029903	26158.740274
HLA A*2501	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.465892	0.435662	-4.030230	29234.232338
HLA A*3201	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.630135	0.599894	-4.030241	42671.193759
HLA A*0216	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.396467	0.365931	-4.030536	24915.336778
HLA A*3002	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.487488	0.456941	-4.030547	30724.736028
HLA A*2403	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.400491	0.369909	-4.030583	25147.303870
HLA B*5401	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.402552	0.371790	-4.030762	25266.898050
HLA B*0702	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.418507	0.387714	-4.030794	26212.429817
HLA B*3801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.512745	0.481784	-4.030961	32564.553219
HLA A*2603	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.631110	0.599894	-4.031216	42767.102649
HLA B*4403	1:128-136	9	DLSGPTPRA	1.059300	-0.424856	-4.665678	0.634444	-4.031234	46310.322124
HLA A*2603	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.613298	0.581978	-4.031320	41048.603168
HLA B*1801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.468135	0.436810	-4.031326	29385.660201
HLA A*2402	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.576515	0.545171	-4.031344	37715.063740
HLA A*0250	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.490768	0.459317	-4.031451	30957.653955
HLA A*2602	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.597188	0.565473	-4.031715	39553.777351
HLA A*0201	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.397839	0.365931	-4.031908	24994.178155
HLA A*0216	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.370303	0.338222	-4.032081	23458.643582
HLA A*8001	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.430062	0.397920	-4.032142	26919.193725
HLA B*1509	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.398074	0.365931	-4.032143	25007.703387
HLA A*3002	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.567512	0.535260	-4.032252	36941.252781
HLA B*3801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.567603	0.535260	-4.032343	36949.047679
HLA A*0301	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.366682	0.334139	-4.032543	23263.890257
HLA A*2603	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.590595	0.557970	-4.032626	38957.879472
HLA A*6801	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.652725	0.620011	-4.032714	44949.523376
HLA A*2602	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.620391	0.587655	-4.032736	41724.532412
HLA B*5301	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.598642	0.565473	-4.033169	39686.453955
HLA A*3001	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.313720	0.280375	-4.033345	20593.029876

HLA A*2601	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.383152	0.349724	-4.033428	24163.076582
HLA A*3301	1:238-246	9	SNVGDLLNN	1.119809	-0.517380	-4.636128	0.602429	-4.033699	43264.165274
HLA B*3901	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.460143	0.426351	-4.033791	28849.779912
HLA B*3901	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.405611	0.371790	-4.033821	25445.498147
HLA B*1509	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.431958	0.398058	-4.033900	27036.973931
HLA A*6901	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.368050	0.334139	-4.033911	23337.253339
HLA B*3501	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.405714	0.371790	-4.033925	25451.555790
HLA B*1501	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.399869	0.365931	-4.033938	25111.278006
HLA B*0801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.352198	0.318175	-4.034023	22500.789950
HLA B*1503	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.374851	0.340384	-4.034468	23705.629903
HLA A*6901	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.251771	0.217020	-4.034751	17855.473788
HLA B*4601	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.406544	0.371790	-4.034754	25500.206833
HLA A*0219	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.446118	0.411293	-4.034825	27933.054480
HLA A*0250	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.431888	0.397004	-4.034884	27032.586276
HLA B*4601	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.404805	0.369909	-4.034896	25398.325465
HLA A*0201	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.388944	0.353947	-4.034996	24487.458381
HLA B*5401	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.461425	0.426351	-4.035074	28935.122357
HLA B*5301	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.604121	0.568895	-4.035226	40190.304332
HLA B*0802	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.494628	0.459317	-4.035311	31234.045976
HLA B*7301	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.594183	0.557970	-4.036213	39281.039606
HLA B*1502	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.557604	0.521317	-4.036287	36108.033876
HLA A*0206	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.408083	0.371790	-4.036293	25590.726522
HLA B*3801	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.550335	0.514013	-4.036321	35508.680532
HLA A*1101	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.493324	0.456941	-4.036383	31140.406759
HLA B*0802	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.459320	0.422812	-4.036508	28795.205657
HLA A*0201	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.386277	0.349724	-4.036553	24337.560571
HLA B*1509	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.513429	0.476646	-4.036782	32615.859245
HLA B*3501	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.469392	0.432524	-4.036869	29470.834043
HLA A*2301	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.520254	0.483198	-4.037056	33132.490198
HLA B*4402	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.401429	0.364208	-4.037220	25201.644103
HLA A*2601	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.403558	0.365931	-4.037627	25325.469631
HLA B*1503	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.219999	0.182285	-4.037714	16595.842051
HLA A*0250	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.220671	0.182878	-4.037794	16621.539482
HLA A*2603	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.528740	0.490659	-4.038082	33786.283196
HLA B*4002	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.625793	0.587655	-4.038138	42246.714954
HLA A*0211	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.514787	0.476646	-4.038140	32718.005913
HLA B*7301	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.579132	0.540972	-4.038160	37943.044251
HLA B*0801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.425934	0.387714	-4.038220	26664.534280
HLA A*3101	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.375425	0.337099	-4.038326	23736.942304
HLA A*0202	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.518344	0.480013	-4.038331	32987.085555
HLA A*6801	1:151-159	9	AGSRGDSAA	0.916861	-0.299446	-4.655768	0.617415	-4.038352	45265.536708
HLA A*6901	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.388093	0.349724	-4.038369	24439.549563
HLA B*1509	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.559920	0.521317	-4.038604	36301.154179
HLA A*6802	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.408548	0.369909	-4.038639	25618.152921
HLA B*4001	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.403038	0.364208	-4.038830	25295.208960
HLA A*0212	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.357345	0.318175	-4.039171	22769.080213
HLA A*2301	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.529990	0.490659	-4.039331	33883.662245
HLA B*4801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.405291	0.365931	-4.039361	25426.783636
HLA A*0203	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.403572	0.364208	-4.039363	25326.291692
HLA B*5101	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.496327	0.456941	-4.039386	31356.452489
HLA A*2402	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.560893	0.521317	-4.039576	36382.548775

HLA B*1801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.403854	0.364208	-4.039645	25342.738522
HLA B*4601	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.308589	0.268910	-4.039679	20351.150891
HLA A*3101	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.242923	0.203022	-4.039901	17495.373481
HLA B*4001	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.389782	0.349724	-4.040058	24534.797453
HLA B*5301	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.580643	0.540487	-4.040156	38075.261187
HLA B*0702	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.451452	0.411293	-4.040159	28278.199845
HLA B*4402	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.438130	0.397920	-4.040210	27423.960796
HLA A*2402	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.520938	0.480013	-4.040924	33184.691019
HLA B*1502	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.581508	0.540487	-4.041020	38151.138414
HLA A*0212	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.411120	0.369909	-4.041212	25770.360850
HLA A*0212	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.330886	0.289672	-4.041214	21423.261402
HLA B*1503	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.515109	0.473842	-4.041267	32742.264009
HLA A*0202	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.381714	0.340384	-4.041330	24083.208497
HLA A*0216	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.473922	0.432524	-4.041398	29779.831350
HLA B*5701	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.413381	0.371790	-4.041591	25904.827483
HLA A*3002	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.563386	0.521317	-4.042069	36591.981174
HLA B*5701	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.376813	0.334728	-4.042085	23812.956565
HLA B*5101	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.440148	0.398058	-4.042090	27551.699117
HLA A*0101	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.366487	0.324195	-4.042293	23253.446631
HLA B*4801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.396312	0.353947	-4.042364	24906.442278
HLA B*4501	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.631857	0.589436	-4.042421	42840.740132
HLA B*2705	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.439434	0.397004	-4.042431	27506.424659
HLA B*4501	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.611386	0.568895	-4.042491	40868.236923
HLA A*3101	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.414375	0.371790	-4.042585	25964.175532
HLA B*4002	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.632118	0.589436	-4.042682	42866.473623
HLA B*1502	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.583657	0.540972	-4.042685	38340.456583
HLA A*2403	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.251341	0.208647	-4.042694	17837.805443
HLA A*8001	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.412603	0.369909	-4.042694	25858.481907
HLA B*0801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.397031	0.353947	-4.043083	24947.707198
HLA A*0250	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.361297	0.318175	-4.043122	22977.211448
HLA B*3901	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.502781	0.459317	-4.043464	31825.919372
HLA A*3201	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.584447	0.540972	-4.043475	38410.212282
HLA B*0802	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.480308	0.436810	-4.043498	30220.951519
HLA A*2601	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.380662	0.337099	-4.043563	24024.910377
HLA B*7301	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.584141	0.540487	-4.043654	38383.208430
HLA B*4501	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.333374	0.289672	-4.043702	21546.349074
HLA B*4601	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.407935	0.364208	-4.043726	25582.006099
HLA B*7301	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.561584	0.517364	-4.044220	36440.461532
HLA B*7301	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.378378	0.334139	-4.044239	23898.909068
HLA A*3001	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.210334	0.166065	-4.044268	16230.560264
HLA B*5101	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.470659	0.426351	-4.044307	29556.894352
HLA A*3002	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.585332	0.540972	-4.044360	38488.630935
HLA B*4601	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.384745	0.340384	-4.044361	24251.867186
HLA A*6901	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.356953	0.312492	-4.044461	22748.518744
HLA A*0301	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.368693	0.324195	-4.044499	23371.872026
HLA B*1502	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.524692	0.480013	-4.044679	33472.816395
HLA A*0211	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.467557	0.422812	-4.044745	29346.578814
HLA B*4001	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.416543	0.371790	-4.044754	26094.147394
HLA B*5301	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.602723	0.557970	-4.044754	40061.144390
HLA B*3901	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.442862	0.398058	-4.044804	27724.392728
HLA B*5701	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.409394	0.364208	-4.045185	25668.094430

HLA B*3801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.566725	0.521317	-4.045408	36874.364303
HLA B*0801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.411518	0.365931	-4.045587	25793.932724
HLA A*3301	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.633278	0.587655	-4.045623	42981.186857
HLA A*2501	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.471989	0.426351	-4.045637	29647.536183
HLA A*0250	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.586284	0.540487	-4.045797	38573.052171
HLA A*2402	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.587102	0.540972	-4.046129	38645.739798
HLA B*4601	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.381188	0.334728	-4.046460	24054.041775
HLA A*0301	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.359213	0.312492	-4.046721	22867.217769
HLA B*5301	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.587698	0.540972	-4.046726	38698.879869
HLA A*0201	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.387144	0.340384	-4.046760	24386.192929
HLA B*1501	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.229054	0.182285	-4.046769	16945.492985
HLA B*4403	1:143-151	9	PARPAEGGA	0.949138	-0.329127	-4.666782	0.620011	-4.046771	46428.222793
HLA A*0206	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.444831	0.398058	-4.046773	27850.366239
HLA B*4001	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.412798	0.365931	-4.046867	25870.095510
HLA B*1501	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.230041	0.182878	-4.047163	16984.039520
HLA B*4002	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.647429	0.599894	-4.047536	44404.742079
HLA B*4001	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.385791	0.338222	-4.047569	24310.321480
HLA B*4402	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.445249	0.397004	-4.048246	27877.197952
HLA A*0202	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.290134	0.241837	-4.048296	19504.452755
HLA A*2603	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.636020	0.587655	-4.048365	43253.400114
HLA B*1517	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.366725	0.318175	-4.048550	23266.155758
HLA A*0212	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.382812	0.334139	-4.048672	24144.129677
HLA A*2501	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.414901	0.365931	-4.048970	25995.658386
HLA A*0203	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.231380	0.182285	-4.049095	17036.492962
HLA B*1801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.475447	0.426351	-4.049096	29884.572642
HLA B*4601	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.387367	0.338222	-4.049145	24398.729178
HLA A*3101	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.389761	0.340384	-4.049377	24533.602908
HLA B*3501	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.460760	0.411293	-4.049467	28890.856619
HLA A*0101	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.386571	0.337099	-4.049472	24354.024075
HLA B*2705	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.413707	0.364208	-4.049499	25924.314581
HLA A*2602	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.526147	0.476646	-4.049500	33585.095421
HLA A*2601	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.387797	0.338222	-4.049575	24422.896117
HLA A*0201	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.387865	0.338222	-4.049643	24426.728047
HLA A*0219	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.414048	0.364208	-4.049840	25944.658471
HLA B*4501	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.637712	0.587655	-4.050057	43422.205852
HLA B*4601	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.404070	0.353947	-4.050122	25355.354991
HLA B*1517	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.447169	0.397004	-4.050165	28000.684502
HLA A*0250	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.595355	0.545171	-4.050184	39387.223394
HLA B*3801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.553267	0.502834	-4.050433	35749.229994
HLA A*6901	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.360630	0.310085	-4.050545	22941.936170
HLA A*0202	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.541270	0.490659	-4.050611	34775.246851
HLA A*1101	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.461921	0.411293	-4.050628	28968.170270
HLA A*2603	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.448651	0.397920	-4.050731	28096.432091
HLA B*5801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.360837	0.310085	-4.050752	22952.860743
HLA B*1501	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.319735	0.268910	-4.050825	20880.213315
HLA B*4601	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.361140	0.310085	-4.051055	22968.884578
HLA A*3201	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.568517	0.517364	-4.051153	37026.886862
HLA A*2602	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.609126	0.557970	-4.051156	40656.098308
HLA A*0212	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.423195	0.371790	-4.051405	26496.865622
HLA A*0202	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.554244	0.502834	-4.051410	35829.774732
HLA B*4002	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.647373	0.595896	-4.051477	44398.977060
HLA A*6802	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.405491	0.353947	-4.051544	25438.478592
HLA B*0702	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.341313	0.289672	-4.051641	21943.838656
HLA B*7301	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.596958	0.545171	-4.051787	39532.812717
HLA B*1501	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.376191	0.324195	-4.051996	23778.842278

HLA A*2301	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.535542	0.483430	-4.052112	34319.596810
HLA B*1517	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.509211	0.456941	-4.052271	32300.667607
HLA A*6801	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.610270	0.557970	-4.052300	40763.352741
HLA A*6901	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.376522	0.324195	-4.052327	23796.987565
HLA A*0250	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.534149	0.481784	-4.052365	34209.673752
HLA B*1501	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.386606	0.334139	-4.052467	24356.000444
HLA B*5701	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.393029	0.340384	-4.052646	24718.918482
HLA A*2403	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.402383	0.349724	-4.052658	25257.058206
HLA B*2705	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.463989	0.411293	-4.052695	29106.407902
HLA B*4001	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.370904	0.318175	-4.052729	23491.154707
HLA A*2301	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.542262	0.489523	-4.052739	34854.728501
HLA A*2501	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.489572	0.436810	-4.052762	30872.525180
HLA A*3002	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.597956	0.545171	-4.052785	39623.811246
HLA A*0101	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.386982	0.334139	-4.052843	24377.091693
HLA A*0201	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.389992	0.337099	-4.052893	24546.613315
HLA A*3301	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.645171	0.592259	-4.052913	44174.485172
HLA B*5401	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.451008	0.397920	-4.053088	28249.301037
HLA B*1501	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.097333	0.044127	-4.053205	12512.171280
HLA B*4801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.403052	0.349724	-4.053328	25296.030039
HLA A*2501	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.451482	0.398058	-4.053424	28280.188680
HLA B*7301	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.451379	0.397920	-4.053459	28273.457803
HLA A*1101	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.451550	0.398058	-4.053492	28284.625816
HLA B*1801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.464931	0.411293	-4.053638	29169.618880
HLA A*0101	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.388410	0.334728	-4.053682	24457.405141
HLA A*0250	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.066963	0.013159	-4.053804	11667.108528
HLA A*6801	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.595008	0.540972	-4.054035	39355.700099
HLA A*2602	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.622992	0.568895	-4.054097	41975.159815
HLA A*3201	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.270922	0.216823	-4.054099	18660.446483
HLA A*3101	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.206180	0.152039	-4.054141	16076.060134
HLA A*0219	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.404145	0.349724	-4.054420	25359.744800
HLA A*3301	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.619950	0.565473	-4.054476	41682.117667
HLA B*3901	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.511584	0.456941	-4.054644	32477.641119
HLA A*0202	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.536508	0.481784	-4.054724	34395.990110
HLA B*5701	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.404521	0.349724	-4.054796	25381.705248
HLA A*3301	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.544846	0.489523	-4.055324	35062.763121
HLA A*2402	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.537156	0.481784	-4.055372	34447.386135
HLA A*0250	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.405099	0.349724	-4.055374	25415.506539
HLA B*5301	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.514904	0.459317	-4.055587	32726.857149
HLA B*3801	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.578014	0.522301	-4.055713	37845.462539
HLA A*0101	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.394002	0.338222	-4.055780	24774.343342
HLA B*5401	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.539036	0.483198	-4.055838	34596.794447
HLA A*2301	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.535953	0.480013	-4.055940	34352.103607
HLA A*8001	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.374123	0.318175	-4.055948	23665.907324
HLA B*4801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.427802	0.371790	-4.056012	26779.461725
HLA B*0801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.366262	0.310085	-4.056177	23241.373104
HLA A*2501	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.479035	0.422812	-4.056222	30132.468643
HLA A*0216	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.239422	0.182878	-4.056545	17354.914776

HLA A*3201	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.601739	0.545171	-4.056568	39970.438891
HLA B*5401	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.538507	0.481784	-4.056723	34554.707982
HLA A*2402	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.559589	0.502834	-4.056755	36273.474421
HLA B*0802	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.489351	0.432524	-4.056827	30856.829579
HLA A*8001	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.428622	0.371790	-4.056832	26830.070484
HLA A*3002	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.516333	0.459317	-4.057016	32834.679969
HLA B*4801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.427085	0.369909	-4.057177	26735.311614
HLA A*0211	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.537274	0.480013	-4.057260	34456.705223
HLA A*2601	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.397667	0.340384	-4.057283	24984.309356
HLA A*2602	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.367425	0.310085	-4.057340	23303.694472
HLA B*1517	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.209422	0.152039	-4.057383	16196.527448
HLA A*3301	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.639855	0.581978	-4.057876	43636.972526
HLA A*0202	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.102032	0.044127	-4.057904	12648.285233
HLA A*0212	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.422245	0.364208	-4.058037	26439.017439
HLA B*1801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.493742	0.435662	-4.058081	31170.408176
HLA B*4001	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.370613	0.312492	-4.058121	23475.401508
HLA B*1503	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.287531	0.229292	-4.058239	19387.889697
HLA B*1502	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.593502	0.535260	-4.058242	39219.461163
HLA A*3001	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.039817	-0.018628	-4.058446	10960.169939
HLA A*2603	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.624021	0.565473	-4.058548	42074.739208
HLA B*5301	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.572629	0.514013	-4.058616	37379.096337
HLA B*1517	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.491214	0.432524	-4.058691	30989.491035
HLA A*0206	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.532544	0.473842	-4.058702	34083.503811
HLA A*6801	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.646363	0.587655	-4.058707	44295.813874
HLA A*0201	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.392884	0.334139	-4.058745	24710.628822
HLA B*4801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.422960	0.364208	-4.058751	26482.534988
HLA A*0206	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.538787	0.480013	-4.058773	34576.960663
HLA A*0203	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.424715	0.365931	-4.058784	26589.772407
HLA A*2501	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.491529	0.432524	-4.059005	31011.964241
HLA A*0201	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.371621	0.312492	-4.059129	23529.947488
HLA B*1503	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.516133	0.456941	-4.059192	32819.584722
HLA A*0219	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.397416	0.338222	-4.059194	24969.851170
HLA A*0211	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.516157	0.456941	-4.059216	32821.360273
HLA B*4403	1:115-123	9	DGSPAEAYA	1.099360	-0.499466	-4.659153	0.599894	-4.059260	45619.790024
HLA B*0702	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.423516	0.364208	-4.059308	26516.511181
HLA B*4001	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.396629	0.337099	-4.059530	24924.638969
HLA B*0801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.423932	0.364208	-4.059724	26541.914237
HLA A*3002	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.377908	0.318175	-4.059733	23873.064962
HLA A*1101	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.400350	0.340384	-4.059967	25139.142547
HLA A*2301	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.519357	0.459317	-4.060039	33064.090036
HLA A*3002	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.540126	0.480013	-4.060113	34683.748014
HLA A*0301	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.350142	0.289672	-4.060470	22394.530714
HLA A*0201	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.395414	0.334728	-4.060686	24855.024329
HLA B*7301	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.517653	0.456941	-4.060712	32934.661053
HLA A*2902	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.448531	0.387714	-4.060818	28088.681233
HLA A*2603	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.370970	0.310085	-4.060886	23494.713343
HLA A*2601	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.395149	0.334139	-4.061010	24839.834661
HLA B*4402	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.431054	0.369909	-4.061145	26980.719728
HLA A*6901	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.350873	0.289672	-4.061201	22432.240678
HLA A*1101	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.448971	0.387714	-4.061257	28117.111505
HLA B*0801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.278114	0.216823	-4.061290	18972.030071
HLA A*0250	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.596655	0.535260	-4.061395	39505.233352
HLA B*3801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.538105	0.476646	-4.061459	34522.756512

HLA B*1801	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.484321	0.422812	-4.061509	30501.489955
HLA B*5301	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.543293	0.481784	-4.061509	34937.604811
HLA A*6802	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.398638	0.337099	-4.061539	25040.193811
HLA A*0202	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.484370	0.422812	-4.061558	30504.955355
HLA A*3001	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.160675	0.099112	-4.061562	14476.874067
HLA B*4601	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.398873	0.337099	-4.061774	25053.743943
HLA A*3001	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.175284	0.113485	-4.061799	14972.140512
HLA A*3002	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.564864	0.502834	-4.062030	36716.709203
HLA B*5301	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.597322	0.535260	-4.062062	39565.976180
HLA A*2403	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.374725	0.312492	-4.062233	23698.705694
HLA A*2402	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.246847	0.184583	-4.062264	17654.151856
HLA B*3901	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.450263	0.387714	-4.062549	28200.896843
HLA A*6801	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.539233	0.476646	-4.062587	34612.519865
HLA A*8001	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.450312	0.387714	-4.062599	28204.100863
HLA B*5801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.352374	0.289672	-4.062702	22509.921311
HLA B*5301	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.584038	0.521317	-4.062721	38374.072966
HLA B*4002	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.631674	0.568895	-4.062778	42822.666380
HLA A*1101	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.495357	0.432524	-4.062833	31286.471470
HLA A*2403	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.397089	0.334139	-4.062950	24951.081534
HLA B*0803	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.522507	0.459317	-4.063190	33304.831003
HLA A*6802	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.429202	0.365931	-4.063271	26865.945932
HLA A*0101	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.376111	0.312492	-4.063619	23774.468890
HLA B*5101	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.496261	0.432524	-4.063737	31351.703070
HLA B*0803	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.461825	0.397920	-4.063905	28961.745684
HLA B*1509	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.490310	0.426351	-4.063958	30925.013067
HLA B*4403	1:8-16	9	GALSKGDGP	0.654001	-0.066346	-4.651633	0.587655	-4.063977	44836.590531
HLA B*4403	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.656430	0.592259	-4.064172	45334.646004
HLA A*2902	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.435997	0.371790	-4.064207	27289.579704
HLA A*2403	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.401307	0.337099	-4.064208	25194.555519
HLA B*4801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.398971	0.334728	-4.064243	25059.437185
HLA B*4501	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.586994	0.522301	-4.064693	38636.123813
HLA A*0250	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.567615	0.502834	-4.064781	36950.047143
HLA B*4501	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.660704	0.595896	-4.064808	45782.967851
HLA B*3501	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.403118	0.338222	-4.064896	25299.862093
HLA A*0250	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.541677	0.476646	-4.065030	34807.808616
HLA B*5401	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.541874	0.476646	-4.065228	34823.629947
HLA A*6801	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.634228	0.568895	-4.065332	43075.229065
HLA A*0219	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.437190	0.371790	-4.065401	27364.680724
HLA B*5101	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.462464	0.397004	-4.065460	29004.393970
HLA B*2705	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.226606	0.161134	-4.065472	16850.238203
HLA A*0203	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.405900	0.340384	-4.065516	25462.435632
HLA B*4403	1:14-22	9	DGPNADGLV	0.733182	-0.137286	-4.661620	0.595896	-4.065724	45879.665328
HLA B*4402	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.419680	0.353947	-4.065732	26283.286777
HLA B*1502	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.579849	0.514013	-4.065836	38005.702567
HLA B*0803	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.522904	0.456941	-4.065963	33335.294577
HLA A*3002	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.549183	0.483198	-4.065985	35414.677149
HLA B*5801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.320520	0.254408	-4.066112	20917.975941
HLA A*0219	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.432332	0.365931	-4.066401	27060.240394
HLA A*2602	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.611588	0.545171	-4.066417	40887.255313
HLA B*4001	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.406873	0.340384	-4.066489	25519.527610
HLA B*5701	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.432470	0.365931	-4.066540	27068.878954
HLA A*2601	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.391239	0.324195	-4.067045	24617.228550
HLA A*0212	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.404514	0.337099	-4.067415	25381.293315
HLA A*2902	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.437439	0.369909	-4.067531	27380.377452

HLA A*2301	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.541458	0.473842	-4.067616	34790.300527
HLA A*0212	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.421681	0.353947	-4.067734	26404.711997
HLA B*4601	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.417466	0.349724	-4.067742	26149.684825
HLA A*0201	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.391984	0.324195	-4.067789	24659.481713
HLA B*7301	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.589211	0.521317	-4.067895	38833.940688
HLA B*4001	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.342729	0.274750	-4.067979	22015.539925
HLA A*0216	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.309940	0.241837	-4.068102	20414.555501
HLA B*4402	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.439916	0.371790	-4.068126	27536.946956
HLA B*7301	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.466326	0.398058	-4.068268	29263.505466
HLA B*3501	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.438212	0.369909	-4.068304	27429.153908
HLA B*1502	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.551958	0.483430	-4.068528	35641.668683
HLA A*2301	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.545349	0.476646	-4.068703	35103.379359
HLA A*0216	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.409102	0.340384	-4.068718	25650.881372
HLA B*1509	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.525797	0.456941	-4.068856	33558.034275
HLA B*3501	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.423014	0.353947	-4.069066	26485.830348
HLA A*2902	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.435085	0.365931	-4.069155	27232.357944
HLA B*4501	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.610174	0.540972	-4.069201	40754.312210
HLA A*2602	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.559869	0.490659	-4.069210	36296.833961
HLA B*4601	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.403511	0.334139	-4.069371	25322.729620
HLA A*2602	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.610070	0.540487	-4.069583	40744.612407
HLA B*4403	1:291-299	9	DLIGGIEVT	0.990693	-0.401257	-4.659092	0.589436	-4.069656	45613.373727
HLA B*5301	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.496130	0.426351	-4.069778	31342.206392
HLA B*5801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.350245	0.280375	-4.069870	22399.862033
HLA B*4001	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.404013	0.334139	-4.069874	25352.063133
HLA A*0301	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.344670	0.274750	-4.069920	22114.138004
HLA B*0702	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.435851	0.365931	-4.069920	27280.427956
HLA A*2402	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.529290	0.459317	-4.069973	33829.080810
HLA B*4601	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.388375	0.318175	-4.070200	24455.420544
HLA A*3101	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.404389	0.334139	-4.070250	25374.016929
HLA B*3501	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.287500	0.217020	-4.070480	19386.526223
HLA A*6802	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.383039	0.312492	-4.070548	24156.802858
HLA A*8001	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.436695	0.365931	-4.070764	27333.462128
HLA B*1509	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.411304	0.340384	-4.070920	25781.237499
HLA A*3201	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.592296	0.521317	-4.070979	39110.767343
HLA B*5801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.345831	0.274750	-4.071081	22173.316753
HLA A*0216	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.442888	0.371790	-4.071098	27726.042622
HLA B*4402	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.458871	0.387714	-4.071158	28765.467259
HLA A*2602	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.560996	0.489523	-4.071474	36391.210131
HLA B*0802	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.482883	0.411293	-4.071590	30400.671021
HLA B*3901	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.412128	0.340384	-4.071744	25830.239254
HLA A*0101	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.381912	0.310085	-4.071827	24094.155133
HLA B*5801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.353091	0.281226	-4.071865	22547.093704
HLA B*4002	1:279-287	9	ATIGAFVYN	0.978908	-0.464895	-4.586218	0.514013	-4.072205	38567.209688
HLA B*5801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.341235	0.268910	-4.072325	21939.921453
HLA B*7301	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.561960	0.489523	-4.072437	36472.017404
HLA B*4001	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.407195	0.334728	-4.072467	25538.448541
HLA B*4801	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.413127	0.340384	-4.072743	25889.696541
HLA A*0219	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.442702	0.369909	-4.072794	27714.195563
HLA A*8001	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.422682	0.349724	-4.072958	26465.634809
HLA B*3901	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.469963	0.397004	-4.072960	29509.601969
HLA B*5101	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.484307	0.411293	-4.073014	30500.499913
HLA A*2602	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.595466	0.522301	-4.073165	39397.239451
HLA A*2402	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.556758	0.483430	-4.073328	36037.779745
HLA A*3301	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.631523	0.557970	-4.073554	

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42807.842330
HLA B*0803	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.499952	0.426351	-4.073601	31619.294695
HLA B*1801	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.038661	-0.035118	-4.073779	10931.036423
HLA A*0212	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.414248	0.340384	-4.073864	25956.591621
HLA B*1503	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.509794	0.435662	-4.074132	32344.032963
HLA A*2902	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.408872	0.334728	-4.074144	25637.285671
HLA A*2403	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.363877	0.289672	-4.074205	23114.103594
HLA B*3901	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.506822	0.432524	-4.074298	32123.441927
HLA A*2603	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.614945	0.540487	-4.074458	41204.568661
HLA A*0212	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.398671	0.324195	-4.074476	25042.090389
HLA B*4002	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.615570	0.540972	-4.074598	41263.905976
HLA A*0211	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.485970	0.411293	-4.074677	30617.546988
HLA A*8001	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.412941	0.338222	-4.074719	25878.634135
HLA B*3501	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.440724	0.365931	-4.074793	27588.240980
HLA A*3002	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.511606	0.436810	-4.074796	32479.222461
HLA A*0211	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.548641	0.473842	-4.074799	35370.447622
HLA A*2603	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.644039	0.568895	-4.075144	44059.447311
HLA A*0250	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.501496	0.426351	-4.075144	31731.879025
HLA A*6901	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.344280	0.268910	-4.075370	22094.287503
HLA A*2602	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.616489	0.540972	-4.075517	41351.282520
HLA A*2902	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.350302	0.274750	-4.075552	22402.770560
HLA B*2705	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.508088	0.432524	-4.075565	32217.248343
HLA B*4002	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.641184	0.565473	-4.075711	43770.793591
HLA A*8001	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.430133	0.353947	-4.076185	26923.562975
HLA B*4002	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.558031	0.481784	-4.076247	36143.603348
HLA B*5401	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.394425	0.318175	-4.076250	24798.479853
HLA A*3201	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.499332	0.422812	-4.076520	31574.167911
HLA B*4001	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.386777	0.310085	-4.076693	24365.621062
HLA B*4002	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.599072	0.522301	-4.076771	39725.763385
HLA A*2501	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.441128	0.364208	-4.076920	27613.923811
HLA B*5101	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.475160	0.397920	-4.077240
29864.855139
HLA B*3901	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.475398	0.397920	-4.077478
29881.177719
HLA B*0802	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.474484	0.397004	-4.077480	29818.360488
HLA B*4801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.415890	0.338222	-4.077668	26054.932619
HLA A*6801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.504242	0.426351	-4.077891	31933.192416
HLA B*1503	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.191397	0.113485	-4.077912	15538.055287
HLA B*1509	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.513584	0.435662	-4.077922	32627.506904
HLA A*2603	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.581204	0.502834	-4.078370	38124.522950
HLA B*0801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.332880	0.254408	-4.078473	21521.884668
HLA A*2601	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.391018	0.312492	-4.078526	24604.713143
HLA A*0219	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.412688	0.334139	-4.078548	25863.518492
HLA B*4403	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.601088	0.522301	-4.078787	39910.586474
HLA B*7301	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.558842	0.480013	-4.078829
36211.125186
HLA B*4801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.416311	0.337099	-4.079212	26080.175658
HLA B*1517	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.490554	0.411293	-4.079261	30942.417255
HLA B*4402	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.429047	0.349724	-4.079323
26856.355086
HLA A*0203	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.095166	0.015810	-4.079356	12449.916987
HLA A*3001	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.296480	0.217020	-4.079459	19791.546389
HLA B*1503	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.449375	0.369909	-4.079466	28143.286680
HLA B*5701	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.397700	0.318175	-4.079525	24986.201700
HLA A*0211	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.477768	0.398058	-4.079710	30044.732444
HLA A*8001	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.414602	0.334728	-4.079874	25977.804049
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HLA B*0702	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.414177	0.334139	-4.080038	25952.379294
HLA A*0250	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.569596	0.489523	-4.080073	37118.944021
HLA A*0203	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.124305	0.044127	-4.080177	13313.883998
HLA A*3101	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.404399	0.324195	-4.080204	25374.566017
HLA A*1101	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.434223	0.353947	-4.080276	27178.343660
HLA A*3301	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.478273	0.397920	-4.080353	30079.698590
HLA A*2601	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.370390	0.289672	-4.080718	23463.339672
HLA A*1101	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.430649	0.349724	-4.080925	26955.625820
HLA A*3001	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.289598	0.208647	-4.080951	19480.409726
HLA A*0206	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.298275	0.216823	-4.081451	19873.517206
HLA A*0201	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.371149	0.289672	-4.081477	23504.375218
HLA A*3002	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.514019	0.432524	-4.081495	32660.177821
HLA B*4002	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.598943	0.517364	-4.081579	39713.944985
HLA B*4403	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.584614	0.502834	-4.081780	38424.968560
HLA A*6801	1:139-147	9	RNPAPARPA	0.811154	-0.218895	-4.674054	0.592259	-4.081795	47212.143218
HLA A*2602	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.264684	0.182878	-4.081807	18394.337390
HLA A*0201	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.392181	0.310085	-4.082097	24670.690285
HLA A*6801	1:124-132	9	SELPDLSGP	0.499243	0.082735	-4.664127	0.581978	-4.082149	46145.264722
HLA B*4501	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.647627	0.565473	-4.082153	44424.925542
HLA B*1502	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.604746	0.522301	-4.082445	40248.181039
HLA B*0803	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.505288	0.422812	-4.082475	32010.161015
HLA B*0802	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.470332	0.387714	-4.082619	29534.676673
HLA A*2402	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.572196	0.489523	-4.082674	37341.906964
HLA A*3101	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.420955	0.338222	-4.082733	26360.609281
HLA A*0301	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.364070	0.281226	-4.082844	23124.359537
HLA B*4002	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.640933	0.557970	-4.082963	43745.463843
HLA B*2705	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.098846	0.015810	-4.083036	12555.839317
HLA A*2601	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.393185	0.310085	-4.083100	24727.746014
HLA B*5701	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.417380	0.334139	-4.083240	26144.451074
HLA B*1517	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.255051	0.171766	-4.083285	17990.832475
HLA A*2602	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.618566	0.535260	-4.083306	41549.512119
HLA B*5401	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.518976	0.435662	-4.083314	33035.125294
HLA B*3501	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.352285	0.268910	-4.083374	22505.294292
HLA A*2902	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.420756	0.337099	-4.083657	26348.490390
HLA B*1801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.418446	0.334728	-4.083718	26208.743111
HLA A*0250	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.567138	0.483198	-4.083940	36909.490599
HLA A*3301	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.624449	0.540487	-4.083962	42116.186390
HLA A*3002	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.396549	0.312492	-4.084057	24920.054847
HLA A*2602	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.482047	0.397920	-4.084127	30342.178089
HLA A*0301	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.326003	0.241837	-4.084166	21183.775105
HLA A*6801	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.605526	0.521317	-4.084209	40320.535078
HLA A*0250	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.520266	0.435662	-4.084604	33133.386426
HLA B*1509	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.567838	0.483198	-4.084640	36969.042112
HLA A*3002	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.574290	0.489523	-4.084767	37522.337350
HLA B*1503	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.403207	0.318175	-4.085032	25305.063667
HLA B*1801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.483125	0.397920	-4.085205	30417.615561
HLA B*4601	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.353518	0.268222	-4.085296	22569.304502
HLA B*0801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.419987	0.334139	-4.085848	26301.920226
HLA A*2301	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.542905	0.456941	-4.085965	34906.432312
HLA B*5301	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.300716	0.214699	-4.086016	19985.538292
HLA B*4402	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.426500	0.340384	-4.086116	26699.321727

HLA B*0803	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.456080	0.369909	-4.086172	28581.185906
HLA A*0202	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.563257	0.476646	-4.086610	36581.095073
HLA A*0301	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.341287	0.254408	-4.086879	21942.532844
HLA B*0803	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.498207	0.411293	-4.086913	31492.454524
HLA B*4402	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.421968	0.334728	-4.087240	26422.145031
HLA A*3101	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.399845	0.312492	-4.087353	25109.919551
HLA A*0203	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.424510	0.337099	-4.087412	26577.260600
HLA B*1517	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.475285	0.387714	-4.087571	29873.419341
HLA B*5701	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.424783	0.337099	-4.087684	26593.944318
HLA A*0301	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.355929	0.268222	-4.087706	22694.924778
HLA B*1517	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.437557	0.349724	-4.087832	27387.784694
HLA B*2705	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.296496	0.208647	-4.087849	19792.295894
HLA B*0802	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.486031	0.398058	-4.087973	30621.853866
HLA B*3801	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.571503	0.483430	-4.088073	37282.359898
HLA B*5701	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.412338	0.324195	-4.088143	25842.678996
HLA A*0219	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.428697	0.340384	-4.088313	26834.715613
HLA B*4001	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.368740	0.280375	-4.088365	23374.400948
HLA B*4002	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.579050	0.490659	-4.088391	37935.860563
HLA B*4402	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.426763	0.338222	-4.088541	26715.503951
HLA A*0301	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.368931	0.280375	-4.088555	23384.645878
HLA B*0803	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.521093	0.432524	-4.088569	33196.541817
HLA B*5401	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.545537	0.456941	-4.088596	35118.575078
HLA A*6901	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.357071	0.268222	-4.088848	22754.672924
HLA B*4002	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.634117	0.545171	-4.088946	43064.277944
HLA B*1502	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.578707	0.489523	-4.089184	37905.908988
HLA A*6901	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.294985	0.205784	-4.089202	19723.566839
HLA A*8001	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.401704	0.312492	-4.089212	25217.600710
HLA A*3001	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.307602	0.218302	-4.089300	20304.962447
HLA B*0801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.439122	0.349724	-4.089397	27486.640485
HLA B*1503	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.240755	0.151290	-4.089465	17408.231095
HLA A*2403	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.427821	0.338222	-4.089599	26780.620742
HLA A*2602	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.611214	0.521317	-4.089897	40852.100347
HLA B*1517	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.319220	0.229292	-4.089929	20855.489803
HLA A*0203	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.424207	0.334139	-4.090068	26558.719446
HLA A*0250	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.332084	0.241837	-4.090246	21482.450726
HLA B*1509	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.549578	0.459317	-4.090261	35446.878813
HLA B*5801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.358971	0.268222	-4.090749	22854.479280
HLA B*1502	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.488827	0.398058	-4.090769	30819.626183
HLA B*4002	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.574259	0.483198	-4.091061	37519.698551
HLA B*0702	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.431509	0.340384	-4.091125	27009.051357
HLA A*1101	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.462931	0.371790	-4.091142	29035.635984
HLA A*6801	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.626587	0.535260	-4.091327	42324.035539
HLA A*3002	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.488454	0.397004	-4.091450	30793.127390
HLA B*4601	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.308462	0.216823	-4.091639	20345.206496
HLA A*0202	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.463657	0.371790	-4.091868	29084.214164
HLA B*3801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.575082	0.483198	-4.091884	37590.807945
HLA B*1502	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.527556	0.435662	-4.091894	33694.287527
HLA A*0301	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.360809	0.268910	-4.091898	22951.370722
HLA B*4403	1:178-186	9	LSARRSRGP	0.516181	0.049292	-4.657485	0.565473	-4.092012	45444.899534
HLA B*0803	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.490171	0.398058	-4.092113	30915.143890
HLA B*5101	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.410296	0.318175	-4.092121	25721.472688
HLA B*5301	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.594982	0.502834	-4.092148	39353.358159
HLA B*1517	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.432914	0.340384	-4.092530	27096.570199
HLA B*4001	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.346996	0.254408	-4.092588	22232.894422

HLA B*0801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.431042	0.338222	-4.092820	26979.989924
HLA A*3301	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.576317	0.483430	-4.092887	37697.928751
HLA A*0101	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.382678	0.289672	-4.093006	24136.685652
HLA A*6802	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.403203	0.310085	-4.093118	25304.789873
HLA A*2501	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.490209	0.397004	-4.093205	30917.819965
HLA B*4402	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.430332	0.337099	-4.093234	26935.946369
HLA A*2402	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.583956	0.490659	-4.093297	38366.807672
HLA B*1509	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.405846	0.312492	-4.093354	25459.267603
HLA A*3001	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.308119	0.214699	-4.093420	20329.143305
HLA B*2705	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.447411	0.353947	-4.093463	28016.291352
HLA A*0203	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.431751	0.338222	-4.093529	27024.105496
HLA A*8001	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.427696	0.334139	-4.093557	26772.943193
HLA A*6801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.573583	0.480013	-4.093569	37461.286573
HLA B*1801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.383253	0.289672	-4.093581	24168.698177
HLA A*0203	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.362221	0.268222	-4.093998	23026.114953
HLA B*3501	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.362404	0.268222	-4.094181	23035.833364
HLA B*5101	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.517266	0.422812	-4.094453	32905.275648
HLA B*1509	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.491485	0.397004	-4.094481	31008.776750
HLA A*2501	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.466580	0.371790	-4.094791	29280.608193
HLA A*2403	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.419120	0.324195	-4.094926	26249.467413
HLA A*0216	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.429085	0.334139	-4.094945	26858.679825
HLA A*0250	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.492918	0.397920	-4.094998	31111.275750
HLA B*3901	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.464921	0.369909	-4.095013	29168.987669
HLA A*0216	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.459240	0.364208	-4.095032	28789.909662
HLA A*3301	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.636077	0.540972	-4.095104	43259.016385
HLA B*0802	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.466935	0.371790	-4.095145	29304.537096
HLA B*7301	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.578376	0.483198	-4.095178	37877.005599
HLA B*0702	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.309898	0.214699	-4.095198	20412.567669
HLA B*3901	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.449147	0.353947	-4.095200	28128.522104
HLA A*0211	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.337140	0.241837	-4.095302	21734.012678
HLA A*0211	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.312146	0.216823	-4.095323	20518.522961
HLA B*4501	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.313718	0.218302	-4.095416	20592.918470
HLA A*0212	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.407935	0.312492	-4.095443	25582.006099
HLA B*0802	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.493376	0.397920	-4.095456	31144.113235
HLA A*3001	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.304853	0.209282	-4.095571	20176.846646
HLA B*1509	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.532387	0.436810	-4.095577	34071.152055
HLA B*1517	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.070036	-0.025677	-4.095714	11749.959349
HLA B*4501	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.640905	0.545171	-4.095734	43742.624038
HLA A*6802	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.429923	0.334139	-4.095784	26910.602935
HLA A*0216	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.465946	0.369909	-4.096037	29237.870105
HLA A*0101	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.365007	0.268910	-4.096097	23174.328436
HLA B*1503	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.460443	0.364208	-4.096235	28869.764317
HLA B*3901	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.313114	0.216823	-4.096291	20564.307175
HLA B*0702	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.364549	0.268222	-4.096327	23149.894070
HLA A*0202	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.586047	0.489523	-4.096524	38551.981659
HLA B*5401	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.433647	0.337099	-4.096549	27142.344725
HLA B*0801	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.409065	0.312492	-4.096573	25648.661173
HLA B*5301	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.532316	0.435662	-4.096654	34065.622869
HLA B*0802	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.461012	0.364208	-4.096803	28907.585167
HLA A*2601	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.378127	0.281226	-4.096901	23885.078993
HLA B*0802	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.450954	0.353947	-4.097006	28245.786268
HLA A*2402	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.573721	0.476646	-4.097075	37473.245505
HLA A*3001	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.303117	0.205784	-4.097333	20096.342499

HLA A*2403	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.432186	0.334728	-4.097458	27051.165557
HLA A*3301	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.642681	0.545171	-4.097510	43921.892297
HLA B*4002	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.638015	0.540487	-4.097528	43452.519730
HLA A*2603	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.618965	0.521317	-4.097648	41587.741999
HLA B*5701	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.436281	0.338222	-4.098059	27307.449218
HLA A*0216	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.387741	0.289672	-4.098069	24419.725319
HLA B*4501	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.656045	0.557970	-4.098075	45294.441954
HLA A*0250	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.581651	0.483430	-4.098221	38163.730491
HLA B*1801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.485935	0.387714	-4.098222	30615.062525
HLA B*4601	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.422431	0.324195	-4.098236	26450.319394
HLA B*4403	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.639321	0.540972	-4.098349	43583.417258
HLA A*2902	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.438755	0.340384	-4.098371	27463.453121
HLA A*6901	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.072715	-0.025677	-4.098392	11822.648480
HLA A*2601	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.281316	0.182878	-4.098439	19112.440765
HLA B*1502	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.580544	0.481784	-4.098760	38066.610886
HLA A*3001	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.142941	0.044127	-4.098813	13897.634434
HLA B*4001	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.308389	0.209282	-4.099107	20341.794757
HLA A*0206	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.510436	0.411293	-4.099142	32391.837149
HLA B*4801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.368120	0.268910	-4.099210	23341.041205
HLA B*0802	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.469153	0.369909	-4.099244	29454.576267
HLA B*1501	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.302419	0.203022	-4.099397	20064.078887
HLA B*5801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.349832	0.250113	-4.099719	22378.544368
HLA A*6901	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.374584	0.274750	-4.099834	23691.014500
HLA B*1502	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.556885	0.456941	-4.099944	36048.309144
HLA A*3301	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.583223	0.483198	-4.100025	38302.103519
HLA A*0219	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.454104	0.353947	-4.100157	28451.444971
HLA B*4403	1:190-198	9	SMQIRRIDP	0.396711	0.172184	-4.669742	0.568895	-4.100847	46745.780010
HLA A*6802	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.450785	0.349724	-4.101060	28234.786337
HLA A*3301	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.591817	0.490659	-4.101158	39067.627830
HLA A*2403	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.411325	0.310085	-4.101240	25782.492792
HLA B*1503	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.450989	0.349724	-4.101264	28248.078459
HLA B*1503	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.533984	0.432524	-4.101461	34196.721267
HLA A*2601	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.370484	0.268910	-4.101573	23468.417584
HLA A*3101	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.376607	0.274750	-4.101857	23801.622623
HLA B*1502	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.575904	0.473842	-4.102062	37662.052109
HLA A*0203	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.370973	0.268910	-4.102062	23494.840448
HLA B*1502	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.585582	0.483198	-4.102383	38510.708502
HLA B*3901	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.466655	0.364208	-4.102447	29285.677586
HLA B*5401	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.500807	0.398058	-4.102749	31681.620745
HLA B*3901	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.437092	0.334139	-4.102953	27358.463755
HLA B*1502	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.605954	0.502834	-4.103120	40360.254220
HLA B*4403	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.586561	0.483430	-4.103131	38597.683793
HLA B*5301	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.594124	0.490659	-4.103465	39275.727314
HLA A*2403	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.332824	0.229292	-4.103532	21519.090505
HLA A*3201	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.580215	0.476646	-4.103569	38037.790741
HLA B*1517	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.440668	0.337099	-4.103569	27584.659228
HLA B*5301	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.583601	0.480013	-4.103587	38335.478883
HLA A*2902	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.457643	0.353947	-4.103695	28684.194081
HLA A*2601	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.378507	0.274750	-4.103757	23906.021100
HLA A*0250	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.583794	0.480013	-4.103780	38352.488692
HLA A*3301	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.639225	0.535260	-4.103965	43573.751290

HLA B*4501	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.644474	0.540487	-4.103986	44103.565379
HLA B*4801	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.416545	0.312492	-4.104054	26094.288561
HLA B*3801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.563835	0.459317	-4.104518	36629.810801
HLA A*2603	1:26-34	9	GAHRAATGP	0.552469	-0.011497	-4.645498	0.540972	-4.104526	44207.715755
HLA A*6901	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.384961	0.280375	-4.104586	24263.940582
HLA B*4002	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.625929	0.521317	-4.104612	42259.972936
HLA A*2301	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.541566	0.436810	-4.104757	34798.959341
HLA A*2402	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.531163	0.426351	-4.104811	33975.255941
HLA A*0211	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.537476	0.432524	-4.104952	34472.739951
HLA A*2603	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.586775	0.481784	-4.104991	38616.690107
HLA A*6901	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.288167	0.182878	-4.105290	19416.334740
HLA A*0203	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.429491	0.324195	-4.105297	26883.828921
HLA B*3801	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.528259	0.422812	-4.105446	33748.834056
HLA A*2403	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.385861	0.280375	-4.105486	24314.267285
HLA A*0216	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.440221	0.334728	-4.105493	27556.320105
HLA A*0212	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.415765	0.310085	-4.105681	26047.463112
HLA B*1509	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.386994	0.281226	-4.105768	24377.751088
HLA B*4402	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.416003	0.310085	-4.105918	26061.699304
HLA A*6802	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.395595	0.289672	-4.105923	24865.380131
HLA B*3501	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.322759	0.216823	-4.105935	21026.099650
HLA B*4002	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.324307	0.218302	-4.106005	21101.193935
HLA A*2301	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.532366	0.426351	-4.106014	34069.493205
HLA B*1501	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.387306	0.281226	-4.106080	24395.297564
HLA A*6802	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.311979	0.205784	-4.106196	20510.643267
HLA B*0702	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.444474	0.338222	-4.106252	27827.474208
HLA B*1509	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.470461	0.364208	-4.106253	29543.465843
HLA B*5301	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.589613	0.483198	-4.106415	38869.882241
HLA A*0212	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.088095	-0.018628	-4.106723	12248.827142
HLA B*5101	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.494466	0.387714	-4.106753	31222.389034
HLA B*7301	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.470992	0.364208	-4.106784	29579.608807
HLA A*6802	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.445021	0.338222	-4.106799	27862.572972
HLA B*5801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.348864	0.241837	-4.107026	22328.720951
HLA A*0101	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.361535	0.254408	-4.107127	22989.769599
HLA A*2601	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.348965	0.241837	-4.107127	22333.915779
HLA A*0216	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.419654	0.312492	-4.107162	26281.722738
HLA B*2705	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.420194	0.312492	-4.107702	26314.444768
HLA A*0202	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.581653	0.473842	-4.107811	38163.936953
HLA A*2602	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.324981	0.216823	-4.108158	21133.981902
HLA A*2402	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.519458	0.411293	-4.108164	33071.782472
HLA A*6801	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.598929	0.490659	-4.108270	39712.655918
HLA B*4501	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.591714	0.483430	-4.108283	39058.329469
HLA A*8001	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.445397	0.337099	-4.108298	27886.700762
HLA B*3801	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.588408	0.480013	-4.108395	38762.157254
HLA A*0216	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.445498	0.337099	-4.108400	27893.188667
HLA B*4501	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.544068	0.435662	-4.108407	35000.033348
HLA B*4403	1:184-192	9	RGPVRASMQ	0.597793	-0.039823	-4.666397	0.557970	-4.108427	46387.048929
HLA A*0202	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.443158	0.334728	-4.108430	27743.297393
HLA B*4601	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.398104	0.289672	-4.108433	25009.462204
HLA B*4801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.376778	0.268222	-4.108556	23811.024261
HLA A*1101	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.398335	0.289672	-4.108663	25022.724965
HLA A*0201	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.377852	0.268910	-4.108941	23869.965548
HLA B*1501	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.389343	0.280375	-4.108968	24509.989394
HLA A*0211	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.447446	0.338222	-4.109224	28018.564920
HLA B*3501	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.201988	0.092742	-4.109246	15921.652495

HLA A*8001	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.433481	0.324195	-4.109286	27131.921295
HLA A*2402	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.546176	0.436810	-4.109366	35170.289744
HLA A*2902	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.378373	0.268910	-4.109463	23898.650488
HLA B*1517	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.443612	0.334139	-4.109472	27772.279536
HLA A*6801	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.654814	0.545171	-4.109643	45166.223911
HLA A*0212	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.378571	0.268910	-4.109660	23909.513236
HLA B*4402	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.427940	0.318175	-4.109766	26788.010651
HLA A*0211	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.480059	0.369909	-4.110150	30203.626335
HLA A*6802	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.434371	0.324195	-4.110176	27187.608244
HLA A*8001	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.450597	0.340384	-4.110213	28222.569216
HLA A*2601	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.390588	0.280375	-4.110213	24580.366292
HLA B*1501	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.213472	0.103191	-4.110281	16348.293406
HLA A*3301	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.445059	0.334728	-4.110331	27864.984811
HLA A*2603	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.567345	0.456941	-4.110404	36927.066292
HLA A*2301	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.533484	0.422812	-4.110672	34157.338861
HLA B*5401	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.543474	0.432524	-4.110950	34952.161502
HLA A*2501	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.465072	0.353947	-4.111124	29179.088681
HLA B*5801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.340464	0.229292	-4.111173	21901.024819
HLA A*2501	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.481394	0.369909	-4.111485	30296.579293
HLA B*7301	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.401227	0.289672	-4.111555	25189.921753
HLA A*3301	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.628951	0.517364	-4.111586	42555.005629
HLA A*2601	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.328440	0.216823	-4.111616	21302.951229
HLA B*4403	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.656823	0.545171	-4.111652	45375.622165
HLA A*0212	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.446490	0.334728	-4.111762	27956.940814
HLA A*2301	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.547461	0.435662	-4.111799	35274.520139
HLA A*6901	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.362056	0.250113	-4.111943	23017.396793
HLA A*3001	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.294913	0.182878	-4.112035	19720.259344
HLA B*0802	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.478003	0.365931	-4.112073	30060.990709
HLA A*0211	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.424614	0.312492	-4.112122	26583.587674
HLA A*0101	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.392515	0.280375	-4.112140	24689.649696
HLA A*6801	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.652697	0.540487	-4.112210	44946.605408
HLA A*3301	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.615253	0.502834	-4.112419	41233.780502
HLA B*4501	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.446570	0.334139	-4.112430	27962.083581
HLA B*1801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.545126	0.432524	-4.112602	35085.342982
HLA A*3002	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.482578	0.369909	-4.112669	30379.298184
HLA A*0250	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.500410	0.387714	-4.112697	31652.668386
HLA A*3002	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.451005	0.338222	-4.112783	28249.148212
HLA B*3801	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.548532	0.435662	-4.112871	35361.646608
HLA A*2601	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.381150	0.268222	-4.112928	24051.959790
HLA A*6901	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.105659	-0.007282	-4.112941	12754.377170
HLA A*0219	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.450108	0.337099	-4.113009	28190.829435
HLA A*2402	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.586914	0.473842	-4.113072	38629.017883
HLA B*0801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.437395	0.324195	-4.113200	27377.563225
HLA A*2301	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.545805	0.432524	-4.113281	35140.240344
HLA B*0802	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.448012	0.334728	-4.113284	28055.118880
HLA B*0702	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.437498	0.324195	-4.113304	27384.080823
HLA B*1509	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.536306	0.422812	-4.113493	34379.991082
HLA A*2603	1:95-103	9	GPAAAVRTP	0.699889	-0.154718	-4.658754	0.545171	-4.113583	45577.853650
HLA B*4001	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.381987	0.268222	-4.113764	24098.326588
HLA B*3501	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.403454	0.289672	-4.113782	25319.441997
HLA A*3201	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.595616	0.481784	-4.113832	39410.882433
HLA A*3001	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.296595	0.182632	-4.113963	19796.793518
HLA B*3501	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.463730	0.349724	-4.114006	29089.092186
HLA A*0212	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-3.940392	-0.173733	-4.114125	8717.496500
HLA A*0301	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.364244	0.250113	-4.114130	23133.618807

HLA B*1501	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.388925	0.274750	-4.114175	24486.398608
HLA A*6901	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.368630	0.254408	-4.114222	23368.458416
HLA A*0201	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.394801	0.280375	-4.114426	24819.954270
HLA A*3101	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.395682	0.281226	-4.114456	24870.357830
HLA B*0801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.297126	0.182632	-4.114494	19821.012572
HLA A*2602	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.617349	0.502834	-4.114515	41433.239975
HLA A*2501	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.451696	0.337099	-4.114597	28294.114442
HLA A*0201	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.389470	0.274750	-4.114720	24517.150642
HLA B*1509	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.547266	0.432524	-4.114742	35258.684701
HLA B*4402	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.080106	-0.034919	-4.115025	12025.586231
HLA B*0702	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.465264	0.349724	-4.115540	29192.035714
HLA A*0201	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.396777	0.281226	-4.115551	24933.135308
HLA A*6801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.552541	0.436810	-4.115731	35689.519510
HLA A*2403	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.396995	0.281226	-4.115770	24945.682815
HLA B*1509	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.513791	0.397920	-4.115871	32643.043587
HLA B*5101	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.487794	0.371790	-4.116004	30746.351892
HLA A*2902	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.300622	0.184583	-4.116039	19981.213978
HLA B*4403	1:129-137	9	LSGPTPRAP	0.608146	-0.067659	-4.656771	0.540487	-4.116284	45370.221990
HLA B*0801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.384745	0.268222	-4.116523	24251.867186
HLA A*3301	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.638015	0.521317	-4.116698	43452.519730
HLA B*3901	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.451602	0.334728	-4.116874	28287.992383
HLA A*1101	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.482937	0.365931	-4.117006	30404.453935
HLA A*1101	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.427158	0.310085	-4.117073	26739.795678
HLA A*3101	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.385391	0.268222	-4.117169	24287.974014
HLA A*0201	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.359084	0.241837	-4.117247	22860.414780
HLA A*2602	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.600494	0.483198	-4.117296	39855.998143
HLA A*0101	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.398875	0.281226	-4.117649	25053.879482
HLA A*3002	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.505504	0.387714	-4.117790	32026.096751
HLA B*4402	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.407580	0.289672	-4.117908	25561.116864
HLA B*2705	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.458347	0.340384	-4.117964	28730.785372
HLA A*0101	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.386247	0.268222	-4.118024	24335.849006
HLA A*6802	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.399277	0.281226	-4.118051	25077.067325
HLA B*4801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.442263	0.324195	-4.118068	27686.172695
HLA A*0212	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.386488	0.268222	-4.118266	24349.413172
HLA A*0250	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.592268	0.473842	-4.118426	39108.228407
HLA B*0801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.321664	0.203022	-4.118642	20973.159437
HLA A*0211	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.485169	0.365931	-4.119239	30561.116655
HLA B*4402	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.431794	0.312492	-4.119302	27026.737177
HLA A*2501	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.454088	0.334728	-4.119360	28450.367558
HLA B*3801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.576355	0.456941	-4.119414	37701.191958
HLA B*3501	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.361314	0.241837	-4.119476	22978.081593
HLA A*0219	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.432071	0.312492	-4.119579	27043.995660
HLA B*5701	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.394472	0.274750	-4.119722	24801.163139
HLA A*3002	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.336973	0.216823	-4.120150	21725.666201
HLA A*3101	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.389122	0.268910	-4.120212	24497.528508
HLA A*0206	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.490207	0.369909	-4.120298	30917.652704
HLA B*7301	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.597000	0.476646	-4.120354	39536.662531
HLA B*4001	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.389341	0.268910	-4.120430	24509.856798
HLA B*2705	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.457596	0.337099	-4.120497	28681.090683
HLA B*5101	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.401777	0.281226	-4.120551	25221.830222
HLA A*2902	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.362392	0.241837	-4.120555	23035.210266
HLA B*0802	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.461139	0.340384	-4.120755	28916.031290
HLA A*3201	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.594740	0.473842	-4.120898	39331.435845
HLA A*2301	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.519232	0.398058	-4.121174	33054.611123

HLA A*2501	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.459619	0.338222	-4.121397	28814.996371
HLA B*7301	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.487399	0.365931	-4.121468	30718.420415
HLA B*4601	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.396281	0.274750	-4.121531	24904.690705
HLA B*3801	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.547969	0.426351	-4.121617	35315.763780
HLA B*0802	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.458723	0.337099	-4.121625	28755.664997
HLA B*5701	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.411313	0.289672	-4.121641	25781.795399
HLA A*3301	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.603588	0.481784	-4.121804	40140.979129
HLA A*2501	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.411995	0.289672	-4.122323	25822.275375
HLA A*3002	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.432454	0.310085	-4.122369	27067.853896
HLA B*3501	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.432604	0.310085	-4.122520	27077.227300
HLA A*0201	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.391105	0.268222	-4.122883	24609.638661
HLA B*3501	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.328712	0.205784	-4.122929	21316.324031
HLA B*4402	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.391866	0.268910	-4.122956	24652.812362
HLA B*4403	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.640346	0.517364	-4.122981	43686.339307
HLA A*2602	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.603057	0.480013	-4.123044	40091.931355
HLA B*1517	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.495117	0.371790	-4.123327	31269.212085
HLA A*2603	1:119-127	9	AEAYASELP	0.543268	-0.008008	-4.658674	0.535260	-4.123414	45569.471003
HLA A*0206	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.457591	0.334139	-4.123452	28680.780362
HLA B*0702	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.441629	0.318175	-4.123454	27645.761852
HLA B*0803	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.520524	0.397004	-4.123521	33153.109568
HLA B*2705	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.365414	0.241837	-4.123576	23196.027694
HLA B*0803	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.511476	0.387714	-4.123763	32469.559904
HLA B*4801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.442019	0.318175	-4.123844	27670.600047
HLA A*0250	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.580972	0.456941	-4.124031	38104.109722
HLA B*3901	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.473774	0.349724	-4.124050	29769.683428
HLA A*3101	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.378810	0.254408	-4.124403	23922.710355
HLA B*5701	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.392722	0.268222	-4.124499	24701.406502
HLA B*2705	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.442740	0.318175	-4.124565	27716.594559
HLA A*0216	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.478840	0.353947	-4.124892	30118.941575
HLA A*3101	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.309761	0.184583	-4.125179	20406.163750
HLA A*2301	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.523106	0.397920	-4.125186	33350.807446
HLA B*7301	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.551629	0.426351	-4.125278	35614.684456
HLA B*1517	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.460032	0.334728	-4.125304	28842.445362
HLA A*0206	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.558309	0.432524	-4.125785	36166.683595
HLA B*4402	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.406262	0.280375	-4.125886	25483.657810
HLA A*8001	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.394972	0.268910	-4.126062	24829.758149
HLA B*4501	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.647559	0.521317	-4.126242	44417.956405
HLA A*1101	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.461019	0.334728	-4.126291	28908.054332
HLA B*5401	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.549148	0.422812	-4.126336	35411.803424
HLA A*2603	1:220-228	9	VAFLYLVLG	1.025116	-0.502815	-4.648726	0.522301	-4.126425	44537.544323
HLA A*0202	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.583373	0.456941	-4.126432	38315.367263
HLA B*4601	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.368292	0.241837	-4.126454	23350.260914
HLA B*0803	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.476208	0.349724	-4.126484	29937.000378
HLA B*7301	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.585816	0.459317	-4.126499	38531.548005
HLA B*0801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.401262	0.274750	-4.126512	25191.965957
HLA A*3001	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.224421	0.097839	-4.126582	16765.674244
HLA B*1503	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.335350	0.208647	-4.126703	21644.602202
HLA A*2301	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.538007	0.411293	-4.126714	34514.913303
HLA A*6801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.343686	0.216823	-4.126862	22064.067694
HLA A*0101	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.368856	0.241837	-4.127018	23380.597962
HLA A*3201	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.617805	0.490659	-4.127146	41476.747754
HLA B*0802	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.445653	0.318175	-4.127478	27903.149783

HLA B*0802	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.437681	0.310085	-4.127597	27395.638559
HLA B*4501	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.609645	0.481784	-4.127861	40704.735219
HLA B*2705	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.493999	0.365931	-4.128068	31188.794098
HLA A*1101	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.465246	0.337099	-4.128147	29190.772336
HLA B*4001	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.409394	0.281226	-4.128168	25668.094430
HLA A*0206	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.468568	0.340384	-4.128184	29414.925827
HLA A*3001	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.279491	0.151290	-4.128201	19032.270543
HLA A*2902	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.408872	0.280375	-4.128497	25637.285671
HLA A*0219	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.463404	0.334728	-4.128676	29067.226151
HLA B*3801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.561267	0.432524	-4.128743	36413.857502
HLA A*0219	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.438861	0.310085	-4.128776	27470.139775
HLA B*1503	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.331830	0.203022	-4.128808	21469.902883
HLA B*5101	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.493176	0.364208	-4.128968	31129.795200
HLA A*0211	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.469378	0.340384	-4.128994	29469.877455
HLA B*4601	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.409504	0.280375	-4.129129	25674.621752
HLA A*0219	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.453364	0.324195	-4.129170	28403.001723
HLA A*2902	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.441805	0.312492	-4.129313	27656.981165
HLA A*2602	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.611165	0.481784	-4.129381	40847.459499
HLA A*0203	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.404138	0.274750	-4.129388	25359.333223
HLA B*5401	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.540702	0.411293	-4.129409	34729.749125
HLA B*0803	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.501200	0.371790	-4.129410	31710.256486
HLA A*3301	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.603273	0.473842	-4.129431	40111.890469
HLA A*0203	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.409943	0.280375	-4.129568	25700.608607
HLA A*1101	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.312118	0.182285	-4.129833	20517.190970
HLA B*4402	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.359589	0.229292	-4.130298	22887.019796
HLA A*0201	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.384874	0.254408	-4.130467	24259.084255
HLA A*3101	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.347400	0.216823	-4.130577	22253.591779
HLA B*4001	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.454790	0.324195	-4.130596	28496.424885
HLA B*2705	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.465448	0.334728	-4.130720	29204.356517
HLA A*0301	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.360228	0.229292	-4.130937	22920.722604
HLA B*1801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.500937	0.369909	-4.131028	31691.048820
HLA B*0802	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.443677	0.312492	-4.131185	27776.486713
HLA A*3201	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.620753	0.489523	-4.131231	41759.308561
HLA A*2403	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.373174	0.241837	-4.131336	23614.239713
HLA A*2902	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.465549	0.334139	-4.131409	29211.150977
HLA B*5301	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.608184	0.476646	-4.131537	40567.995967
HLA A*2603	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.648942	0.517364	-4.131578	44559.716613
HLA B*1502	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.529582	0.397920	-4.131661	33851.781859
HLA A*0301	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.348488	0.216823	-4.131664	22309.401968
HLA B*1501	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.298637	0.166065	-4.132571	19890.081188
HLA B*5301	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.569497	0.436810	-4.132687	37110.510986
HLA B*5801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.335740	0.203022	-4.132717	21664.048686
HLA B*4801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.413414	0.280375	-4.133038	25906.789549
HLA B*5301	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.414607	0.281226	-4.133381	25978.085124
HLA B*4601	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.414638	0.281226	-4.133412	25979.912190
HLA B*1509	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.468147	0.334728	-4.133419	29386.455078
HLA A*6802	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.408524	0.274750	-4.133774	25616.767045
HLA B*4402	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.383918	0.250113	-4.133805	24205.728761
HLA B*1801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.499875	0.365931	-4.133944	31613.650321
HLA B*0702	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.414419	0.280375	-4.134044	25966.844472
HLA A*3101	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.384181	0.250113	-4.134068	24220.399639
HLA A*0216	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.115541	-0.018628	-4.134169	13047.917126
HLA B*1801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.505997	0.371790	-4.134208	32062.501529
HLA A*8001	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.423892	0.289672	-4.134221	26539.473339
HLA B*3801	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.571118	0.436810	-4.134308	37249.296844

HLA A*8001	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.388718	0.254408	-4.134311	24474.744137
HLA B*3501	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.468535	0.334139	-4.134396	29412.698070
HLA B*3801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.504430	0.369909	-4.134522	31947.015809
HLA A*3301	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.614555	0.480013	-4.134542	41167.581855
HLA B*5801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.351671	0.217020	-4.134651	22473.539666
HLA B*1801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.453073	0.318175	-4.134898	28383.954633
HLA B*0702	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.409875	0.274750	-4.135125	25696.576837
HLA B*7301	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.571938	0.436810	-4.135128	37319.691862
HLA B*5801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.353513	0.218302	-4.135211	22569.060308
HLA A*3201	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.615324	0.480013	-4.135310	41240.473151
HLA A*0211	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.445418	0.310085	-4.135334	27888.058570
HLA A*0206	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.472555	0.337099	-4.135456	29686.215354
HLA B*5801	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.350450	0.214699	-4.135750	22410.407242
HLA B*3901	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.454116	0.318175	-4.135941	28452.214578
HLA A*3201	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.571623	0.435662	-4.135961	37292.647682
HLA B*5701	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.416447	0.280375	-4.136071	26088.360212
HLA A*0101	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.353175	0.216823	-4.136352	22551.485314
HLA B*4501	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.460697	0.324195	-4.136502	28886.636926
HLA B*3901	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.473892	0.337099	-4.136793	29777.737051
HLA B*0702	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.378693	0.241837	-4.136855	23916.240269
HLA B*3901	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.475175	0.338222	-4.136953	29865.824548
HLA B*4402	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.340056	0.203022	-4.137033	21880.418631
HLA A*3301	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.563433	0.426351	-4.137081	36595.940560
HLA B*4501	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.563661	0.426351	-4.137309	36615.149658
HLA A*2402	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.569852	0.432524	-4.137328	37140.838698
HLA B*7301	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.611245	0.473842	-4.137403	40854.973518
HLA A*0212	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.417819	0.280375	-4.137443	26170.913472
HLA B*1801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.447559	0.310085	-4.137474	28025.841576
HLA A*3201	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.491647	0.353947	-4.137699	31020.353940
HLA A*0219	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.427468	0.289672	-4.137796	26758.897529
HLA B*1501	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.289861	0.152039	-4.137823	19492.216631
HLA B*1502	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.549223	0.411293	-4.137930	35417.934320
HLA A*0206	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.472715	0.334728	-4.137987	29697.138104
HLA A*0203	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.419278	0.281226	-4.138052	26258.983587
HLA A*3002	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.611943	0.473842	-4.138101	40920.669482
HLA B*4501	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.560961	0.422812	-4.138149	36388.257164
HLA B*5701	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.341580	0.203022	-4.138558	21957.376196
HLA A*0212	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.355433	0.216823	-4.138610	22669.033606
HLA A*0101	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.367935	0.229292	-4.138643	23331.067813
HLA B*3501	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.393297	0.254408	-4.138890	24734.168017
HLA B*3501	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.463089	0.324195	-4.138894	29046.162223
HLA A*1101	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.355828	0.216823	-4.139004	22689.645980
HLA B*3901	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.280294	0.141159	-4.139135	19067.516305
HLA B*5701	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.420420	0.281226	-4.139194	26328.114708
HLA A*0250	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.562056	0.422812	-4.139244	36480.107994
HLA A*0212	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.420533	0.281226	-4.139307	26334.952340
HLA B*4001	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.381176	0.241837	-4.139339	24053.391135
HLA B*0802	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.473593	0.334139	-4.139454	29757.285107
HLA B*1509	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.527326	0.387714	-4.139613	33676.428590
HLA A*2601	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.394023	0.254408	-4.139616	24775.549609
HLA A*0206	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.489398	0.349724	-4.139674	30860.168400
HLA A*2602	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.566062	0.426351	-4.139711	36818.152078
HLA B*0702	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.476819	0.337099	-4.139720	29979.138528

HLA A*2501	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.421007	0.281226	-4.139781	26363.746844
HLA A*2501	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.480226	0.340384	-4.139842	30215.229841
HLA A*2602	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.613815	0.473842	-4.139973	41097.487299
HLA A*2403	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.408214	0.268222	-4.139992	25598.480504
HLA B*5101	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.506124	0.365931	-4.140194	32071.869445
HLA A*2501	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.474352	0.334139	-4.140213	29809.328271
HLA B*4801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.421486	0.281226	-4.140261	26392.858394
HLA B*4402	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.421618	0.281226	-4.140392	26400.855422
HLA A*2602	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.623979	0.483430	-4.140549	42070.642253
HLA B*4601	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.370023	0.229292	-4.140732	23443.546311
HLA A*2301	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.537913	0.397004	-4.140909	34507.445237
HLA A*2603	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.624160	0.483198	-4.140962	42088.170912
HLA A*0206	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.323250	0.182285	-4.140965	21049.886609
HLA A*2902	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.422288	0.281226	-4.141062	26441.592143
HLA B*1502	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.564081	0.422812	-4.141269	36650.623849
HLA B*5801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.350614	0.209282	-4.141332	22418.895496
HLA A*1101	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.475609	0.334139	-4.141470	29895.730108
HLA A*2403	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.358415	0.216823	-4.141591	22825.195330
HLA A*0206	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.130498	-0.011592	-4.142090	13505.106432
HLA A*0212	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.416935	0.274750	-4.142186	26117.732843
HLA A*2501	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.460624	0.318175	-4.142449	28881.792853
HLA A*3301	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.619231	0.476646	-4.142584	41613.173085
HLA A*6802	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.411560	0.268910	-4.142649	25796.444608
HLA A*0206	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.411720	0.268910	-4.142809	25805.936156
HLA A*8001	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.453026	0.310085	-4.142941	28380.883718
HLA B*0803	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.508930	0.365931	-4.142999	32279.705248
HLA B*5101	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.480132	0.337099	-4.143033	30208.692106
HLA A*2603	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.632632	0.489523	-4.143110	42917.290449
HLA B*0801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.412349	0.268910	-4.143439	25843.378036
HLA A*0101	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.349254	0.205784	-4.143470	22348.782077
HLA B*4403	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.477667	0.334139	-4.143528	30037.744094
HLA B*5801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.315309	0.171766	-4.143542	20668.478214
HLA A*1101	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.456050	0.312492	-4.143558	28579.175903
HLA A*3101	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.385455	0.241837	-4.143617	24291.521944
HLA B*4403	1:94-102	9	TGPAAAVRT	0.939479	-0.418162	-4.665229	0.521317	-4.143912	46262.494899
HLA B*1509	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.481161	0.337099	-4.144062	30280.357425
HLA B*0803	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.462379	0.318175	-4.144204	28998.745740
HLA A*2902	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.454436	0.310085	-4.144351	28473.155853
HLA B*5701	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.413327	0.268910	-4.144416	25901.604412
HLA A*2402	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.601361	0.456941	-4.144420	39935.640109
HLA A*3301	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.462706	0.318175	-4.144531	29020.560261
HLA B*5101	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.485040	0.340384	-4.144656	30552.024733
HLA A*0201	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.361652	0.216823	-4.144829	22995.989045
HLA A*0202	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.494633	0.349724	-4.144908	31234.383924
HLA B*4002	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.624931	0.480013	-4.144917	42162.920299
HLA B*1517	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.348042	0.203022	-4.145019	22286.482385
HLA A*3301	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.602004	0.456941	-4.145064	39994.880989
HLA A*2501	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.455162	0.310085	-4.145077	28520.792973
HLA B*0801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.387012	0.241837	-4.145175	24378.806159
HLA A*0206	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.499163	0.353947	-4.145215	31561.871789
HLA B*5301	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.602350	0.456941	-4.145409	40026.699716
HLA B*3801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.533181	0.387714	-4.145467	34133.509600
HLA A*8001	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.426806	0.281226	-4.145580	26718.105580
HLA A*2402	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.581275	0.435662	-4.145613	38130.710935

HLA B*1801	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.486149	0.340384	-4.145765	30630.138028
HLA B*5401	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.039268	-0.106651	-4.145918	10946.304084
HLA A*2902	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.435649	0.289672	-4.145977	27267.738676
HLA A*0201	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.396145	0.250113	-4.146032	24896.877497
HLA A*0212	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.400515	0.254408	-4.146107	25148.664348
HLA B*1502	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.534008	0.387714	-4.146294	34198.571322
HLA B*0802	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.427534	0.281226	-4.146308	26762.951190
HLA B*0802	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.496033	0.349724	-4.146309	31335.255290
HLA A*3001	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.307614	0.161134	-4.146480	20305.511692
HLA A*3002	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.481234	0.334728	-4.146506	30285.436066
HLA A*2301	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.496421	0.349724	-4.146696	31363.238620
HLA B*1501	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.318494	0.171766	-4.146728	20820.655727
HLA B*5101	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.516666	0.369909	-4.146758	32859.913401
HLA B*1502	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.606189	0.459317	-4.146872	40382.094578
HLA A*3301	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.583711	0.436810	-4.146902	38345.227485
HLA B*5101	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.481798	0.334728	-4.147070	30324.783408
HLA A*3201	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.329546	0.182285	-4.147261	21357.301594
HLA A*2301	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.535028	0.387714	-4.147314	34278.960205
HLA A*0101	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.037933	-0.109508	-4.147441	10912.719720
HLA A*3002	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.513528	0.365931	-4.147597	32623.270910
HLA A*6901	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.377152	0.229292	-4.147860	23831.514658
HLA B*0801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.251132	0.103191	-4.147941	17829.218961
HLA A*3001	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.248421	0.100401	-4.148020	17718.257659
HLA A*3301	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.512242	0.364208	-4.148034	32526.874521
HLA A*2603	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.622135	0.473842	-4.148293	41892.357043
HLA B*1517	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.514239	0.365931	-4.148309	32676.790712
HLA A*0201	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.136912	-0.011592	-4.148504	13706.043480
HLA A*0219	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.331539	0.182878	-4.148661	21455.505138
HLA A*6901	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.363668	0.214699	-4.148968	23102.977291
HLA B*4601	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.403520	0.254408	-4.149112	25323.277598
HLA B*1503	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.417344	0.268222	-4.149122	26142.329581
HLA B*5101	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.461827	0.312492	-4.149335	28961.902365
HLA A*2501	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.424137	0.274750	-4.149387	26554.409404
HLA B*3801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.547508	0.398058	-4.149450	35278.336970
HLA B*5701	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.403962	0.254408	-4.149554	25349.045971
HLA A*2403	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.418528	0.268910	-4.149618	26213.706105
HLA A*0301	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.352658	0.203022	-4.149636	22524.661052
HLA A*0301	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.368261	0.218302	-4.149959	23348.618782
HLA A*8001	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.430346	0.280375	-4.149971	26936.820706
HLA A*2902	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.474199	0.324195	-4.150005	29798.847879
HLA A*2403	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.367143	0.217020	-4.150123	23288.570933
HLA A*0219	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.138585	-0.011592	-4.150177	13758.938788
HLA A*0301	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.367387	0.217020	-4.150367	23301.677432
HLA A*0250	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.561760	0.411293	-4.150467	36455.249946
HLA A*0301	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.365298	0.214699	-4.150599	23189.879600
HLA A*3001	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.270248	0.119542	-4.150706	18631.496041
HLA A*6901	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.392642	0.241837	-4.150804	24696.863436
HLA A*0202	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.583331	0.432524	-4.150807	38311.636371
HLA A*3101	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.380232	0.229292	-4.150940	24001.137252
HLA A*3201	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.440839	0.289672	-4.151167	27595.555166
HLA B*5401	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.538921	0.387714	-4.151207	34587.624586
HLA A*2602	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.583794	0.432524	-4.151270	38352.488692
HLA B*3501	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.426021	0.274750	-4.151271	26669.872145
HLA A*0250	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.583998	0.432524	-4.151474	38370.543937

HLA B*5801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.360158	0.208647	-4.151511	22917.002949
HLA B*2705	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.489863	0.338222	-4.151642	30893.242229
HLA A*2402	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.501449	0.349724	-4.151724	31728.445891
HLA B*0702	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.401981	0.250113	-4.151868	25233.703932
HLA A*0216	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.420796	0.268910	-4.151885	26350.913723
HLA B*5801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.334306	0.182285	-4.152022	21592.674457
HLA B*0702	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.293205	0.141159	-4.152046	19642.852094
HLA A*2602	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.575143	0.422812	-4.152330	37596.095732
HLA B*1503	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.318480	0.166065	-4.152415	20819.979913
HLA A*8001	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.394453	0.241837	-4.152616	24800.089789
HLA B*1509	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.522568	0.369909	-4.152660	33309.515894
HLA A*0206	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.134036	-0.018628	-4.152665	13615.585935
HLA A*3002	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.355736	0.203022	-4.152714	22684.859295
HLA B*0803	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.442470	0.289672	-4.152798	27699.356396
HLA A*2601	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.403217	0.250113	-4.153104	25305.611263
HLA A*6901	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.371717	0.218302	-4.153415	23535.167137
HLA A*1101	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.491818	0.338222	-4.153596	31032.606977
HLA A*6801	1:136-144	9	APQRNPAPA	0.774750	-0.257386	-4.670964	0.517364	-4.153600	46877.467685
HLA B*4501	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.643440	0.489523	-4.153917	43998.708251
HLA A*3201	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.613251	0.459317	-4.153934	41044.162041
HLA B*5301	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.552031	0.398058	-4.153973	35647.646526
HLA A*3201	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.565500	0.411293	-4.154207	36770.578313
HLA A*0211	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.488536	0.334139	-4.154397	30798.958501
HLA A*6901	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.357447	0.203022	-4.154424	22774.377492
HLA A*0219	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.422711	0.268222	-4.154488	26467.352978
HLA A*3002	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.135925	-0.018628	-4.154554	13674.936599
HLA A*2603	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.551575	0.397004	-4.154571	35610.253288
HLA A*0216	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.478863	0.324195	-4.154669	30120.571020
HLA B*3901	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.464766	0.310085	-4.154682	29158.574663
HLA B*4002	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.644241	0.489523	-4.154719	44079.950758
HLA A*0101	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.363508	0.208647	-4.154861	23094.479905
HLA B*3801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.526743	0.371790	-4.154954	33631.276821
HLA B*0802	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.493207	0.338222	-4.154985	31131.984591
HLA A*6802	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.423488	0.268222	-4.155266	26514.789820
HLA B*4601	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.405590	0.250113	-4.155477	25444.259261
HLA A*3002	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.495906	0.340384	-4.155522	31326.102533
HLA B*4801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.430579	0.274750	-4.155829	26951.251366
HLA B*5101	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.505572	0.349724	-4.155848	32031.121616
HLA B*5801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.361640	0.205784	-4.155857	22995.367025
HLA A*0101	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.370625	0.214699	-4.155925	23476.036513
HLA A*0206	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.466056	0.310085	-4.155972	29245.305211
HLA B*3501	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.406088	0.250113	-4.155975	25473.457934
HLA B*7301	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.588563	0.432524	-4.156039	38775.999857
HLA A*3002	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.527967	0.371790	-4.156178	33726.202044
HLA A*3201	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.425119	0.268910	-4.156208	26614.525729
HLA A*0219	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.425156	0.268910	-4.156246	26616.829535
HLA A*3001	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.259515	0.103191	-4.156324	18176.710115
HLA A*6802	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.255469	0.099112	-4.156357	18008.165276
HLA B*4501	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.365750	0.209282	-4.156467	23213.979412
HLA A*3001	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.299240	0.142630	-4.156610	19917.754427
HLA A*1101	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.425795	0.268910	-4.156885	26656.024760
HLA A*6802	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.407469	0.250113	-4.157356	25554.618399
HLA B*2705	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.481819	0.324195	-4.157624	30326.259928

HLA A*2603	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.637684	0.480013	-4.157670	43419.387031
HLA A*6801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.432557	0.274750	-4.157807	27074.297763
HLA A*2402	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.545525	0.387714	-4.157812	35117.625153
HLA B*5101	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.511784	0.353947	-4.157837	32492.579090
HLA A*3001	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.299062	0.141159	-4.157903	19909.566894
HLA A*2602	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.614901	0.456941	-4.157960	41200.333548
HLA B*1517	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.496341	0.338222	-4.158119	31357.470315
HLA B*4001	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.387433	0.229292	-4.158141	24402.425301
HLA A*2601	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.387522	0.229292	-4.158231	24407.442365
HLA A*2402	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.581193	0.422812	-4.158380	38123.491717
HLA B*5101	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.496792	0.338222	-4.158570	31390.058201
HLA B*0801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.408729	0.250113	-4.158615	25628.826679
HLA B*0801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.341508	0.182878	-4.158630	21953.694109
HLA A*0206	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.524810	0.365931	-4.158879	33481.871831
HLA B*5701	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.375754	0.216823	-4.158930	23754.927105
HLA A*0301	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.341226	0.182285	-4.158941	21939.446688
HLA A*0301	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.368491	0.209282	-4.159209	23361.000781
HLA B*0801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.325291	0.166065	-4.159226	21149.079182
HLA A*0211	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.531214	0.371790	-4.159425	33979.299834
HLA B*0803	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.513673	0.353947	-4.159726	32634.215019
HLA A*0301	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.368374	0.208647	-4.159727	23354.682614
HLA A*2501	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.509728	0.349724	-4.160004	32339.133960
HLA B*1503	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.441358	0.281226	-4.160133	27628.567742
HLA B*1501	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.368856	0.208647	-4.160209	23380.597962
HLA A*6801	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.619717	0.459317	-4.160400	41659.799576
HLA B*0702	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.429334	0.268910	-4.160423	26874.086305
HLA A*3002	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.558602	0.398058	-4.160544	36191.149085
HLA B*4403	1:68-76	9	EGRPTNPPA	0.968641	-0.477982	-4.651257	0.490659	-4.160598	44797.797566
HLA B*5701	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.410815	0.250113	-4.160702	25752.243298
HLA B*0803	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.525078	0.364208	-4.160869	33502.527386
HLA A*3201	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.501254	0.340384	-4.160870	31714.202357
HLA A*6901	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.343570	0.182632	-4.160939	22058.219625
HLA B*5401	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.415352	0.254408	-4.160944	26022.674071
HLA B*1801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.499174	0.338222	-4.160953	31562.725531
HLA A*0216	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.377939	0.216823	-4.161115	23874.743979
HLA B*0801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.441492	0.280375	-4.161117	27637.088703
HLA B*4001	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.411236	0.250113	-4.161122	25777.193080
HLA A*0206	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.525399	0.364208	-4.161191	33527.367149
HLA A*0301	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.344170	0.182878	-4.161292	22088.670418
HLA B*5301	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.525503	0.364208	-4.161294	33535.348790
HLA A*0206	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.442012	0.280375	-4.161636	27670.150966
HLA B*0803	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.496679	0.334728	-4.161951	31381.908056
HLA A*2403	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.436803	0.274750	-4.162053	27340.265041
HLA B*3801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.559373	0.397004	-4.162369	36255.425249
HLA B*4501	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.621771	0.459317	-4.162454	41857.243651
HLA B*3901	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.431476	0.268910	-4.162566	27007.005811
HLA A*0301	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.368416	0.205784	-4.162633	23356.956957
HLA B*1501	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.379677	0.217020	-4.162657	23970.513741
HLA A*6802	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.443043	0.280375	-4.162668	27735.944048
HLA A*2402	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.560834	0.398058	-4.162776	36377.628469
HLA B*4402	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.431058	0.268222	-4.162836	26981.011655
HLA A*2402	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.560888	0.397920	-4.162968	36382.155126
HLA A*2902	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.431237	0.268222	-4.163014	26992.107221

HLA B*5301	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.595743	0.432524	-4.163219	39422.397375
HLA B*0801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.176773	0.013159	-4.163614	15023.581170
HLA B*0802	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.488188	0.324195	-4.163994	30774.308766
HLA A*2403	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.378820	0.214699	-4.164120	23923.228037
HLA A*3301	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.599848	0.435662	-4.164186	39796.747682
HLA A*3101	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.178249	0.013159	-4.165090	15074.709243
HLA A*6901	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.317597	0.152039	-4.165558	20777.672654
HLA A*3101	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.446029	0.280375	-4.165654	27927.312710
HLA B*1801	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.478320	0.312492	-4.165829	30082.953323
HLA B*5801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.350541	0.184583	-4.165959	22415.136015
HLA A*1101	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.490185	0.324195	-4.165991	30916.147391
HLA B*4402	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.440978	0.274750	-4.166228	27604.364617
HLA B*3901	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.446701	0.280375	-4.166326	27970.556084
HLA A*2402	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.520444	0.353947	-4.166497	33147.012071
HLA B*1502	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.592919	0.426351	-4.166567	39166.877557
HLA A*6901	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.375371	0.208647	-4.166724	23733.988960
HLA B*5401	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.351493	0.184583	-4.166910	22464.301534
HLA A*2301	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.536898	0.369909	-4.166989	34426.893014
HLA A*0202	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.531259	0.364208	-4.167051	33982.792674
HLA B*0801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.384160	0.217020	-4.167140	24219.220401
HLA B*4501	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.647204	0.480013	-4.167190	44381.686492
HLA A*0101	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.370282	0.203022	-4.167260	23457.501432
HLA A*0212	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.409170	0.241837	-4.167333	25654.905972
HLA A*6901	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.349618	0.182285	-4.167333	22367.530124
HLA B*4002	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.626770	0.459317	-4.167453	42341.898838
HLA A*0211	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.457138	0.289672	-4.167466	28650.850140
HLA A*3301	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.626956	0.459317	-4.167639	42359.998839
HLA A*0219	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.449055	0.281226	-4.167829	28122.588015
HLA A*0201	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.397181	0.229292	-4.167889	24956.346410
HLA A*0219	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.422309	0.254408	-4.167901	26442.879589
HLA B*5301	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.590764	0.422812	-4.167952	38973.056990
HLA B*0803	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.508483	0.340384	-4.168099	32246.542666
HLA A*2301	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.539893	0.371790	-4.168104	34665.177100
HLA A*6802	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.422558	0.254408	-4.168150	26458.047561
HLA B*5801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.351133	0.182878	-4.168256	22445.715232
HLA A*6802	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.350649	0.182285	-4.168365	22420.714826
HLA B*1517	1:120-128	9	EAYASELPD	0.526970	-0.706526	-3.988993	-0.179556	-4.168549	9749.744357
HLA B*4002	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.642507	0.473842	-4.168665	43904.312486
HLA A*2602	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.604406	0.435662	-4.168744	40216.621380
HLA A*0212	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.418886	0.250113	-4.168772	26235.270583
HLA A*3002	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.505967	0.337099	-4.168868	32060.246699
HLA A*0206	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.059492	-0.109508	-4.169000	11468.110672
HLA B*1502	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.481586	0.312492	-4.169094	30310.022168
HLA B*1502	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.601692	0.432524	-4.169168	39966.114412
HLA A*6801	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.658867	0.489523	-4.169344	45589.690602
HLA A*1101	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.444096	0.274750	-4.169346	27803.247249
HLA B*1801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.519077	0.349724	-4.169353	33042.810992
HLA B*1801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.523607	0.353947	-4.169659	33389.259945
HLA A*2301	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.510135	0.340384	-4.169751	32369.414674
HLA B*0802	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.459515	0.289672	-4.169843	28808.138206
HLA B*2705	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.438093	0.268222	-4.169870	27421.587129
HLA A*0101	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.388526	0.218302	-4.170223	24463.889281
HLA B*5701	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.399552	0.229292	-4.170260	25092.945056
HLA A*2501	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.482792	0.312492	-4.170300	30394.257592

HLA B*0802	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.445221	0.274750	-4.170471	27875.388260
HLA A*0101	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.352893	0.182285	-4.170608	22536.849941
HLA B*4002	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.647281	0.476646	-4.170635	44389.610500
HLA A*2402	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.540617	0.369909	-4.170708	34722.985956
HLA B*3801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.568865	0.397920	-4.170945	37056.544814
HLA A*0216	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.425365	0.254408	-4.170958	26629.648096
HLA A*0206	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.509233	0.338222	-4.171011	32302.240333
HLA B*1801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.439939	0.268910	-4.171029	27538.436714
HLA A*2301	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.535298	0.364208	-4.171089	34300.293058
HLA B*1502	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.520820	0.349724	-4.171096	33175.715957
HLA A*2602	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.559049	0.387714	-4.171335	36228.368330
HLA B*1502	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.535742	0.364208	-4.171534	34335.381982
HLA A*3201	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.628692	0.456941	-4.171751	42529.689198
HLA A*2403	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.421961	0.250113	-4.171848	26421.716211
HLA B*1503	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.413707	0.241837	-4.171870	25924.314581
HLA B*1517	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.269714	0.097839	-4.171875	18608.629772
HLA B*5101	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.506155	0.334139	-4.172016	32074.125092
HLA B*5301	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.490216	0.318175	-4.172041	30918.321755
HLA A*0301	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.356648	0.184583	-4.172065	22732.525663
HLA A*2902	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.422241	0.250113	-4.172127	26438.731376
HLA B*4501	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.646013	0.473842	-4.172171	44260.122580
HLA A*0202	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.583587	0.411293	-4.172294	38334.234559
HLA B*4403	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.654156	0.481784	-4.172372	45097.859308
HLA A*2602	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.490719	0.318175	-4.172544	30954.137128
HLA A*6901	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.357155	0.184583	-4.172573	22759.104965
HLA A*0201	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.391016	0.218302	-4.172714	24604.580035
HLA A*0301	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.325005	0.152039	-4.172966	21135.125258
HLA A*6801	1:221-229	9	AFLYLVLGG	0.924667	-0.441469	-4.656367	0.483198	-4.173169	45328.024592
HLA A*2301	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.527129	0.353947	-4.173181	33661.128464
HLA B*7301	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.596735	0.422812	-4.173922	39512.500464
HLA B*7301	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.609631	0.435662	-4.173969	40703.413992
HLA B*5401	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.514491	0.340384	-4.174107	32695.711414
HLA B*5301	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.571196	0.397004	-4.174192	37255.947418
HLA A*6801	1:80-88	9	ARLNRFISG	1.008296	-0.505462	-4.677146	0.502834	-4.174312	47549.465360
HLA B*4002	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.597134	0.422812	-4.174322	39548.856082
HLA A*0101	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.391345	0.217020	-4.174325	24623.222221
HLA A*0216	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.454863	0.280375	-4.174488	28501.204323
HLA A*6802	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.403792	0.229292	-4.174501	25339.174136
HLA A*6802	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.416437	0.241837	-4.174600	26087.795678
HLA B*1501	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.383883	0.209282	-4.174601	24203.764586
HLA B*1501	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.389447	0.214699	-4.174747	24515.824327
HLA B*5401	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.540683	0.365931	-4.174752	34728.246085
HLA B*4402	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.391683	0.216823	-4.174860	24642.411776
HLA A*2403	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.380711	0.205784	-4.174927	24027.639946
HLA A*0211	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.443863	0.268910	-4.174953	27788.360400
HLA A*2402	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.515386	0.340384	-4.175002	32763.172260
HLA A*2603	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.597853	0.422812	-4.175040	39614.380510
HLA B*3901	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.487601	0.312492	-4.175109	30732.715499
HLA B*2705	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.378277	0.203022	-4.175255	23893.350225
HLA A*6802	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.392343	0.217020	-4.175323	24679.901138
HLA A*6901	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.273422	0.097839	-4.175583	18768.168022
HLA A*0203	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.425748	0.250113	-4.175635	26653.140793
HLA A*0211	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.529652	0.353947	-4.175705	33857.276337
HLA A*0203	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.066291	-0.109508	-4.175799	11649.070806

HLA A*2603	1:263-271	9	GAFLIGLVN	1.072286	-0.588856	-4.659280	0.483430	-4.175850	45633.119064
HLA A*6801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.457128	0.281226	-4.175902	28650.230155
HLA B*7301	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.457222	0.281226	-4.175996	28656.430609
HLA B*4601	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.347851	0.171766	-4.176085	22276.718565
HLA A*2602	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.546284	0.369909	-4.176375	35179.043132
HLA A*2501	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.500622	0.324195	-4.176427	31668.083507
HLA A*0250	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.548302	0.371790	-4.176513	35342.903923
HLA A*2602	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.588020	0.411293	-4.176727	38727.572361
HLA B*4002	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.500923	0.324195	-4.176728	31690.020167
HLA B*1801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.431199	0.254408	-4.176792	26989.770933
HLA B*0801	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.391528	0.214699	-4.176829	24633.614708
HLA A*6901	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.318090	0.141159	-4.176931	20801.291098
HLA A*0216	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.487169	0.310085	-4.177084	30702.138773
HLA A*0219	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.418930	0.241837	-4.177093	26237.967390
HLA A*2301	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.543152	0.365931	-4.177221	34926.266137
HLA A*0203	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.406516	0.229292	-4.177224	25498.551447
HLA A*2602	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.636636	0.459317	-4.177319	43314.750561
HLA A*0201	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.383155	0.205784	-4.177371	24163.207302
HLA A*0211	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.541616	0.364208	-4.177407	34802.912995
HLA B*5801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.343538	0.166065	-4.177472	22056.549033
HLA B*1509	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.338655	0.161134	-4.177521	21809.983343
HLA A*2601	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.392259	0.214699	-4.177559	24675.095047
HLA A*2602	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.614374	0.436810	-4.177565	41150.436598
HLA B*4501	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.654222	0.476646	-4.177575	45104.691109
HLA A*0219	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.458089	0.280375	-4.177714	28713.693118
HLA A*0101	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.387111	0.209282	-4.177829	24384.346027
HLA B*5701	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.349740	0.171766	-4.177974	22373.823314
HLA A*6802	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.330221	0.152039	-4.178182	21390.487513
HLA A*0212	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.384019	0.205784	-4.178236	24211.360279
HLA A*0203	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.432677	0.254408	-4.178269	27081.768710
HLA B*1503	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.339440	0.161134	-4.178306	21849.427492
HLA B*4002	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.387680	0.209282	-4.178397	24416.290753
HLA A*3101	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.361058	0.182285	-4.178773	22964.535920
HLA B*1517	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.468460	0.289672	-4.178788	29407.606689
HLA A*2601	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.395830	0.217020	-4.178810	24878.835665
HLA B*4601	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.397132	0.218302	-4.178830	24953.511339
HLA A*0212	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.408139	0.229292	-4.178847	25594.049369
HLA A*0201	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.395992	0.217020	-4.178972	24888.124229
HLA A*3201	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.611665	0.432524	-4.179142	40894.555417
HLA A*2601	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.397545	0.218302	-4.179243	24977.281902
HLA B*5701	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.421484	0.241837	-4.179647	26392.715612
HLA B*1509	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.529405	0.349724	-4.179681	33838.049566
HLA A*1101	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.331755	0.152039	-4.179716	21466.186412
HLA B*7301	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.533733	0.353947	-4.179786	34176.931945
HLA A*0219	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.454605	0.274750	-4.179855	28484.248649
HLA A*3101	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.394592	0.214699	-4.179892	24808.006831
HLA A*0201	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.362225	0.182285	-4.179940	23026.364092
HLA B*1503	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.518476	0.338222	-4.180254	32997.080632
HLA A*3101	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.397418	0.217020	-4.180398	24969.986254
HLA B*5101	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.397545	0.217020	-4.180525	24977.281902
HLA B*5801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.363388	0.182632	-4.180757	23088.108916
HLA A*6901	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.390064	0.209282	-4.180782	24550.730289
HLA A*1101	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.430934	0.250113	-4.180820	26973.276657
HLA B*0803	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.515125	0.334139	-4.180986	32743.503957
HLA B*3501	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.461479	0.280375	-4.181104	28938.722905

HLA B*7301	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.384148	0.203022	-4.181126	24218.565293
HLA A*0201	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.395922	0.214699	-4.181222	24884.085297
HLA B*4402	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.435738	0.254408	-4.181331	27273.344839
HLA A*0250	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.520898	0.338222	-4.182676	33181.639225
HLA A*2601	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.391359	0.208647	-4.182712	24624.021487
HLA A*6801	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.656710	0.473842	-4.182868	45363.840794
HLA A*0202	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.549026	0.365931	-4.183095	35401.842980
HLA B*7301	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.580807	0.397004	-4.183804	38089.682723
HLA B*4501	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.640762	0.456941	-4.183821	43728.191212
HLA B*1517	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.508192	0.324195	-4.183997	32224.918092
HLA B*4601	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.366332	0.182285	-4.184047	23245.145408
HLA B*4403	1:42-50	9	DPPPWQRAA	1.009754	-0.520231	-4.673657	0.489523	-4.184134	47168.998238
HLA B*1501	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.390560	0.205784	-4.184777	24578.770619
HLA B*1801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.459576	0.274750	-4.184826	28812.190561
HLA A*2601	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.390708	0.205784	-4.184925	24587.149058
HLA A*0301	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.367563	0.182632	-4.184932	23311.133813
HLA B*5401	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.549186	0.364208	-4.184977	35414.868739
HLA A*6801	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.641974	0.456941	-4.185033	43850.429114
HLA B*1502	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.495192	0.310085	-4.185108	31274.625769
HLA A*0201	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.388131	0.203022	-4.185109	24441.665098
HLA B*3501	1:3-11	9	APNEPGALS	0.822079	-1.082447	-3.924838	-0.260368	-4.185206	8410.817138
HLA A*2601	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.388340	0.203022	-4.185318	24453.436108
HLA B*1801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.519935	0.334139	-4.185795	33108.122102
HLA B*2705	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.460603	0.274750	-4.185853	28880.386662
HLA B*4002	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.642907	0.456941	-4.185966	43944.709028
HLA A*2403	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.389113	0.203022	-4.186091	24496.998398
HLA B*5701	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.368473	0.182285	-4.186188	23359.989759
HLA A*0301	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.352301	0.166065	-4.186236	22506.146566
HLA B*2705	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.436354	0.250113	-4.186241	27312.029241
HLA A*0250	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.584585	0.398058	-4.186527	38422.474143
HLA B*4801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.441067	0.254408	-4.186659	27610.039989
HLA A*0211	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.521455	0.334728	-4.186727	33224.210141
HLA A*6901	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.286046	0.099112	-4.186933	19321.714726
HLA B*2705	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.371612	0.184583	-4.187029	23529.438316
HLA A*2601	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.396389	0.209282	-4.187107	24910.889131
HLA A*0201	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.396488	0.209282	-4.187205	24916.549910
HLA A*1101	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.390281	0.203022	-4.187258	24562.952469
HLA B*3801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.524366	0.337099	-4.187267	33447.655149
HLA A*2402	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.584313	0.397004	-4.187309	38398.369794
HLA A*3201	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.521631	0.334139	-4.187492	33237.693323
HLA B*4001	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.390553	0.203022	-4.187531	24578.371717
HLA A*0212	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.369901	0.182285	-4.187616	23436.952235
HLA A*6901	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.280369	0.092742	-4.187628	19070.817492
HLA B*0803	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.524789	0.337099	-4.187690	33480.241672
HLA B*1501	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.406001	0.218302	-4.187699	25468.359526
HLA A*0101	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.370641	0.182878	-4.187764	23476.925549
HLA B*5701	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.402590	0.214699	-4.187890	25269.085202
HLA B*4801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.438057	0.250113	-4.187944	27419.362003
HLA A*3101	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.396622	0.208647	-4.187975	24924.234454
HLA A*0201	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.396753	0.208647	-4.188106	24931.786489
HLA B*0803	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.498202	0.310085	-4.188117	31492.113785
HLA B*3801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.554087	0.365931	-4.188156	35816.790133
HLA B*3901	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.403217	0.214699	-4.188517	25305.611263
HLA B*5301	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.599815	0.411293	-4.188522	39793.733652
HLA B*0803	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.527096	0.338222	-4.188874	33658.579119

HLA B*4403	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.615295	0.426351	-4.188944	41237.795961
HLA B*5801	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.341000	0.152039	-4.188961	21928.055408
HLA B*4801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.430849	0.241837	-4.189012	26968.023960
HLA B*5801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.350189	0.161134	-4.189055	22396.953883
HLA B*0801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.394857	0.205784	-4.189074	24823.177036
HLA A*0301	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.202336	0.013159	-4.189177	15934.405487
HLA B*4601	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.392395	0.203022	-4.189373	24682.838654
HLA A*0212	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.406445	0.217020	-4.189425	25494.413453
HLA A*6901	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.042994	-0.146721	-4.189715	11040.628371
HLA B*4402	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.406840	0.217020	-4.189819	25517.594873
HLA A*0212	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.399180	0.209282	-4.189898	25071.505712
HLA A*0211	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.080501	-0.109508	-4.190009	12036.520790
HLA B*2705	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.458930	0.268910	-4.190020	28769.357972
HLA A*0301	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.361988	0.171766	-4.190222	23013.785951
HLA A*0203	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.393295	0.203022	-4.190273	24734.034208
HLA B*3501	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.362059	0.171766	-4.190292	23017.521315
HLA A*0216	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.465194	0.274750	-4.190444	29187.298329
HLA B*1801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.527615	0.337099	-4.190516	33698.844894
HLA B*4002	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.626204	0.435662	-4.190542	42286.730150
HLA B*0801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.399425	0.208647	-4.190778	25085.615623
HLA B*0702	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.407718	0.216823	-4.190895	25569.276852
HLA B*4403	1:233-241	9	WAKLNSNVG	1.055248	-0.575235	-4.671199	0.480013	-4.191186	46902.834736
HLA A*0202	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.561163	0.369909	-4.191255	36405.190757
HLA A*2501	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.179706	-0.011592	-4.191297	15125.356688
HLA B*5401	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-3.882491	-0.308836	-4.191327	7629.412091
HLA A*6901	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.342739	0.151290	-4.191449	22016.016337
HLA B*5401	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.561396	0.369909	-4.191487	36424.693836
HLA B*4601	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.400365	0.208647	-4.191717	25139.958560
HLA B*4402	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.363729	0.171766	-4.191963	23106.227118
HLA B*4002	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.590135	0.398058	-4.192077	38916.592835
HLA B*5301	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.527004	0.334728	-4.192276	33651.478390
HLA B*1501	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.376879	0.184583	-4.192296	23816.563951
HLA B*4001	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.409290	0.216823	-4.192467	25661.985249
HLA A*0211	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.529589	0.337099	-4.192490	33852.331267
HLA B*0802	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.460883	0.268222	-4.192660	28898.985171
HLA B*0702	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.395875	0.203022	-4.192852	24881.393040
HLA A*8001	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.461096	0.268222	-4.192874	28913.215641
HLA B*3901	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.517108	0.324195	-4.192914	32893.350878
HLA A*0216	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.474228	0.281226	-4.193002	29800.782443
HLA A*0202	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.462090	0.268910	-4.193180	28979.455918
HLA A*6801	1:193-201	9	IRRIDPWST	0.689528	-0.207744	-4.674994	0.481784	-4.193209	47314.418823
HLA B*2705	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.447737	0.254408	-4.193330	28037.366814
HLA B*4402	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.408076	0.214699	-4.193376	25590.311196
HLA A*1101	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.461665	0.268222	-4.193443	28951.093415
HLA B*1509	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.503629	0.310085	-4.193545	31888.135170
HLA A*3301	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.626077	0.432524	-4.193553	42274.378562
HLA B*0803	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.506124	0.312492	-4.193632	32071.869445
HLA A*2603	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.653002	0.459317	-4.193685	44978.226826
HLA B*3901	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.186435	-0.007282	-4.193716	15361.532714
HLA A*0206	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.517921	0.324195	-4.193726	32954.979025
HLA A*6802	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.175124	-0.018628	-4.193752	14966.633687
HLA A*0216	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.462048	0.268222	-4.193825	28976.634094
HLA A*0101	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.360195	0.166065	-4.194130	22918.986690
HLA A*0250	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.564117	0.369909	-4.194208	36653.598107
HLA B*5701	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.411290	0.217020	-4.194269	25780.400670

HLA B*5101	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.518497	0.324195	-4.194302	32998.687266
HLA A*0202	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.532767	0.338222	-4.194545	34101.025171
HLA B*5301	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.592632	0.397920	-4.194712	39141.035693
HLA B*4002	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.631568	0.436810	-4.194758	42812.242685
HLA B*4601	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.411792	0.217020	-4.194772	25810.264343
HLA B*4601	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.409528	0.214699	-4.194828	25676.010758
HLA A*2501	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.463105	0.268222	-4.194883	29047.262200
HLA A*1101	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.437139	0.241837	-4.195301	27361.424040
HLA B*7301	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.532483	0.337099	-4.195384	34078.710061
HLA A*2603	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.631185	0.435662	-4.195523	42774.506979
HLA A*0206	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.437540	0.241837	-4.195703	27386.747560
HLA A*3201	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.593964	0.398058	-4.195906	39261.281512
HLA A*3002	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.464186	0.268222	-4.195964	29119.637753
HLA B*3801	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.560233	0.364208	-4.196025	36327.282812
HLA A*1101	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.476495	0.280375	-4.196120	29956.765514
HLA B*4001	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.378425	0.182285	-4.196140	23901.495017
HLA B*4601	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.380812	0.184583	-4.196229	24033.230032
HLA B*5101	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.378984	0.182632	-4.196353	23932.289293
HLA B*0801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.316074	0.119542	-4.196532	20704.961798
HLA A*6901	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.368381	0.171766	-4.196615	23355.061656
HLA B*0702	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.451048	0.254408	-4.196640	28251.899192
HLA B*1502	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.178028	-0.018628	-4.196656	15067.045256
HLA B*5701	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.415162	0.218302	-4.196859	26011.273407
HLA A*2602	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.594171	0.397004	-4.197168	39279.977090
HLA B*1801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.521518	0.324195	-4.197324	33229.063457
HLA B*4403	1:293-301	9	IGGIEVTLA	0.846461	-0.387144	-4.656658	0.459317	-4.197341	45358.442022
HLA B*4403	1:130-138	9	SGPTPRAPQ	0.602245	-0.125599	-4.674030	0.476646	-4.197384	47209.589163
HLA A*0203	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.406067	0.208647	-4.197420	25472.217687
HLA B*4601	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.403294	0.205784	-4.197511	25310.129385
HLA B*4403	1:66-74	9	HPEGRPTNP	0.640941	-0.167099	-4.671389	0.473842	-4.197547	46923.392110
HLA B*1502	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.564142	0.365931	-4.198212	36655.779383
HLA A*0101	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.381404	0.182632	-4.198773	24066.016687
HLA B*3801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.508908	0.310085	-4.198824	32278.133620
HLA A*1101	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.480172	0.281226	-4.198946	30211.470470
HLA B*1502	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.569011	0.369909	-4.199102	37068.976150
HLA B*4601	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.408454	0.209282	-4.199171	25612.609866
HLA B*3801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.553175	0.353947	-4.199228	35741.688214
HLA B*4402	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.441083	0.241837	-4.199246	27611.085579
HLA A*0219	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.449375	0.250113	-4.199262	28143.286680
HLA A*0202	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.383913	0.184583	-4.199331	24205.466861
HLA B*4001	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.383930	0.184583	-4.199347	24206.383521
HLA A*8001	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.417697	0.218302	-4.199395	26163.552256
HLA A*0206	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.480630	0.281226	-4.199404	30243.358225
HLA B*5401	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.298545	0.099112	-4.199432	19885.885108
HLA A*2603	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.625894	0.426351	-4.199542	42256.543749
HLA B*5401	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.553589	0.353947	-4.199641	35775.735529
HLA A*2501	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.468587	0.268910	-4.199676	29416.198906
HLA A*0219	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.416910	0.216823	-4.200086	26116.178655
HLA A*3201	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.518323	0.318175	-4.200148	32985.479486
HLA B*1501	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.160947	-0.039278	-4.200225	14485.961839
HLA B*4001	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.417441	0.217020	-4.200420	26148.128735
HLA A*2301	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.538658	0.338222	-4.200436	34566.674030
HLA B*1509	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.534581	0.334139	-4.200442	34243.743686
HLA A*2301	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.535589	0.334728	-4.200861	34323.310315

HLA B*5701	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.406739	0.205784	-4.200955	25511.659527
HLA A*6802	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.419402	0.218302	-4.201100	26266.513751
HLA A*6802	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.404126	0.203022	-4.201104	25358.647276
HLA B*5101	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.342274	0.141159	-4.201115	21992.446330
HLA B*1801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.216964	0.015810	-4.201154	16480.248584
HLA B*5101	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.511342	0.310085	-4.201258	32459.549015
HLA A*8001	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.451452	0.250113	-4.201338	28278.199845
HLA A*0202	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.407178	0.205784	-4.201394	25537.481438
HLA A*2501	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.443304	0.241837	-4.201466	27752.604420
HLA A*0202	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.555456	0.353947	-4.201509	35929.933380
HLA B*3901	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.469923	0.268222	-4.201701	29506.888151
HLA A*0212	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.416534	0.214699	-4.201834	26093.582735
HLA A*0203	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.419071	0.217020	-4.202051	26246.485442
HLA A*0212	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.420413	0.218302	-4.202111	26327.687415
HLA A*1101	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.456637	0.254408	-4.202229	28617.854597
HLA A*2402	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.574029	0.371790	-4.202240	37499.812037
HLA A*6801	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.600313	0.397920	-4.202393	39839.399127
HLA A*2402	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.566807	0.364208	-4.202598	36881.346982
HLA B*1517	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.471836	0.268910	-4.202925	29637.112673
HLA B*4001	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.417814	0.214699	-4.203115	26170.630310
HLA B*7301	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.590938	0.387714	-4.203225	38988.662268
HLA A*0201	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.387926	0.184583	-4.203344	24430.164082
HLA A*0101	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.375152	0.171766	-4.203386	23722.050926
HLA A*3201	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.540727	0.337099	-4.203629	34731.815911
HLA A*0202	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.540772	0.337099	-4.203673	34735.386105
HLA B*3501	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.386820	0.182878	-4.203942	24367.993853
HLA A*0219	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.420974	0.217020	-4.203954	26361.750170
HLA B*5401	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.542248	0.338222	-4.204026	34853.597158
HLA B*4501	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.641166	0.436810	-4.204356	43768.899271
HLA B*1517	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.410157	0.205784	-4.204374	25713.264129
HLA B*5801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.355802	0.151290	-4.204512	22688.295787
HLA A*2601	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.386965	0.182285	-4.204681	24376.168569
HLA A*0101	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.389421	0.184583	-4.204838	24514.365463
HLA A*2301	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.542351	0.337099	-4.205252	34861.894526
HLA B*4801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.422161	0.216823	-4.205337	26433.868783
HLA B*5401	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.555097	0.349724	-4.205372	35900.206010
HLA B*4801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.423718	0.218302	-4.205416	26528.850870
HLA B*4001	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.414170	0.208647	-4.205523	25951.958099
HLA A*2301	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.539865	0.334139	-4.205726	34662.926756
HLA A*3101	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.411529	0.205784	-4.205746	25794.630445
HLA A*2403	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.372042	0.166065	-4.205976	23552.744223
HLA B*1517	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.487225	0.281226	-4.205999	30706.125316
HLA A*2403	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.424374	0.218302	-4.206072	26568.922666
HLA B*4801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.435496	0.229292	-4.206205	27258.151858
HLA A*2603	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.617692	0.411293	-4.206399	41465.978691
HLA A*3101	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.378207	0.171766	-4.206440	23889.472728
HLA B*4002	1:255-263	9	VSSGTIFGG	0.968346	-0.541995	-4.632888	0.426351	-4.206537	42942.605290
HLA A*2403	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.388955	0.182285	-4.206671	24488.120762
HLA B*4403	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.530949	0.324195	-4.206754	33958.534042
HLA A*3301	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.630114	0.422812	-4.207301	42669.116191
HLA B*2705	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.389985	0.182285	-4.207700	24546.214935
HLA B*5101	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.482453	0.274750	-4.207703	30370.588955
HLA B*4501	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.605012	0.397004	-4.208008	40272.792978
HLA A*0301	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.369161	0.161134	-4.208027	23397.046983

HLA A*6801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.098733	-0.109508	-4.208241	12552.579307
HLA B*3801	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.543326	0.334728	-4.208598	34940.251031
HLA B*1517	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.450519	0.241837	-4.208682	28217.531193
HLA A*0250	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.574689	0.365931	-4.208759	37556.861810
HLA A*0203	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.427144	0.218302	-4.208842	26738.927736
HLA B*0803	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.533066	0.324195	-4.208871	34124.462533
HLA B*0801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.391157	0.182285	-4.208872	24612.567814
HLA A*6901	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.375230	0.166065	-4.209165	23726.286315
HLA A*6801	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.563198	0.353947	-4.209251	36576.147916
HLA B*0802	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.489821	0.280375	-4.209446	30890.234053
HLA A*0250	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.253602	0.044127	-4.209474	17930.880959
HLA A*2403	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.418848	0.209282	-4.209566	26232.999803
HLA A*6802	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.381573	0.171766	-4.209807	24075.392516
HLA B*4001	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.416061	0.205784	-4.210278	26065.224314
HLA B*5101	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.464738	0.254408	-4.210330	29156.681788
HLA B*4403	1:19-27	9	DGLVDRGGA	0.866546	-0.409605	-4.667438	0.456941	-4.210497	46498.352565
HLA A*3201	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.560280	0.349724	-4.210555	36331.213556
HLA B*5701	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.419285	0.208647	-4.210638	26259.409765
HLA B*4001	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.393603	0.182878	-4.210725	24751.569319
HLA A*0212	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.362059	0.151290	-4.210769	23017.521315
HLA A*2902	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.393699	0.182878	-4.210822	24757.059961
HLA A*0250	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.545692	0.334728	-4.210964	35131.116498
HLA B*1509	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.491612	0.280375	-4.211236	31017.836792
HLA B*2705	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.428143	0.216823	-4.211319	26800.476685
HLA A*2603	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.643851	0.432524	-4.211327	44040.382899
HLA A*0202	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.465786	0.254408	-4.211378	29227.116276
HLA A*6801	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.644302	0.432524	-4.211778	44086.151353
HLA B*0802	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.466199	0.254408	-4.211792	29254.957849
HLA A*3101	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.377915	0.166065	-4.211850	23873.452417
HLA B*4801	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.426571	0.214699	-4.211871	26703.655290
HLA B*4402	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.420570	0.208647	-4.211923	26337.231946
HLA A*3001	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.304820	0.092742	-4.212079	20175.318541
HLA B*0702	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.364185	0.152039	-4.212146	23130.490260
HLA A*2601	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.395153	0.182632	-4.212522	24840.103424
HLA B*3801	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.493787	0.281226	-4.212561	31173.612282
HLA A*3101	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.395717	0.182878	-4.212840	24872.376100
HLA A*2301	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.531071	0.318175	-4.212896	33968.088405
HLA B*1503	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.194282	-0.018628	-4.212910	15641.623570
HLA B*4002	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.610857	0.397920	-4.212937	40818.521345
HLA B*3801	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.553382	0.340384	-4.212998	35758.707819
HLA A*3101	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.395666	0.182632	-4.213034	24869.416027
HLA B*5801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.354197	0.141159	-4.213038	22604.618259
HLA B*4801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.421790	0.208647	-4.213142	26411.283757
HLA A*3101	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.312336	0.099112	-4.213224	20527.516169
HLA B*1517	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.467879	0.254408	-4.213472	29368.337234
HLA A*0203	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.419323	0.205784	-4.213539	26261.682832
HLA B*5401	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.482505	0.268910	-4.213594	30374.203804
HLA A*8001	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.443059	0.229292	-4.213768	27736.994406
HLA B*1509	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.532112	0.318175	-4.213937	34049.593304
HLA A*0202	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.548215	0.334139	-4.214076	35335.830187
HLA B*0801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.398741	0.184583	-4.214158	25046.154966
HLA A*3201	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.578394	0.364208	-4.214186	37878.644918
HLA B*1509	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.568146	0.353947	-4.214199	36995.251191

HLA A*0206	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.468657	0.254408	-4.214249	29420.973445
HLA A*2403	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.375385	0.161134	-4.214251	23734.759362
HLA A*0202	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.526797	0.312492	-4.214306	33635.461735
HLA B*4403	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.651374	0.436810	-4.214564	44809.916760
HLA B*1503	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.483666	0.268910	-4.214755	30455.486980
HLA B*5401	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.548899	0.334139	-4.214760	35391.502408
HLA A*0201	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.397569	0.182632	-4.214937	24978.633182
HLA B*4403	1:251-259	9	SAELVSSGT	0.736295	-0.300633	-4.650735	0.435662	-4.215073	44744.027912
HLA B*0702	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.444450	0.229292	-4.215159	27825.968814
HLA A*0211	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.539421	0.324195	-4.215227	34627.503099
HLA B*5801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.314413	0.099112	-4.215301	20625.920887
HLA B*0802	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.444643	0.229292	-4.215351	27838.315455
HLA B*1801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.457257	0.241837	-4.215420	28658.756125
HLA A*8001	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.424837	0.209282	-4.215554	26597.253540
HLA A*0101	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.376834	0.161134	-4.215700	23814.116022
HLA A*3201	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.367763	0.152039	-4.215724	23321.855683
HLA B*0802	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.465847	0.250113	-4.215734	29231.227567
HLA A*0206	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.490552	0.274750	-4.215802	30942.249861
HLA A*0301	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.367110	0.151290	-4.215820	23286.807159
HLA B*5401	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.525914	0.310085	-4.215829	33567.112765
HLA A*0203	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.430558	0.214699	-4.215858	26949.939169
HLA B*4002	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.627290	0.411293	-4.215996	42392.552473
HLA B*1502	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.556469	0.340384	-4.216085	36013.807593
HLA B*5401	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.528780	0.312492	-4.216289	33789.390600
HLA A*2601	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.401015	0.184583	-4.216433	25177.660017
HLA A*2601	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.388366	0.171766	-4.216599	24454.891345
HLA B*0801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.426047	0.209282	-4.216764	26671.459284
HLA A*0211	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.422666	0.205784	-4.216882	26464.632595
HLA B*0801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.388674	0.171766	-4.216907	24472.228559
HLA A*0101	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.369255	0.152039	-4.217216	23402.110548
HLA B*0802	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.486281	0.268910	-4.217370	30639.418951
HLA B*5701	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.427083	0.209282	-4.217800	26735.166980
HLA A*0202	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.492612	0.274750	-4.217862	31089.403330
HLA B*7301	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.587853	0.369909	-4.217945	38712.699875
HLA B*0802	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.460058	0.241837	-4.218220	28844.161791
HLA B*5101	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.498620	0.280375	-4.218245	31522.454045
HLA A*3201	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.584402	0.365931	-4.218471	38406.264380
HLA A*0212	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.427280	0.208647	-4.218633	26747.319021
HLA A*0212	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.360108	0.141159	-4.218950	22914.399549
HLA A*0301	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.361699	0.142630	-4.219069	22998.477295
HLA B*3901	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.493900	0.274750	-4.219150	31181.708330
HLA B*5401	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.494036	0.274750	-4.219286	31191.493861
HLA A*2601	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.362040	0.142630	-4.219410	23016.525159
HLA B*3801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.557822	0.338222	-4.219600	36126.205110
HLA B*4001	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.360783	0.141159	-4.219624	22950.004955
HLA A*3201	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.095740	-0.123980	-4.219720	12466.361890
HLA B*1509	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.544054	0.324195	-4.219860	34998.897288
HLA B*1502	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.591657	0.371790	-4.219868	39053.258568
HLA A*2603	1:274-282	9	LMTALATIG	0.983162	-0.546352	-4.656757	0.436810	-4.219947	45368.749327
HLA B*5801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.362587	0.142630	-4.219957	23045.555877
HLA A*2602	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.591763	0.371790	-4.219973	39062.767047
HLA B*4002	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.617058	0.397004	-4.220054	41405.454790
HLA A*2902	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.434862	0.214699	-4.220163	27218.365756
HLA A*2402	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.554909	0.334728	-4.220181	35884.672081
HLA B*3901	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.462229	0.241837	-4.220391	28988.707158

HLA B*4403	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.618453	0.398058	-4.220395	41538.724163
HLA B*4002	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.652993	0.432524	-4.220469	44977.253527
HLA B*4601	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.403560	0.182878	-4.220682	25325.606639
HLA A*3201	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.617706	0.397004	-4.220702	41467.324671
HLA A*3301	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.632061	0.411293	-4.220768	42860.908316
HLA A*2902	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.450103	0.229292	-4.220812	28190.524418
HLA B*5101	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.489856	0.268910	-4.220946	30892.740846
HLA B*4801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.424125	0.203022	-4.221103	26553.691131
HLA A*3002	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.387297	0.166065	-4.221232	24394.769666
HLA A*2402	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.539525	0.318175	-4.221350	34635.746642
HLA B*4601	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.387447	0.166065	-4.221382	24403.217401
HLA A*8001	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.438501	0.217020	-4.221481	27447.411790
HLA B*0803	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.496245	0.274750	-4.221495	31350.515828
HLA A*8001	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.436234	0.214699	-4.221535	27304.494773
HLA B*2705	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.451088	0.229292	-4.221796	28254.497585
HLA A*6802	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.387865	0.166065	-4.221800	24426.728047
HLA A*6901	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.211179	-0.010665	-4.221844	16262.201056
HLA A*2403	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.374295	0.152039	-4.222256	23675.255355
HLA B*5301	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.610122	0.387714	-4.222408	40749.462020
HLA A*3201	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.557195	0.334728	-4.222467	36074.060629
HLA B*1503	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.546745	0.324195	-4.222550	35216.364601
HLA A*2301	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.535241	0.312492	-4.222750	34295.839889
HLA B*1509	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.561133	0.338222	-4.222911	36402.630522
HLA A*2501	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.503472	0.280375	-4.223096	31876.579009
HLA B*3801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.573033	0.349724	-4.223308	37413.893808
HLA A*0201	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.395111	0.171766	-4.223345	24837.684662
HLA B*3901	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.432069	0.208647	-4.223421	27043.849356
HLA B*5301	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.595238	0.371790	-4.223448	39376.570809
HLA A*0219	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.429444	0.205784	-4.223661	26880.920308
HLA B*4402	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.405985	0.182285	-4.223700	25467.395078
HLA B*1503	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.478172	0.254408	-4.223765	30072.702107
HLA A*2602	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.621940	0.398058	-4.223882	41873.550726
HLA B*3801	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.536435	0.312492	-4.223943	34390.222161
HLA B*5301	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.594028	0.369909	-4.224119	39267.016709
HLA B*4801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.433405	0.209282	-4.224123	27127.224719
HLA B*4801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.406433	0.182285	-4.224148	25493.723853
HLA B*5101	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.438870	0.214699	-4.224171	27470.734223
HLA A*2602	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.513882	0.289672	-4.224211	32649.931528
HLA A*2902	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.441189	0.216823	-4.224366	27617.808179
HLA A*2902	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.376475	0.152039	-4.224436	23794.412923
HLA A*3101	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.442796	0.218302	-4.224494	27720.193441
HLA A*3002	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.406877	0.182285	-4.224592	25519.803727
HLA A*6802	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.439317	0.214699	-4.224617	27498.985329
HLA B*1517	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.441699	0.217020	-4.224679	27650.249031
HLA A*6901	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.385908	0.161134	-4.224774	24316.898177
HLA A*2301	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.549019	0.324195	-4.224824	35401.268425
HLA A*3201	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.537445	0.312492	-4.224953	34470.315618
HLA B*5701	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.409603	0.184583	-4.225020	25680.456083
HLA B*4501	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.636333	0.411293	-4.225040	43284.532794
HLA B*1501	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.244714	0.019638	-4.225075	17567.644141
HLA B*0803	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.493491	0.268222	-4.225269	31152.370153
HLA A*2402	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.562503	0.337099	-4.225404	36517.624406
HLA A*2501	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.475694	0.250113	-4.225580	29901.553048
HLA A*0203	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.408224	0.182632	-4.225592	25599.034450
HLA A*2501	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.480099	0.254408	-4.225691	30206.404233

HLA B*4001	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.377741	0.152039	-4.225703	23863.897028
HLA A*2402	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.591667	0.365931	-4.225736	39054.103673
HLA A*0216	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.377845	0.152039	-4.225806	23869.578149
HLA B*1517	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.506185	0.280375	-4.225810	32076.380899
HLA B*0803	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.506216	0.280375	-4.225840	32078.636864
HLA A*3101	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.435196	0.209282	-4.225913	27239.283054
HLA B*5101	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.215282	-0.010665	-4.225946	16416.536135
HLA A*2902	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.431862	0.205784	-4.226078	27030.977648
HLA B*1517	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.444399	0.218302	-4.226096	27822.657232
HLA B*4601	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.387231	0.161134	-4.226097	24391.074702
HLA B*1517	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.325221	0.099112	-4.226109	21145.647035
HLA B*1503	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.476394	0.250113	-4.226281	29949.797625
HLA B*4002	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.279639	0.053318	-4.226320	19038.758285
HLA B*5101	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.516446	0.289672	-4.226774	32843.207411
HLA A*0301	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.367993	0.141159	-4.226834	23334.223489
HLA A*0201	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.392926	0.166065	-4.226861	24713.035211
HLA B*4002	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.561043	0.334139	-4.226904	36395.147792
HLA A*8001	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.430074	0.203022	-4.227052	26919.921884
HLA B*0801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.445829	0.218302	-4.227527	27914.473551
HLA A*0203	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.378895	0.151290	-4.227605	23927.369900
HLA B*3901	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.119460	-0.108442	-4.227902	13166.190380
HLA B*3801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.517644	0.289672	-4.227972	32933.948370
HLA A*6802	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.437261	0.209282	-4.227978	27369.122281
HLA A*0216	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.457288	0.229292	-4.227996	28660.771725
HLA A*0101	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.379358	0.151290	-4.228068	23952.884044
HLA A*3001	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.281532	0.053318	-4.228214	19121.955581
HLA B*1501	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.193441	-0.034919	-4.228360	15611.359124
HLA B*4501	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.661040	0.432524	-4.228516	45818.399906
HLA A*6802	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.437167	0.208647	-4.228520	27363.200365
HLA A*0219	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.457939	0.229292	-4.228647	28703.753214
HLA A*2403	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.412124	0.182878	-4.229246	25829.959779
HLA A*6901	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.372063	0.142630	-4.229433	23553.891010
HLA B*1503	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.438743	0.209282	-4.229461	27462.710260
HLA B*1801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.446332	0.216823	-4.229509	27946.809305
HLA B*4501	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.595510	0.365931	-4.229580	39401.289219
HLA A*0212	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.414269	0.184583	-4.229686	25957.855452
HLA A*0219	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.444415	0.214699	-4.229716	27823.710874
HLA B*1801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.248776	0.019002	-4.229773	17732.737497
HLA B*4402	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.435581	0.205784	-4.229797	27263.461064
HLA B*4001	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.395933	0.166065	-4.229868	24884.758407
HLA A*2601	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.396081	0.166065	-4.230016	24893.241150
HLA B*4002	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.519904	0.289672	-4.230232	33105.793738
HLA B*4501	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.540403	0.310085	-4.230319	34705.896040
HLA A*2602	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.565078	0.334728	-4.230350	36734.789286
HLA A*0206	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.480623	0.250113	-4.230510	30242.867389
HLA B*7301	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.568867	0.338222	-4.230645	37056.745286
HLA B*1501	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.381966	0.151290	-4.230676	24097.153293
HLA B*3801	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.548932	0.318175	-4.230757	35394.183007
HLA B*7301	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.580589	0.349724	-4.230864	38070.523874
HLA B*4801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.448007	0.217020	-4.230987	28054.815332
HLA B*1501	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.244180	0.013159	-4.231021	17546.083527
HLA A*0211	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.499299	0.268222	-4.231077	31571.776624
HLA A*3301	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.629331	0.398058	-4.231273	42592.317271
HLA A*0301	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.275461	0.044127	-4.231334	18856.506528

HLA B*1502	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.549531	0.318175	-4.231356	35443.043746
HLA A*6901	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.057819	-0.173733	-4.231552	11424.022298
HLA B*1509	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.506432	0.274750	-4.231682	32094.606689
HLA B*0802	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.448811	0.217020	-4.231791	28106.769896
HLA A*3301	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.628866	0.397004	-4.231862	42546.718593
HLA B*7301	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.566764	0.334728	-4.232037	36877.755725
HLA A*3002	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.513286	0.281226	-4.232060	32605.097681
HLA A*6802	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.414706	0.182632	-4.232074	25983.988415
HLA B*3801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.566243	0.334139	-4.232104	36833.492296
HLA A*2601	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.384393	0.152039	-4.232354	24232.195182
HLA A*0250	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.596589	0.364208	-4.232380	39499.249675
HLA B*1801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.500655	0.268222	-4.232432	31670.482090
HLA A*8001	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.449523	0.216823	-4.232699	28152.880194
HLA A*2403	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.415474	0.182632	-4.232842	26029.995649
HLA A*3002	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.567300	0.334139	-4.233161	36923.270832
HLA B*3901	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.439028	0.205784	-4.233244	27480.693141
HLA B*5701	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.416132	0.182878	-4.233254	26069.454957
HLA B*4801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.439241	0.205784	-4.233458	27494.225215
HLA A*2601	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.207834	-0.025677	-4.233511	16137.403546
HLA A*0219	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.415866	0.182285	-4.233582	26053.523114
HLA A*0203	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.442925	0.209282	-4.233643	27728.442643
HLA A*0250	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.574452	0.340384	-4.234068	37536.346391
HLA A*0201	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.395259	0.161134	-4.234125	24846.151360
HLA A*2603	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.546752	0.312492	-4.234260	35216.936156
HLA B*2705	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.515583	0.281226	-4.234357	32778.064234
HLA A*1101	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.463740	0.229292	-4.234448	29089.721668
HLA A*8001	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.406302	0.171766	-4.234535	25486.001602
HLA A*0216	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.484817	0.250113	-4.234704	30536.326876
HLA B*7301	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.558924	0.324195	-4.234730	36217.982272
HLA B*4001	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.417690	0.182632	-4.235058	26163.127634
HLA B*1502	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.569344	0.334139	-4.235205	37097.463636
HLA A*3002	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.419797	0.184583	-4.235214	26290.397222
HLA B*0803	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.516478	0.281226	-4.235253	32845.694999
HLA B*3501	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.417603	0.182285	-4.235318	26157.891192
HLA B*5301	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.589294	0.353947	-4.235346	38841.294441
HLA A*6801	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.646884	0.411293	-4.235591	44349.044901
HLA B*4601	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.418526	0.182632	-4.235894	26213.564292
HLA A*3002	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.516288	0.280375	-4.235913	32831.305135
HLA A*0201	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.388011	0.152039	-4.235972	24434.922467
HLA A*3201	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.574219	0.338222	-4.235997	37516.248094
HLA B*0802	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.452911	0.216823	-4.236087	28373.361381
HLA B*4001	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.407878	0.171766	-4.236112	25578.684815
HLA B*4002	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.546199	0.310085	-4.236115	35172.192469
HLA B*4501	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.634202	0.398058	-4.236144	43072.665787
HLA B*1502	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.121119	-0.115163	-4.236282	13216.573242
HLA A*3301	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.586188	0.349724	-4.236463	38564.497407
HLA A*0203	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.408242	0.171766	-4.236476	25600.142377
HLA A*0212	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.224971	-0.011592	-4.236562	16786.911587
HLA B*4402	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.387973	0.151290	-4.236684	24432.807515
HLA A*2403	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.408903	0.171766	-4.237136	25639.088767
HLA A*0216	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.419466	0.182285	-4.237181	26270.350702
HLA A*0216	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.443017	0.205784	-4.237233	27734.293564
HLA A*2603	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.555435	0.318175	-4.237260	35928.184030
HLA B*3801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.517703	0.280375	-4.237327	32938.402896
HLA B*5401	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.561621	0.324195	-4.237427	36443.615890

HLA B*1502	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.575754	0.338222	-4.237532	37649.014524
HLA B*4501	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.609325	0.371790	-4.237536	40674.797931
HLA A*0203	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.403633	0.166065	-4.237568	25329.854266
HLA B*0801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.388873	0.151290	-4.237583	24483.484470
HLA A*2301	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.547701	0.310085	-4.237616	35293.990297
HLA A*0206	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.505856	0.268222	-4.237634	32052.095943
HLA B*0702	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.455944	0.218302	-4.237642	28572.219292
HLA A*0219	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.456097	0.218302	-4.237795	28582.268274
HLA A*0203	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.337123	0.099112	-4.238011	21733.189644
HLA B*5801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.351878	0.113485	-4.238394	22484.241197
HLA A*3001	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.301543	0.063148	-4.238395	20023.632632
HLA B*7301	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.557066	0.318175	-4.238891	36063.328609
HLA A*0250	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.593036	0.353947	-4.239089	39177.473413
HLA A*1101	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.405472	0.166065	-4.239407	25437.377661
HLA B*3901	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.390898	0.151290	-4.239609	24597.925532
HLA A*6802	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.424219	0.184583	-4.239636	26559.437854
HLA B*1801	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.454349	0.214699	-4.239649	28467.457068
HLA A*0212	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.442773	0.203022	-4.239751	27718.693850
HLA B*1502	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.574534	0.334728	-4.239806	37543.454426
HLA B*4403	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.604039	0.364208	-4.239831	40182.695174
HLA B*3901	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.490138	0.250113	-4.240025	30912.802513
HLA B*5101	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.508396	0.268222	-4.240174	32240.088654
HLA A*2902	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.458695	0.218302	-4.240393	28753.798278
HLA B*5701	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.406609	0.166065	-4.240544	25504.069818
HLA B*0702	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.449231	0.208647	-4.240584	28134.000836
HLA B*4403	1:65-73	9	SHPEGRPTN	0.940880	-0.529587	-4.651884	0.411293	-4.240591	44862.552070
HLA A*2603	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.606663	0.365931	-4.240733	40426.248155
HLA B*7301	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.459200	0.218302	-4.240898	28787.262030
HLA B*5401	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.509150	0.268222	-4.240928	32296.124608
HLA B*5301	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.606920	0.365931	-4.240989	40450.093651
HLA B*0801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.260011	0.019002	-4.241009	18197.470433
HLA B*0801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.258007	0.016895	-4.241112	18113.689199
HLA B*7301	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.553751	0.312492	-4.241259	35789.092472
HLA A*6801	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.639685	0.398058	-4.241627	43619.978710
HLA B*2705	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.456355	0.214699	-4.241656	28599.282295
HLA B*0702	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.402850	0.161134	-4.241716	25284.263787
HLA B*5701	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.424456	0.182632	-4.241824	26573.953864
HLA A*1101	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.456524	0.214699	-4.241825	28610.424229
HLA A*6802	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.393163	0.151290	-4.241874	24726.542074
HLA B*1801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.451348	0.209282	-4.242066	28271.469441
HLA A*0250	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.579224	0.337099	-4.242125	37951.050534
HLA B*4002	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.629944	0.387714	-4.242231	42652.499294
HLA B*7301	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.582868	0.340384	-4.242484	38270.827565
HLA B*0803	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.492713	0.250113	-4.242600	31096.636351
HLA A*0201	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.394080	0.151290	-4.242790	24778.766609
HLA B*5101	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.461404	0.218302	-4.243102	28933.713569
HLA B*5101	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.472569	0.229292	-4.243277	29687.178964
HLA B*4801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.425972	0.182632	-4.243340	26666.842415
HLA A*2902	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.425699	0.182285	-4.243414	26650.112964
HLA B*1501	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.426209	0.182632	-4.243577	26681.417127
HLA B*4501	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.613515	0.369909	-4.243606	41069.038545
HLA A*2603	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.631331	0.387714	-4.243617	42788.856516
HLA B*4002	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.556175	0.312492	-4.243684	35989.461987
HLA B*3501	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.446844	0.203022	-4.243822	27979.787981
HLA B*5401	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.533510	0.289672	-4.243838	34159.371583

HLA A*0216	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.395160	0.151290	-4.243871	24840.506574
HLA B*2705	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.415643	0.171766	-4.243877	26040.136620
HLA B*7301	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.512374	0.268222	-4.244151	32536.730153
HLA B*5301	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.581266	0.337099	-4.244167	38129.885813
HLA A*2602	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.610150	0.365931	-4.244219	40752.107506
HLA A*3001	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.261129	0.016895	-4.244235	18244.391258
HLA B*5801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.347426	0.103191	-4.244235	22254.916103
HLA B*4403	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.667191	0.422812	-4.244378	46471.947217
HLA B*4601	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.395694	0.151290	-4.244404	24871.030568
HLA B*1517	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.459308	0.214699	-4.244609	28794.426773
HLA B*4501	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.642700	0.397920	-4.244780	43923.793239
HLA B*0803	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.461808	0.216823	-4.244985	28960.648946
HLA A*3301	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.615060	0.369909	-4.245152	41215.492804
HLA B*4002	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.616980	0.371790	-4.245190	41398.063486
HLA A*2601	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.396603	0.151290	-4.245313	24923.155778
HLA B*3901	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.499891	0.254408	-4.245483	31614.847529
HLA B*0702	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.454840	0.209282	-4.245557	28499.662481
HLA A*2902	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.462732	0.217020	-4.245711	29022.287290
HLA A*6801	1:24-32	9	RGGAHRAAT	0.870371	-0.447559	-4.668561	0.422812	-4.245748	46618.749512
HLA B*4801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.417532	0.171766	-4.245766	26153.646198
HLA B*0702	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.428128	0.182285	-4.245844	26799.606774
HLA B*5801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.344104	0.097839	-4.246265	22085.324748
HLA B*3501	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.464839	0.218302	-4.246537	29163.465157
HLA A*3101	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.398118	0.151290	-4.246829	25010.274008
HLA A*0206	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.476267	0.229292	-4.246975	29941.049548
HLA A*8001	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.455725	0.208647	-4.247078	28557.847662
HLA A*2601	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.408249	0.161134	-4.247115	25600.557862
HLA A*2601	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.388338	0.141159	-4.247179	24453.303818
HLA B*3901	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.464242	0.217020	-4.247222	29123.418815
HLA B*4501	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.611532	0.364208	-4.247323	40881.946965
HLA B*4001	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.398624	0.151290	-4.247334	25039.381036
HLA A*0101	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.390017	0.142630	-4.247387	24548.074098
HLA A*0206	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.346507	0.099112	-4.247395	22207.890774
HLA B*4801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.432014	0.184583	-4.247432	27040.484568
HLA B*1503	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.522207	0.274750	-4.247457	33281.776529
HLA A*2402	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.586023	0.338222	-4.247801	38549.896096
HLA A*2902	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.450857	0.203022	-4.247835	28239.521893
HLA A*0202	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.572056	0.324195	-4.247861	37329.787997
HLA A*0301	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.367538	0.119542	-4.247995	23309.746637
HLA A*2403	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.399364	0.151290	-4.248074	25082.087401
HLA A*3201	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.619877	0.371790	-4.248087	41675.127889
HLA B*4402	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.432708	0.184583	-4.248125	27083.673399
HLA B*4601	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.400318	0.152039	-4.248279	25137.238619
HLA A*6801	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.645338	0.397004	-4.248335	44191.455945
HLA A*2301	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.517254	0.268910	-4.248343	32904.385590
HLA B*3901	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.430645	0.182285	-4.248360	26955.334167
HLA A*0250	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.582605	0.334139	-4.248466	38247.646004
HLA B*7301	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.558588	0.310085	-4.248504	36189.974363
HLA A*3201	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.517162	0.268222	-4.248940	32897.443968
HLA A*8001	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.433542	0.184583	-4.248959	27135.737861
HLA B*4403	1:63-71	9	PVSHPEGRP	0.601892	-0.169368	-4.681593	0.432524	-4.249069	48038.917581
HLA A*0202	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.517341	0.268222	-4.249118	32910.972585
HLA A*0201	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.390356	0.141159	-4.249197	24567.205088
HLA B*4001	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.214281	-0.034919	-4.249200	

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16378.745938
HLA A*0203	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.433793	0.184583	-4.249210	27151.450151
HLA A*6801	1:87-95 9	SGASAPVTG	1.027552	-0.687168	-4.589672	0.340384	-4.249288	38875.139641
HLA A*0219	1:67-75 9	PEGRPTNPP	0.513566	-0.304284	-4.458651	0.209282	-4.249368	28750.842887
HLA B*0702	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.434094	0.184583	-4.249511	27170.258113
HLA A*3301	1:36-44 9	RIPDAGDPP	0.201291	0.186423	-4.637331	0.387714	-4.249618	43384.167213
HLA A*0212	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.410846	0.161134	-4.249712	25754.054480
HLA B*0801	1:31-39 9	ATGPGRIPD	0.891200	-0.739161	-4.401856	0.152039	-4.249818	25226.469857
HLA A*0301	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.348948	0.099112	-4.249836
22333.070027
HLA B*5301	1:87-95 9	SGASAPVTG	1.027552	-0.687168	-4.590365	0.340384	-4.249981	38937.230681
HLA A*8001	1:43-51 9	PPPWQRAAT	0.896839	-0.714207	-4.432701	0.182632	-4.250069	27083.233843
HLA B*5701	1:31-39 9	ATGPGRIPD	0.891200	-0.739161	-4.402136	0.152039	-4.250097	25242.715302
HLA B*5701	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.411292	0.161134	-4.250158	25780.540140
HLA A*2603	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.621980	0.371790	-4.250190	41877.401934
HLA B*4002	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.215282	-0.034919	-4.250201
16416.536135
HLA B*3501	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.458991	0.208647	-4.250344	28773.404872
HLA B*0802	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.453446	0.203022	-4.250424	28408.380230
HLA A*0211	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.504947	0.254408	-4.250540	31985.061004
HLA A*0212	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.422447	0.171766	-4.250681	26451.321066
HLA A*0250	1:64-72 9	VSHPEGRPT	0.625300	-0.312808	-4.563372	0.312492	-4.250880	36590.793442
HLA B*3901	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.416980	0.166065	-4.250915	26120.417568
HLA B*5101	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.435659	0.184583	-4.251076	27268.328745
HLA B*0801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.240419	-0.010665	-4.251084	17394.769049
HLA A*6901	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.370655	0.119542	-4.251113	23477.687607
HLA A*0211	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.525921	0.274750	-4.251171	33567.657552
HLA A*0301	1:71-79 9	PTNPPAAAD	1.087869	-0.990030	-4.349212	0.097839	-4.251372	22346.605903
HLA B*0802	1:17-25 9	NADGLVDRG	0.911402	-0.705618	-4.457161	0.205784	-4.251377	28652.400161
HLA A*2603	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.434298	0.182878	-4.251421	27183.049086
HLA A*2402	1:64-72 9	VSHPEGRPT	0.625300	-0.312808	-4.564037	0.312492	-4.251545	36646.856802
HLA B*1501	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.350736	0.099112	-4.251624
22425.203138
HLA A*3002	1:54-62 9	SQAGHRQPP	0.204349	0.085323	-4.541296	0.289672	-4.251624	34777.316345
HLA A*2301	1:54-62 9	SQAGHRQPP	0.204349	0.085323	-4.541397	0.289672	-4.251725	34785.407368
HLA A*0101	1:37-45 9	IPDAGDPPP	0.238307	-0.097148	-4.392891	0.141159	-4.251732	24711.029871
HLA B*1501	1:37-45 9	IPDAGDPPP	0.238307	-0.097148	-4.392891	0.141159	-4.251732	24711.029871
HLA B*0702	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.435139	0.182878	-4.252262	27235.746607
HLA A*6802	1:71-79 9	PTNPPAAAD	1.087869	-0.990030	-4.350144	0.097839	-4.252305	22394.651866
HLA B*4402	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.435203	0.182878	-4.252325	27239.725142
HLA B*5301	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.602176	0.349724	-4.252451
40010.678963
HLA B*1509	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.520722	0.268222	-4.252499	33168.178782
HLA A*2902	1:75-83 9	PAAADARLN	0.953438	-0.810808	-4.395243	0.142630	-4.252613	24845.210473
HLA B*4002	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.616982	0.364208	-4.252774	41398.287445
HLA B*1501	1:75-83 9	PAAADARLN	0.953438	-0.810808	-4.395508	0.142630	-4.252878	24860.403428
HLA A*0206	1:46-54 9	WQRAATRQS	1.013661	-0.997851	-4.268756	0.015810	-4.252946	18567.601454
HLA A*0219	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.404328	0.151290	-4.253038	25370.448144
HLA A*0301	1:57-65 9	GHRQPPPVS	1.076955	-0.963470	-4.366579	0.113485	-4.253094	23258.353293
HLA A*0216	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.461761	0.208647	-4.253114	28957.515638
HLA A*2603	1:286-294	9	YNLITDLIG	1.049859	-0.651801	-4.651184	0.398058	-4.253126	44790.285311
HLA B*5101	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.503415	0.250113	-4.253302	31872.440508
HLA A*8001	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.436345	0.182878	-4.253467	27311.438227
HLA A*2301	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.534866	0.281226	-4.253640	34266.166862
HLA A*0216	1:37-45 9	IPDAGDPPP	0.238307	-0.097148	-4.394886	0.141159	-4.253727	24824.788576
HLA B*0702	1:27-35 9	AHRAATGPG	0.551366	-0.531728	-4.273377	0.019638	-4.253739	18766.238980
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HLA B*3801	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.528606	0.274750	-4.253857	33775.866340
HLA A*6801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.074312	-0.179556	-4.253869	11866.220844
HLA A*6801	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.623897	0.369909	-4.253988	42062.677095
HLA B*5801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.373733	0.119542	-4.254191	23644.663895
HLA A*2902	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.464047	0.209282	-4.254765	29110.344729
HLA B*5701	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.397407	0.142630	-4.254776	24969.310839
HLA B*4801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.437827	0.182878	-4.254950	27404.828957
HLA B*1517	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.421071	0.166065	-4.255005	26367.597998
HLA B*1502	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.536381	0.281226	-4.255155	34385.943339
HLA B*1503	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.244540	-0.010665	-4.255205	17560.612662
HLA A*0201	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.398041	0.142630	-4.255411	25005.809414
HLA B*5801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.355870	0.100401	-4.255469	22691.855560
HLA A*6801	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.643268	0.387714	-4.255555	43981.335628
HLA A*2902	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.421627	0.166065	-4.255562	26401.426731
HLA A*2602	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.619954	0.364208	-4.255746	41682.568661
HLA B*1801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.505885	0.250113	-4.255771	32054.176790
HLA A*0250	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.082371	-0.173733	-4.256104	12088.465082
HLA A*2902	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.464975	0.208647	-4.256328	29172.617317
HLA A*2603	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.626317	0.369909	-4.256408	42297.712369
HLA B*3801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.580857	0.324195	-4.256662	38094.010249
HLA A*0212	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.439333	0.182632	-4.256701	27500.026714
HLA B*0702	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.408047	0.151290	-4.256758	25588.649961
HLA A*2603	1:237-245	9	NSNVGDLLN	0.919525	-0.555317	-4.621061	0.364208	-4.256853	41788.913684
HLA B*3901	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.486163	0.229292	-4.256872	30631.132278
HLA A*0101	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.376637	0.119542	-4.257095	23803.296615
HLA A*8001	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.423232	0.166065	-4.257167	26499.159243
HLA B*4801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.423263	0.166065	-4.257197	26501.022956
HLA B*0802	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.466599	0.209282	-4.257316	29281.875459
HLA A*2402	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.547085	0.289672	-4.257413	35244.000350
HLA B*3501	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.466773	0.209282	-4.257490	29293.600271
HLA A*8001	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.408858	0.151290	-4.257568	25636.453515
HLA A*0216	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.474735	0.217020	-4.257715	29835.626086
HLA A*0216	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.442301	0.184583	-4.257718	27688.569264
HLA B*4403	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.623655	0.365931	-4.257724	42039.245518
HLA A*0202	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.567819	0.310085	-4.257735	36967.442159
HLA B*2705	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.474874	0.217020	-4.257854	29845.150644
HLA A*3301	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.595066	0.337099	-4.257968	39361.023209
HLA A*3101	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.302133	0.044127	-4.258005	20050.840834
HLA B*4801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.419170	0.161134	-4.258036	26252.449723
HLA A*2301	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.538519	0.280375	-4.258144	34555.642680
HLA B*1502	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.612157	0.353947	-4.258209	40940.819684
HLA B*5401	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.487697	0.229292	-4.258406	30739.532939
HLA B*1501	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.419590	0.161134	-4.258456	26277.884125
HLA A*0211	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.488076	0.229292	-4.258784	30766.318495
HLA B*2705	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.464585	0.205784	-4.258802	29146.430854
HLA A*2501	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.488193	0.229292	-4.258901	30774.641739
HLA B*1501	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.233234	-0.025677	-4.258911	17109.366989
HLA A*3301	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.630793	0.371790	-4.259003	42735.879738
HLA A*6901	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.362279	0.103191	-4.259088	23029.229382
HLA A*0219	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.462273	0.203022	-4.259251	28991.686999
HLA A*0216	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.477618	0.218302	-4.259316	30034.331770
HLA B*1801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.400553	0.141159	-4.259394	25150.841266
HLA A*8001	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.420624	0.161134	-4.259490	26340.509224
HLA A*3201	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.509653	0.250113	-4.259540	32333.536009
HLA A*1101	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.476636	0.217020	-4.259616	29966.490859
HLA B*1503	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.474413	0.214699	-4.259714	29813.521460

HLA A*0216	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.474531	0.214699	-4.259831	29821.586943
HLA A*0301	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.363090	0.103191	-4.259899	23072.251543
HLA B*0803	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.529053	0.268910	-4.260142	33810.601690
HLA B*5101	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.476970	0.216823	-4.260146	29989.520089
HLA B*1509	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.279805	0.019638	-4.260167	19046.072517
HLA B*0801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.401427	0.141159	-4.260268	25201.507765
HLA B*1801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.359401	0.099112	-4.260289	22877.116640
HLA B*3501	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.241791	-0.018628	-4.260419	17449.812558
HLA B*4403	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.614379	0.353947	-4.260432	41150.881839
HLA A*0219	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.401819	0.141159	-4.260660	25224.286393
HLA B*3501	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.445508	0.184583	-4.260925	27893.792269
HLA B*4601	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.402089	0.141159	-4.260930	25239.984244
HLA A*3201	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.535789	0.274750	-4.261039	34339.097195
HLA B*0803	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.515912	0.254408	-4.261505	32802.899235
HLA B*5301	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.599765	0.338222	-4.261543	39789.213035
HLA A*2602	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.574046	0.312492	-4.261554	37501.232153
HLA B*0803	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.490850	0.229292	-4.261559	30963.516222
HLA A*2501	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.464729	0.203022	-4.261706	29156.050857
HLA A*2402	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.595861	0.334139	-4.261721	39433.062357
HLA A*0203	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.364960	0.103191	-4.261769	23171.821161
HLA A*1101	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.467659	0.205784	-4.261875	29353.406363
HLA A*1101	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.480186	0.218302	-4.261884	30212.451131
HLA B*5801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.354679	0.092742	-4.261937	22629.701303
HLA B*4001	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.423126	0.161134	-4.261992	26492.708940
HLA B*3901	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.465107	0.203022	-4.262085	29181.456611
HLA A*1101	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.471293	0.208647	-4.262646	29600.098769
HLA A*8001	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.414760	0.152039	-4.262721	25987.221737
HLA B*3901	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.481130	0.218302	-4.262828	30278.227926
HLA A*2602	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.601112	0.338222	-4.262890	39912.745651
HLA A*3002	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.513142	0.250113	-4.263029	32594.339669
HLA B*1801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.543486	0.280375	-4.263110	34953.106952
HLA A*0211	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.543528	0.280375	-4.263153	34956.510781
HLA A*0212	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.429242	0.166065	-4.263177	26868.416856
HLA B*1501	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.376710	0.113485	-4.263225	23807.288919
HLA B*4402	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.316782	0.053318	-4.263463	20738.704739
HLA B*1502	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.531846	0.268222	-4.263624	34028.784554
HLA B*1502	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.600888	0.337099	-4.263790	39892.238186
HLA B*4002	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.633725	0.369909	-4.263816	43025.389027
HLA A*2403	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.405197	0.141159	-4.264039	25421.281988
HLA A*3002	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.518473	0.254408	-4.264066	32996.902122
HLA A*3301	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.618284	0.353947	-4.264337	41522.547482
HLA B*1801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.447051	0.182632	-4.264419	27993.111497
HLA B*4402	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.447079	0.182632	-4.264448	27994.928831
HLA B*5101	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.506564	0.241837	-4.264726	32104.331345
HLA B*3501	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.426477	0.161134	-4.265343	26697.877363
HLA A*0203	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.426641	0.161134	-4.265507	26707.989556
HLA B*4403	1:111-119	9	LGCGDGSPA	0.715203	-0.318199	-4.662675	0.397004	-4.265672	45991.244341
HLA B*3901	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.448557	0.182878	-4.265680	28090.352806
HLA B*4402	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.417779	0.152039	-4.265740	26168.506693
HLA A*0206	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.471530	0.205784	-4.265747	29616.276647
HLA B*0802	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.484086	0.218302	-4.265784	30484.993449
HLA A*0219	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.474646	0.208647	-4.265999	29829.493234
HLA B*1509	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.469028	0.203022	-4.266006	29446.132140
HLA B*4001	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.408757	0.142630	-4.266127	25630.490523
HLA A*2602	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.603259	0.337099	-4.266160	40110.588485

HLA A*0301	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.366600	0.100401	-4.266199	23259.485747
HLA A*2603	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.620274	0.353947	-4.266327	41713.247684
HLA B*4403	1:231-239	9	GVWAKLNSN	0.894678	-0.496758	-4.664334	0.397920	-4.266414	46167.238340
HLA B*4501	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.603560	0.337099	-4.266461	40138.373315
HLA B*1503	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.483527	0.217020	-4.266507	30445.767644
HLA B*5701	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.418557	0.151290	-4.267267	26215.407919
HLA A*0211	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.548518	0.281226	-4.267293	35360.498811
HLA B*2705	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.485719	0.218302	-4.267417	30599.828900
HLA B*4601	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.410056	0.142630	-4.267426	25707.283271
HLA A*0219	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.439281	0.171766	-4.267515	27496.753923
HLA A*2902	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.366635	0.099112	-4.267523	23261.373292
HLA B*5301	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.601772	0.334139	-4.267633	39973.466304
HLA B*4501	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.655399	0.387714	-4.267685	45227.106630
HLA B*5401	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.548105	0.280375	-4.267729	35326.846672
HLA A*3001	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.199329	-0.068483	-4.267812	15824.446331
HLA A*3101	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.409363	0.141159	-4.268204	25666.289293
HLA A*0219	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.452918	0.184583	-4.268335	28373.821875
HLA A*0216	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.434510	0.166065	-4.268444	27196.287464
HLA B*1517	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.199996	-0.068483	-4.268479	15848.777832
HLA A*2402	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.578564	0.310085	-4.268479	37893.401979
HLA A*2301	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.453317	0.184583	-4.268735	28399.928748
HLA A*0203	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.420930	0.152039	-4.268891	26359.040640
HLA A*2501	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.487234	0.218302	-4.268932	30706.789790
HLA B*4501	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.581576	0.312492	-4.269084	38157.124293
HLA B*0702	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.474876	0.205784	-4.269092	29845.312103
HLA B*3501	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.421132	0.152039	-4.269093	26371.307050
HLA A*2301	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.543873	0.274750	-4.269124	34984.321133
HLA B*4002	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.635139	0.365931	-4.269208	43165.740525
HLA A*8001	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.475066	0.205784	-4.269283	29858.393216
HLA B*4402	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.435412	0.166065	-4.269347	27252.843686
HLA B*1517	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.372542	0.103191	-4.269351	23579.899843
HLA A*0212	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.421437	0.152039	-4.269398	26389.860133
HLA A*0206	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.478078	0.208647	-4.269431	30066.195211
HLA A*6802	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.430656	0.161134	-4.269522	26956.063304
HLA A*2501	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.421775	0.152039	-4.269737	26410.426478
HLA A*0250	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.580253	0.310085	-4.270168	38041.083367
HLA A*2602	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.610737	0.340384	-4.270353	40807.260891
HLA A*0250	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.560064	0.289672	-4.270392	36313.135654
HLA A*0201	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.251988	-0.018628	-4.270616	17864.362844
HLA B*5301	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.583150	0.312492	-4.270658	38295.680543
HLA B*5401	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.442434	0.171766	-4.270668	27697.108730
HLA B*5301	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.488061	0.217020	-4.271041	30765.319857
HLA A*2402	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.545889	0.274750	-4.271139	35147.084784
HLA A*2902	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.442942	0.171766	-4.271176	27729.492717
HLA B*3901	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.384710	0.113485	-4.271225	24249.899267
HLA B*0801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.231989	-0.039278	-4.271266	17060.380568
HLA A*1101	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.480604	0.209282	-4.271322	30241.558533
HLA A*0301	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.252768	-0.018628	-4.271396	17896.477558
HLA B*3501	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.414330	0.142630	-4.271700	25961.506866
HLA B*0801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.364664	0.092742	-4.271922	23156.031563
HLA B*1501	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.391521	0.119542	-4.271979	24633.214916
HLA A*0202	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.501362	0.229292	-4.272070	31722.095574
HLA B*0803	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.514162	0.241837	-4.272324	32670.957564
HLA A*0212	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.325794	0.053318	-4.272476	21173.577993

HLA B*3901	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.444286	0.171766	-4.272519	27815.433330
HLA A*8001	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.454936	0.182285	-4.272651	28505.984563
HLA A*3101	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.433845	0.161134	-4.272711	27154.681842
HLA B*4002	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.626780	0.353947	-4.272832	42342.815108
HLA A*3301	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.638818	0.365931	-4.272888	43532.989223
HLA B*0802	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.487627	0.214699	-4.272927	30734.544420
HLA A*6802	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.317087	0.044127	-4.272960	20753.295102
HLA B*1501	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.370958	0.097839	-4.273119	23494.077833
HLA B*0702	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.439204	0.166065	-4.273139	27491.845466
HLA B*2705	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.456083	0.182878	-4.273205	28581.340528
HLA B*3501	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.261768	-0.011592	-4.273360	18271.257456
HLA B*1509	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.158438	-0.115163	-4.273601	14402.506729
HLA A*2902	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.286765	0.013159	-4.273606	19353.726886
HLA A*0101	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.372814	0.099112	-4.273702	23594.701986
HLA B*0702	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.445491	0.171766	-4.273725	27892.735973
HLA A*3101	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.393471	0.119542	-4.273929	24744.071873
HLA A*0219	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.255512	-0.018628	-4.274140	18009.918961
HLA A*3101	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.387687	0.113485	-4.274202	24416.687024
HLA A*2501	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.456672	0.182285	-4.274387	28620.176982
HLA A*2501	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.489262	0.214699	-4.274563	30850.486814
HLA B*4501	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.624289	0.349724	-4.274565	42100.695854
HLA B*4601	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.298672	0.023895	-4.274777	19891.695301
HLA A*6901	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.338082	0.063148	-4.274934	21781.212875
HLA A*0216	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.484328	0.209282	-4.275046	30501.984988
HLA A*2601	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.394620	0.119542	-4.275078	24809.617386
HLA B*4402	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.436283	0.161134	-4.275149	27307.596949
HLA B*0801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.374311	0.099112	-4.275199	23676.151936
HLA A*6901	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.388685	0.113485	-4.275201	24472.890528
HLA A*0301	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.368031	0.092742	-4.275289	23336.243346
HLA A*0101	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.388873	0.113485	-4.275389	24483.484470
HLA A*2603	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.610141	0.334728	-4.275413	40751.225658
HLA A*2403	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.394998	0.119542	-4.275456	24831.235782
HLA B*4801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.426944	0.151290	-4.275655	26726.634918
HLA B*1517	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.460993	0.184583	-4.276410	28906.334100
HLA A*2301	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.544656	0.268222	-4.276433	35047.401948
HLA B*4402	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.419163	0.142630	-4.276533	26252.023658
HLA A*0250	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.601137	0.324195	-4.276943	39915.120881
HLA A*0201	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.396782	0.119542	-4.277239	24933.405080
HLA A*0216	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.103714	-0.173733	-4.277447	12697.373130
HLA A*6901	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.377856	0.100401	-4.277455	23870.223817
HLA A*0219	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.443630	0.166065	-4.277565	27773.481522
HLA B*1501	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.294689	0.016895	-4.277795	19710.126929
HLA A*0206	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.494875	0.217020	-4.277855	31251.793153
HLA B*0802	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.430111	0.152039	-4.278073	26922.252126
HLA B*4801	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.430292	0.152039	-4.278254	26933.469235
HLA A*0206	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.291696	0.013159	-4.278537	19574.747882
HLA A*2402	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.602862	0.324195	-4.278667	40073.933285
HLA B*1501	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.302734	0.023895	-4.278839	20078.629116
HLA B*0803	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.496066	0.217020	-4.279046	31337.628664
HLA A*0211	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.430633	0.151290	-4.279343	26954.605050
HLA B*5701	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.420511	0.141159	-4.279352	26333.670149
HLA A*2501	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.462266	0.182878	-4.279389	28991.216477
HLA B*4601	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.392943	0.113485	-4.279458	24713.971092

HLA B*1509	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.488785	0.209282	-4.279503	30816.625175
HLA B*7301	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.548483	0.268910	-4.279573	35357.629482
HLA A*0216	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.451365	0.171766	-4.279598	28272.540080
HLA A*6801	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.616726	0.337099	-4.279628	41373.882986
HLA B*4501	1:165-173	9	RSITAESRD	1.002229	-0.648282	-4.633593	0.353947	-4.279646	43012.356297
HLA A*2601	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.380220	0.100401	-4.279819	24000.488043
HLA B*5401	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.422490	0.142630	-4.279860	26453.896968
HLA B*0801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.422680	0.142630	-4.280050	26465.491633
HLA A*2902	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.377894	0.097839	-4.280055	23872.290071
HLA B*1517	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.431556	0.151290	-4.280267	27011.973834
HLA A*6801	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.629991	0.349724	-4.280267	42657.114450
HLA A*3101	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.378178	0.097839	-4.280339	23887.921906
HLA A*0206	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.498846	0.218302	-4.280543	31538.829463
HLA B*4601	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.400153	0.119542	-4.280611	25127.721144
HLA A*2601	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.383852	0.103191	-4.280661	24202.062430
HLA A*2501	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.421912	0.141159	-4.280753	26418.714672
HLA A*3101	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.423545	0.142630	-4.280914	26518.232653
HLA B*1503	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.463794	0.182878	-4.280916	29093.341453
HLA A*2501	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.463758	0.182632	-4.281127	29090.980673
HLA A*2902	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.464240	0.182632	-4.281608	29123.261261
HLA A*2902	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.422859	0.141159	-4.281700	26476.375199
HLA A*3002	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.550685	0.268910	-4.281774	35537.314677
HLA B*4002	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.297631	0.015810	-4.281821	19844.080323
HLA B*4402	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.395407	0.113485	-4.281922	24854.620943
HLA A*1101	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.295086	0.013159	-4.281927	19728.155572
HLA A*0101	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.382703	0.100401	-4.282302	24138.122040
HLA A*0219	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.465065	0.182632	-4.282433	29178.615118
HLA A*2602	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.616581	0.334139	-4.282441	41360.007969
HLA B*1509	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.511953	0.229292	-4.282662	32505.237806
HLA A*0101	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.380779	0.097839	-4.282940	24031.409861
HLA B*1503	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.501461	0.218302	-4.283158	31729.304140
HLA B*4801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.426270	0.142630	-4.283640	26685.170322
HLA B*3901	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.168536	-0.115163	-4.283699	14741.313195
HLA A*0201	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.383075	0.099112	-4.283962	24158.763221
HLA A*0201	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.387203	0.103191	-4.284012	24389.491317
HLA B*4801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.383260	0.099112	-4.284148	24169.090430
HLA A*3201	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.526095	0.241837	-4.284257	33581.098443
HLA A*0216	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.466918	0.182632	-4.284287	29303.427377
HLA B*0801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.445449	0.161134	-4.284315	27890.019966
HLA A*2501	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.493641	0.209282	-4.284359	31163.157996
HLA A*6802	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.426998	0.142630	-4.284368	26729.960652
HLA B*1509	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.526335	0.241837	-4.284497	33599.633899
HLA A*0206	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.206917	-0.077944	-4.284861	16103.391828
HLA A*3301	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.623328	0.338222	-4.285106	42007.644957
HLA A*3002	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.609718	0.324195	-4.285523	40711.562243
HLA B*4801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.426895	0.141159	-4.285736	26723.598740
HLA B*5101	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.491666	0.205784	-4.285882	31021.696502
HLA B*5301	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.596004	0.310085	-4.285919	39446.077543
HLA B*0802	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.494666	0.208647	-4.286019	31236.749657
HLA A*0216	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.447155	0.161134	-4.286021	27999.775634
HLA A*0201	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.399704	0.113485	-4.286220	25101.770360
HLA B*4403	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.495641	0.209282	-4.286358	31306.958192
HLA B*5301	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.610557	0.324195	-4.286362	40790.265698

HLA A*3101	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.310384	0.023895	-4.286489	20435.439427
HLA A*2602	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.636572	0.349724	-4.286848	43308.424167
HLA A*0211	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.537098	0.250113	-4.286984	34442.727537
HLA A*0212	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.390389	0.103191	-4.287198	24569.065841
HLA B*1502	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.556171	0.268910	-4.287260	35989.072592
HLA B*0802	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.470156	0.182878	-4.287278	29522.695654
HLA A*0101	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.380281	0.092742	-4.287539	24003.864120
HLA A*3101	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.306651	0.019002	-4.287648	20260.522872
HLA B*1501	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.276157	-0.011592	-4.287748	18886.726153
HLA B*4403	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.491292	0.203022	-4.288270	30995.023969
HLA A*0203	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.430985	0.142630	-4.288355	26976.487141
HLA B*4403	1:36-44	9	RIPDAGDPP	0.201291	0.186423	-4.676180	0.387714	-4.288466	47443.858265
HLA B*1801	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.440585	0.152039	-4.288547	27579.436675
HLA B*1801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.491698	0.203022	-4.288676	31024.046127
HLA A*6802	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.408313	0.119542	-4.288771	25604.297532
HLA B*0803	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.507252	0.218302	-4.288950	32155.260194
HLA A*3001	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.281706	-0.007282	-4.288988	19129.612241
HLA A*2602	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.570749	0.281226	-4.289523	37217.672489
HLA A*2601	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.388662	0.099112	-4.289549	24471.566608
HLA A*2501	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.495380	0.205784	-4.289596	31288.164079
HLA A*2601	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.403149	0.113485	-4.289664	25301.641459
HLA B*0802	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.455772	0.166065	-4.289707	28560.937725
HLA B*1517	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.499515	0.209282	-4.290233	31587.494117
HLA A*3201	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.519589	0.229292	-4.290298	33081.803212
HLA B*1801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.474902	0.184583	-4.290319	29847.088214
HLA A*2902	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.441638	0.151290	-4.290348	27646.360100
HLA B*4402	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.255237	-0.035118	-4.290355	17998.523063
HLA A*2403	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.390840	0.100401	-4.290438	24594.598956
HLA A*6801	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.662306	0.371790	-4.290517	45952.198143
HLA B*5101	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.462715	0.171766	-4.290949	29021.188260
HLA B*1801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.473842	0.182878	-4.290965	29774.354264
HLA A*0101	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.394178	0.103191	-4.290987	24784.397365
HLA B*5801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.354181	0.063148	-4.291033	22603.762256
HLA B*4002	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.640877	0.349724	-4.291152	43739.784417
HLA B*4601	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.394479	0.103191	-4.291288	24801.565656
HLA A*3301	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.566135	0.274750	-4.291385	36824.327241
HLA B*0802	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.473690	0.182285	-4.291405	29763.886168
HLA B*0802	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.474087	0.182632	-4.291455	29791.110877
HLA B*3901	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.474228	0.182632	-4.291596	29800.782443
HLA A*2602	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.559852	0.268222	-4.291630	36295.459454
HLA B*1503	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.476436	0.184583	-4.291854	29952.714218
HLA A*1101	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.475109	0.182878	-4.292231	29861.300908
HLA B*4403	1:175-183	9	RVQLSARRS	1.127184	-0.757275	-4.662252	0.369909	-4.292344	45946.480783
HLA A*6802	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.253212	-0.039278	-4.292489	17914.785510
HLA B*5101	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.501888	0.209282	-4.292606	31760.560192
HLA B*1517	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.501430	0.208647	-4.292783	31727.072742
HLA A*2403	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.435421	0.142630	-4.292791	27253.433432
HLA B*4501	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.633365	0.340384	-4.292981	42989.791086
HLA B*3901	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.454407	0.161134	-4.293273	28471.307473
HLA B*4002	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.630492	0.337099	-4.293393	42706.296846
HLA B*3501	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.444711	0.151290	-4.293421	27842.683262
HLA B*0802	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.478027	0.184583	-4.293444	30062.617019
HLA A*0203	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.434646	0.141159	-4.293487	27204.822279

HLA B*4403	1:134-142	9	PRAPQRNPA	0.710811	-0.339021	-4.665332	0.371790	-4.293543	46273.508309
HLA B*1801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.510614	0.217020	-4.293594	32405.157842
HLA A*2603	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.631826	0.338222	-4.293604	42837.727310
HLA A*3301	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.603933	0.310085	-4.293849	40172.914088
HLA A*6901	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.184372	-0.109508	-4.293879	15288.740251
HLA A*3201	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.618221	0.324195	-4.294026	41516.482850
HLA B*4403	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.643818	0.349724	-4.294094	44037.047475
HLA B*3901	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.503852	0.209282	-4.294570	31904.527954
HLA A*2501	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.511744	0.217020	-4.294724	32489.590946
HLA A*8001	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.436157	0.141159	-4.294998	27299.620636
HLA A*8001	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.394141	0.099112	-4.295028	24782.252164
HLA B*1502	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.619377	0.324195	-4.295182	41627.133030
HLA A*2601	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.393093	0.097839	-4.295254	24722.529364
HLA B*1801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.524575	0.229292	-4.295283	33463.763408
HLA A*3301	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.635898	0.340384	-4.295514	43241.234028
HLA A*0211	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.480101	0.184583	-4.295519	30206.567647
HLA A*2601	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.388429	0.092742	-4.295687	24458.463659
HLA B*5401	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.501632	0.205784	-4.295848	31741.837212
HLA B*1503	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.315574	0.019638	-4.295936	20681.117079
HLA A*2603	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.630100	0.334139	-4.295960	42667.731203
HLA B*1501	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.349329	0.053318	-4.296011	22352.651354
HLA A*2902	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.457220	0.161134	-4.296086	28656.275581
HLA A*2501	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.504935	0.208647	-4.296288	31984.195838
HLA A*0206	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.447589	0.151290	-4.296299	28027.812663
HLA A*2403	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.316081	0.019638	-4.296443	20705.297835
HLA B*4501	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.634733	0.338222	-4.296511	43125.360140
HLA A*0216	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.499548	0.203022	-4.296526	31589.886596
HLA B*3501	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.181364	-0.115163	-4.296528	15183.236662
HLA A*0219	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.448581	0.152039	-4.296542	28091.872504
HLA B*1509	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.505215	0.208647	-4.296568	32004.793151
HLA A*0201	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.309738	0.013159	-4.296579	20405.059829
HLA B*4801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.410141	0.113485	-4.296656	25712.290406
HLA B*5401	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.506618	0.209282	-4.297335	32108.326254
HLA A*0206	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.480050	0.182632	-4.297418	30202.972749
HLA A*3301	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.578714	0.281226	-4.297488	37906.524193
HLA A*0211	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.479876	0.182285	-4.297591	30190.883959
HLA B*5401	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.515947	0.218302	-4.297645	32805.561244
HLA B*2705	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.464014	0.166065	-4.297949	29108.140041
HLA A*2301	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.548267	0.250113	-4.298154	35340.036022
HLA A*0203	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.417758	0.119542	-4.298216	26167.232605
HLA A*6802	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.439382	0.141159	-4.298224	27503.151106
HLA A*8001	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.440926	0.142630	-4.298296	27601.079408
HLA B*4001	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.397472	0.099112	-4.298360	24973.093399
HLA A*1101	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.470400	0.171766	-4.298634	29539.310637
HLA A*0219	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.459804	0.161134	-4.298670	28827.313992
HLA A*0250	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.553154	0.254408	-4.298746	35739.948029
HLA B*1509	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.515903	0.217020	-4.298883	32802.189403
HLA A*0201	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.399286	0.100401	-4.298885	25077.609988
HLA B*5701	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.418604	0.119542	-4.299061	26218.244521
HLA B*4001	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.402265	0.103191	-4.299074	25250.227235
HLA A*0202	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.580471	0.281226	-4.299246	38060.227401
HLA A*6802	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.402608	0.103191	-4.299417	25270.178850
HLA B*1801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.505332	0.205784	-4.299549	32013.451441

HLA B*5401	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.516373	0.216823	-4.299549	32837.699852
HLA B*5701	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.413221	0.113485	-4.299736	25895.299563
HLA A*2603	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.574490	0.274750	-4.299740	37539.595611
HLA A*0202	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.580305	0.280375	-4.299929	38045.611194
HLA B*5101	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.503023	0.203022	-4.300001	31843.658307
HLA A*0201	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.393062	0.092742	-4.300321	24720.790725
HLA B*5301	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.506110	0.205784	-4.300327	32070.828430
HLA B*1509	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.554885	0.254408	-4.300478	35882.730812
HLA B*1517	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.483619	0.182878	-4.300741	30452.191943
HLA A*0211	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.517771	0.217020	-4.300750	32943.570902
HLA A*3301	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.613254	0.312492	-4.300762	41044.384086
HLA A*0201	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.398741	0.097839	-4.300902	25046.154966
HLA B*4402	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.398774	0.097839	-4.300935	25048.051995
HLA B*3801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.569328	0.268222	-4.301105	37096.058811
HLA B*4801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.420850	0.119542	-4.301308	26354.192704
HLA A*0206	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.486027	0.184583	-4.301444	30621.522546
HLA B*2705	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.510807	0.209282	-4.301524	32419.536313
HLA A*0206	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.442683	0.141159	-4.301525	27712.996143
HLA B*0802	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.473349	0.171766	-4.301583	29740.547521
HLA A*0201	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.192242	-0.109508	-4.301750	15568.346070
HLA A*2501	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.486339	0.184583	-4.301757	30643.563127
HLA A*8001	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.314923	0.013159	-4.301764	20650.148822
HLA B*0702	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.415394	0.113485	-4.301910	26025.208230
HLA A*3301	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.636058	0.334139	-4.301919	43257.144214
HLA B*4001	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.421524	0.119542	-4.301982	26395.143012
HLA B*4002	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.640301	0.338222	-4.302079	43681.849111
HLA B*5101	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.510927	0.208647	-4.302280	32428.482238
HLA A*6901	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.355720	0.053318	-4.302401	22684.000253
HLA A*2501	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.474362	0.171766	-4.302595	29809.973339
HLA B*3501	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.276993	-0.025677	-4.302670	18923.135537
HLA A*2403	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.416179	0.113485	-4.302694	26072.275767
HLA A*3301	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.557378	0.254408	-4.302971	36089.286061
HLA B*5401	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.553415	0.250113	-4.303301	35761.416231
HLA B*4002	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.638109	0.334728	-4.303381	43461.923680
HLA A*2402	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.584729	0.281226	-4.303503	38435.155776
HLA A*6802	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.322547	0.019002	-4.303545	21015.864744
HLA A*2501	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.469613	0.166065	-4.303548	29485.824645
HLA B*1509	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.572483	0.268910	-4.303573	37366.561000
HLA B*5701	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.404145	0.100401	-4.303743	25359.744800
HLA A*0301	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.366920	0.063148	-4.303772	23276.605092
HLA B*4601	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.403158	0.099112	-4.304046	25302.188981
HLA A*2301	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.546047	0.241837	-4.304209	35159.826596
HLA B*5801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.357686	0.053318	-4.304368	22786.948060
HLA B*0803	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.513701	0.209282	-4.304419	32636.333658
HLA A*0206	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.470520	0.166065	-4.304455	29547.461785
HLA A*0203	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.328545	0.023895	-4.304651	21308.137958
HLA B*4801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.402810	0.097839	-4.304971	25281.938547
HLA B*1509	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.521875	0.216823	-4.305052	33256.399058
HLA B*4001	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.418662	0.113485	-4.305178	26221.790706
HLA A*0219	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.447897	0.142630	-4.305267	28047.682887
HLA B*0702	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.408651	0.103191	-4.305460	25624.251667
HLA B*0801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.293155	-0.012369	-4.305525	19640.620642
HLA B*5701	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.408853	0.103191	-4.305662	25636.176136
HLA A*3001	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.280038	-0.025677	-4.305715	19056.275926
HLA A*6801	1:11-19	9	SKGDGPNAD	1.160358	-0.794427	-4.672033	0.365931	-4.306102	46992.998683

HLA B*5301	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.575065	0.268910	-4.306155	37589.384437
HLA B*1509	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.556269	0.250113	-4.306156	35997.250790
HLA A*2402	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.586542	0.280375	-4.306167	38596.013356
HLA A*2603	1:55-63	9	QAGHRQPPP	0.312125	0.024974	-4.643395	0.337099	-4.306297	43994.185949
HLA B*3801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.575246	0.268910	-4.306336	37605.045988
HLA B*3501	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.409558	0.103191	-4.306367	25677.816578
HLA B*4402	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.447782	0.141159	-4.306623	28040.248864
HLA A*3002	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.458749	0.152039	-4.306711	28757.376262
HLA B*4801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.409943	0.103191	-4.306752	25700.608607
HLA A*2402	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.407166	0.100401	-4.306765	25536.790673
HLA A*3101	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.410108	0.103191	-4.306917	25710.343071
HLA A*0250	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.587381	0.280375	-4.307006	38670.627039
HLA B*4402	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.400057	0.092742	-4.307315	25122.148297
HLA A*2602	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.631627	0.324195	-4.307432	42818.033313
HLA B*0802	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.448644	0.141159	-4.307485	28095.976099
HLA B*7301	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.549508	0.241837	-4.307670	35441.126369
HLA B*4501	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.642815	0.334728	-4.308087	43935.438302
HLA A*0211	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.479925	0.171766	-4.308159	30194.314070
HLA B*1517	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.449396	0.141159	-4.308237	28144.656982
HLA B*1503	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.321474	0.013159	-4.308314	20963.970991
HLA B*4002	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.648754	0.340384	-4.308371	44540.435735
HLA B*1501	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.408940	0.100401	-4.308539	25641.308138
HLA B*0801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.289993	-0.018628	-4.308621	19498.122767
HLA A*0203	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.422586	0.113485	-4.309101	26459.765238
HLA B*3801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.450263	0.141159	-4.309104	28200.896843
HLA A*0250	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.577800	0.268222	-4.309578	37826.835806
HLA B*0803	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.515487	0.205784	-4.309703	32770.794687
HLA A*3001	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.299264	-0.010665	-4.309929	19918.831984
HLA B*5701	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.409286	0.099112	-4.310173	25661.707593
HLA B*5701	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.408116	0.097839	-4.310276	25592.664797
HLA A*0101	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.373895	0.063148	-4.310747	23653.491678
HLA A*0250	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.591974	0.281226	-4.310749	39081.790949
HLA A*0206	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.513781	0.203022	-4.310759	32642.337214
HLA B*1502	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.137171	-0.173733	-4.310904	13714.202207
HLA A*0212	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.453550	0.142630	-4.310920	28415.143228
HLA A*3002	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.540485	0.229292	-4.311194	34712.468089
HLA B*2705	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.494241	0.182632	-4.311609	31206.177916
HLA A*2403	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.415300	0.103191	-4.312109	26019.577100
HLA B*4403	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.601856	0.289672	-4.312185	39981.252135
HLA B*4601	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.410127	0.097839	-4.312287	25711.455816
HLA B*3801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.554206	0.241837	-4.312369	35826.673504
HLA B*0803	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.515468	0.203022	-4.312446	32769.376427
HLA B*0702	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.410310	0.097839	-4.312471	25722.307603
HLA B*5101	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.494823	0.182285	-4.312538	31248.073862
HLA A*0212	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.426176	0.113485	-4.312691	26679.396395
HLA B*3501	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.410770	0.097839	-4.312931	25749.596415
HLA B*1509	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.464252	0.151290	-4.312962	29124.049039
HLA B*1502	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.593424	0.280375	-4.313049	39212.460081
HLA B*0802	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.464367	0.151290	-4.313077	29131.770399
HLA A*6802	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.413552	0.100401	-4.313151	25915.059887
HLA A*0250	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.582393	0.268910	-4.313483	38229.028139
HLA B*0803	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.498080	0.184583	-4.313497	31483.255851
HLA B*0801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.427125	0.113485	-4.313641	26737.770524
HLA A*2501	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.475069	0.161134	-4.313935	29858.554747
HLA B*4402	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.433638	0.119542	-4.314096	27141.757383

HLA A*2603	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.654607	0.340384	-4.314223	45144.726733
HLA A*6802	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.327415	0.013159	-4.314256	21252.762923
HLA B*4403	1:87-95	9	SGASAPVTG	1.027552	-0.687168	-4.654673	0.340384	-4.314289	45151.565634
HLA B*1503	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.466329	0.152039	-4.314290	29263.663779
HLA B*4601	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.414821	0.100401	-4.314419	25990.877282
HLA B*2705	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.466545	0.152039	-4.314506	29278.232216
HLA B*1801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.480628	0.166065	-4.314563	30243.194612
HLA A*0301	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.368327	0.053318	-4.315009	23352.155826
HLA B*5801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.359375	0.044127	-4.315248	22875.755291
HLA A*1101	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.476525	0.161134	-4.315391	29958.872404
HLA A*2603	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.583636	0.268222	-4.315414	38338.589870
HLA B*5301	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.605099	0.289672	-4.315427	40280.855024
HLA B*1517	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.477026	0.161134	-4.315892	29993.414101
HLA B*3501	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.435520	0.119542	-4.315978	27259.626534
HLA A*2601	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.379283	0.063148	-4.316135	23948.737764
HLA A*2402	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.585069	0.268910	-4.316159	38465.317445
HLA B*4402	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.415387	0.099112	-4.316275	26024.785853
HLA B*0801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.332145	0.015810	-4.316335	21485.472598
HLA A*3002	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.154956	-0.161502	-4.316458	14287.496928
HLA B*5101	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.499604	0.182878	-4.316727	31593.988409
HLA B*4501	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.519812	0.203022	-4.316790	33098.809626
HLA B*0803	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.525498	0.208647	-4.316851	33534.985947
HLA A*1101	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.468187	0.151290	-4.316897	29389.157819
HLA A*3001	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.305307	-0.011592	-4.316898	20197.924467
HLA B*1502	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.571330	0.254408	-4.316922	37267.437571
HLA B*5401	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.519960	0.203022	-4.316938	33110.092385
HLA A*3001	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.239206	-0.077944	-4.317150	17346.279214
HLA A*0250	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.592101	0.274750	-4.317351	39093.209737
HLA A*0250	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.547113	0.229292	-4.317822	35246.288418
HLA A*1101	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.500563	0.182632	-4.317931	31663.800776
HLA B*0803	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.532634	0.214699	-4.317934	34090.511275
HLA A*2603	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.586925	0.268910	-4.318015	38630.062791
HLA B*5401	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.559880	0.241837	-4.318043	36297.815784
HLA B*4001	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.410994	0.092742	-4.318252	25762.833551
HLA A*2902	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.431775	0.113485	-4.318290	27025.567509
HLA B*5301	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.598849	0.280375	-4.318474	39705.351993
HLA A*2301	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.547903	0.229292	-4.318611	35310.414663
HLA B*1502	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.593520	0.274750	-4.318770	39221.158583
HLA B*1503	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.422170	0.103191	-4.318979	26434.440806
HLA A*0212	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.438560	0.119542	-4.319018	27451.124227
HLA B*1509	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.490820	0.171766	-4.319053	30961.338679
HLA A*0202	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.569330	0.250113	-4.319217	37096.259497
HLA B*3901	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.503826	0.184583	-4.319244	31902.629410
HLA A*8001	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.412004	0.092742	-4.319262	25822.834163
HLA B*0702	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.418629	0.099112	-4.319517	26219.804784
HLA A*3201	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.574027	0.254408	-4.319619	37499.609168
HLA B*1509	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.534480	0.214699	-4.319781	34235.778654
HLA B*7301	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.574678	0.254408	-4.320270	37555.845932
HLA A*0203	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.418122	0.097839	-4.320283	26189.183891
HLA A*2603	1:229-237	9	GMGVWAKLN	1.028283	-0.678559	-4.670008	0.349724	-4.320283	46774.365259
HLA A*2301	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.538881	0.218302	-4.320579	34584.443774
HLA A*0211	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.529229	0.208647	-4.320582	33824.322844
HLA A*3301	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.644812	0.324195	-4.320617	44137.936502

HLA A*1101	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.461829	0.141159	-4.320670	28962.059046
HLA B*5301	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.595463	0.274750	-4.320714	39397.026317
HLA A*0250	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.537565	0.216823	-4.320742	34479.827440
HLA B*2705	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.419962	0.099112	-4.320849	26300.355077
HLA B*5401	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.211363	-0.109508	-4.320870	16269.064687
HLA B*0803	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.504033	0.182878	-4.321156	31917.820919
HLA A*0101	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.374922	0.053318	-4.321604	23709.477560
HLA A*2501	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.473048	0.151290	-4.321758	29719.960337
HLA B*4601	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.414666	0.092742	-4.321924	25981.598826
HLA A*0211	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.536625	0.214699	-4.321926	34405.295293
HLA A*3001	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.287164	-0.034919	-4.322083	19371.534332
HLA B*3801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.572267	0.250113	-4.322154	37347.967924
HLA B*4501	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.590494	0.268222	-4.322272	38948.817941
HLA B*3501	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.341503	0.019002	-4.322501	21953.456576
HLA B*4501	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.572763	0.250113	-4.322649	37390.624470
HLA B*5101	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.483807	0.161134	-4.322672	30465.374234
HLA A*0206	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.532133	0.209282	-4.322851	34051.251185
HLA A*6802	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.415721	0.092742	-4.322979	26044.785886
HLA B*3801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.577549	0.254408	-4.323141	37804.945771
HLA B*1517	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.505788	0.182632	-4.323157	32047.067787
HLA A*2602	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.598438	0.274750	-4.323688	39667.779510
HLA B*4001	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.424348	0.100401	-4.323947	26567.341629
HLA A*0211	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.542398	0.218302	-4.324096	34865.666710
HLA A*3002	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.347999	0.023895	-4.324105	22284.312277
HLA A*2902	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.427442	0.103191	-4.324251	26757.305187
HLA B*0803	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.368444	0.044127	-4.324317	23358.473309
HLA B*4403	1:64-72	9	VSHPEGRPT	0.625300	-0.312808	-4.636918	0.312492	-4.324426	43342.879050
HLA B*1509	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.530282	0.205784	-4.324498	33906.399921
HLA B*2705	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.467292	0.142630	-4.324662	29328.644220
HLA B*0802	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.485808	0.161134	-4.324674	30606.120130
HLA B*1502	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.541519	0.216823	-4.324696	34795.194375
HLA B*0803	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.338162	0.013159	-4.325003	21785.219598
HLA B*4501	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.554597	0.229292	-4.325305	35858.861798
HLA A*2402	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.593894	0.268222	-4.325672	39254.910054
HLA A*1101	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.510398	0.184583	-4.325815	32389.033490
HLA B*1502	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.555146	0.229292	-4.325855	35904.284780
HLA A*3101	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.426411	0.100401	-4.326010	26693.833557
HLA A*6901	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.370197	0.044127	-4.326070	23452.933387
HLA A*0206	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.540857	0.214699	-4.326157	34742.151689
HLA A*3002	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.534875	0.208647	-4.326228	34266.908375
HLA B*1801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.534917	0.208647	-4.326270	34270.245380
HLA A*0203	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.319007	-0.007282	-4.326288	20845.225174
HLA B*7301	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.439780	0.113485	-4.326295	27528.307945
HLA B*4501	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.644523	0.318175	-4.326348	44108.576167
HLA B*4002	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.645040	0.318175	-4.326865	44161.104371
HLA A*3101	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.314599	-0.012369	-4.326968	20634.737903
HLA B*1502	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.544125	0.217020	-4.327105	35004.577954
HLA B*4402	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.430372	0.103191	-4.327181	26938.423731
HLA B*7301	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.601939	0.274750	-4.327189	39988.823147
HLA A*0206	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.479267	0.152039	-4.327229	30148.611283
HLA B*5301	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.581794	0.254408	-4.327386	38176.326724
HLA A*2301	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.499306	0.171766	-4.327540	31572.289027
HLA B*5101	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.420330	0.092742	-4.327589	26322.702841
HLA A*1101	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.426747	0.099112	-4.327634	

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HLA B*1503	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.426824	0.099112	-4.327712
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HLA B*4403	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.596885	0.268910	-4.327974	39526.183361
HLA A*2603	1:18-26 9	ADGLVDRGG	1.009719	-0.685524	-4.652187	0.324195	-4.327993	44893.871482
HLA B*4403	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.666218	0.338222	-4.327996	46367.980741
HLA B*4001	1:71-79 9	PTNPPAAAD	1.087869	-0.990030	-4.425946	0.097839	-4.328107	26665.255551
HLA A*6801	1:112-120	9	GCGDGSPAE	1.135648	-0.797426	-4.666390	0.338222	-4.328168	46386.296089
HLA B*4403	1:55-63 9	QAGHRQPPP	0.312125	0.024974	-4.665323	0.337099	-4.328224	46272.506981
HLA B*1501	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.391559	0.063148	-4.328411	24635.347215
HLA B*2705	1:37-45 9	IPDAGDPPP	0.238307	-0.097148	-4.469703	0.141159	-4.328544	29491.886840
HLA B*5301	1:49-57 9	AATRQSQAG	0.707385	-0.478093	-4.557945	0.229292	-4.328653	36136.369355
HLA A*3101	1:6-14  9	EPGALSKGD	1.111689	-1.018947	-4.421430	0.092742	-4.328688	26389.431838
HLA B*1801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.511218	0.182285	-4.328933	32450.243413
HLA A*2403	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.373139	0.044127	-4.329011	23612.323535
HLA A*6801	1:64-72 9	VSHPEGRPT	0.625300	-0.312808	-4.641739	0.312492	-4.329247	43826.712934
HLA B*0801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.429909	0.100401	-4.329508	26909.729449
HLA B*1517	1:75-83 9	PAAADARLN	0.953438	-0.810808	-4.472202	0.142630	-4.329572	29662.135255
HLA B*5101	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.429064	0.099112	-4.329951
26857.372134
HLA A*0212	1:6-14  9	EPGALSKGD	1.111689	-1.018947	-4.422711	0.092742	-4.329969	26467.352978
HLA A*2301	1:15-23 9	GPNADGLVD	1.314613	-1.099914	-4.544870	0.214699	-4.330170	35064.660029
HLA A*0212	1:71-79 9	PTNPPAAAD	1.087869	-0.990030	-4.428058	0.097839	-4.330219	26795.257639
HLA A*0101	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.374480	0.044127	-4.330353	23685.375878
HLA B*5101	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.496555	0.166065	-4.330490	31372.911395
HLA B*0702	1:75-83 9	PAAADARLN	0.953438	-0.810808	-4.473163	0.142630	-4.330533	29727.839684
HLA B*5701	1:6-14  9	EPGALSKGD	1.111689	-1.018947	-4.423345	0.092742	-4.330603	26506.041297
HLA A*6901	1:79-87 9	DARLNRFIS	1.021930	-1.002928	-4.349658	0.019002	-4.330656	22369.587318
HLA B*1501	1:6-14  9	EPGALSKGD	1.111689	-1.018947	-4.423599	0.092742	-4.330857	26521.532455
HLA A*2301	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.547846	0.216823	-4.331023	35305.830350
HLA A*2602	1:9-17  9	ALSKGDGPN	0.754582	-0.512745	-4.573014	0.241837	-4.331177	37412.274603
HLA A*6802	1:57-65 9	GHRQPPPVS	1.076955	-0.963470	-4.444725	0.113485	-4.331241	27843.587031
HLA A*0212	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.430393	0.099112	-4.331281
26939.735368
HLA A*6801	1:234-242	9	AKLNSNVGD	1.055238	-0.721099	-4.665626	0.334139	-4.331487	46304.810710
HLA B*4403	1:96-104	9	PAAAVRTPQ	0.573431	-0.238703	-4.666486	0.334728	-4.331758	46396.585963
HLA B*3901	1:31-39 9	ATGPGRIPD	0.891200	-0.739161	-4.483816	0.152039	-4.331777	30466.033498
HLA A*0201	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.394954	0.063148	-4.331806	24828.683563
HLA A*2301	1:67-75 9	PEGRPTNPP	0.513566	-0.304284	-4.541181	0.209282	-4.331899	34768.098637
HLA B*1801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.503834	0.171766	-4.332067	31903.147184
HLA A*2301	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.549240	0.217020	-4.332219	35419.275595
HLA B*1517	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.325143	-0.007282	-4.332425	21141.872317
HLA A*2402	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.549921	0.216823	-4.333098	35474.887370
HLA B*5301	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.601377	0.268222	-4.333155	39937.152469
HLA A*0216	1:25-33 9	GGAHRAATG	0.837696	-0.734505	-4.436370	0.103191	-4.333179	27313.063546
HLA A*0219	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.452777	0.119542	-4.333235	28364.613416
HLA A*2902	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.434040	0.100401	-4.333638	27166.877597
HLA A*2301	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.536764	0.203022	-4.333742	34416.278647
HLA A*3301	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.602228	0.268222	-4.334005	40015.441219
HLA A*0301	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.358043	0.023895	-4.334149	22805.693545
HLA B*0803	1:43-51 9	PPPWQRAAT	0.896839	-0.714207	-4.517000	0.182632	-4.334368	32885.166225
HLA A*0201	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.387687	0.053318	-4.334369	24416.687024
HLA A*2602	1:49-57 9	AATRQSQAG	0.707385	-0.478093	-4.563917	0.229292	-4.334625	36636.747170
HLA A*0202	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.553365	0.218302	-4.335063	35757.353690
HLA B*1517	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.348295	0.013159	-4.335136	22299.507469
HLA B*5801	1:27-35 9	AHRAATGPG	0.551366	-0.531728	-4.355097	0.019638	-4.335459	22651.503302
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HLA B*2705	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.328414	-0.007282	-4.335696	21301.683554
HLA A*2601	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.348951	0.013159	-4.335792	22333.190846
HLA B*4501	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.590374	0.254408	-4.335967	38938.073275
HLA B*3501	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.351855	0.015810	-4.336045	22483.024857
HLA A*0219	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.435238	0.099112	-4.336126	27241.935690
HLA B*5801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.353105	0.016895	-4.336210	22547.825580
HLA A*0202	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.539405	0.203022	-4.336383	34626.191807
HLA A*0206	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.508253	0.171766	-4.336487	32229.451075
HLA A*2403	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.435647	0.099112	-4.336534	27267.591161
HLA B*1502	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.551359	0.214699	-4.336659	35592.534126
HLA A*0211	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.545969	0.209282	-4.336687	35153.550201
HLA B*0801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.190175	-0.146721	-4.336896	15494.405950
HLA A*0219	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.450491	0.113485	-4.337006	28215.699408
HLA B*4001	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.400334	0.063148	-4.337186	25138.190565
HLA B*0803	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.519704	0.182285	-4.337419	33090.573850
HLA B*1509	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.503798	0.166065	-4.337733	31900.558401
HLA A*3301	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.627442	0.289672	-4.337771	42407.462130
HLA B*3801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.567119	0.229292	-4.337828	36907.893223
HLA B*4403	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.647916	0.310085	-4.337831	44454.496452
HLA B*5101	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.480534	0.142630	-4.337904	30236.650827
HLA A*2902	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.457544	0.119542	-4.338002	28677.677333
HLA A*1101	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.441210	0.103191	-4.338019	27619.152895
HLA A*3201	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.618697	0.280375	-4.338322	41562.101608
HLA B*4402	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.438814	0.100401	-4.338412	27467.167728
HLA B*5301	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.588605	0.250113	-4.338492	38779.775970
HLA B*7301	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.555358	0.216823	-4.338534	35921.770475
HLA A*0211	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.504646	0.166065	-4.338581	31962.920110
HLA A*0216	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.481290	0.142630	-4.338660	30289.368501
HLA B*7301	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.548011	0.209282	-4.338728	35319.202926
HLA B*5801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.352061	0.013159	-4.338902	22493.730904
HLA A*2602	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.439312	0.100401	-4.338911	27498.687798
HLA A*0211	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.542243	0.203022	-4.339221	34853.220052
HLA B*1502	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.589404	0.250113	-4.339291	38851.171670
HLA A*3101	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.356598	0.016895	-4.339704	22729.943220
HLA A*0101	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.352889	0.013159	-4.339729	22536.606099
HLA A*0211	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.491987	0.152039	-4.339949	31044.696905
HLA B*4801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.440468	0.100401	-4.340066	27571.977599
HLA B*5801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.364192	0.023895	-4.340297	23130.865664
HLA A*2301	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.548986	0.208647	-4.340339	35398.587289
HLA A*2403	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.433488	0.092742	-4.340746	27132.361640
HLA B*3501	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.234155	-0.106651	-4.340805	17145.688922
HLA A*0301	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.357884	0.016895	-4.340989	22797.305501
HLA B*3801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.558095	0.217020	-4.341075	36148.883122
HLA A*0206	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.502278	0.161134	-4.341144	31789.095307
HLA A*8001	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.439021	0.097839	-4.341181	27480.247142
HLA A*2601	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.394557	0.053318	-4.341238	24805.993785
HLA A*6901	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.357061	0.015810	-4.341251	22754.180528
HLA B*5801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.357306	0.015810	-4.341495	22766.986280
HLA A*3001	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.306637	-0.035118	-4.341754	20259.865239
HLA A*8001	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.442197	0.100401	-4.341796	27681.979197
HLA A*0250	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.592097	0.250113	-4.341983	39092.786760
HLA A*2301	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.547938	0.205784	-4.342154	35313.280160
HLA A*2601	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.386378	0.044127	-4.342251	24343.222760
HLA A*2902	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.232778	-0.109508	-4.342286	17091.419811

HLA A*6901	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.355520	0.013159	-4.342361	22673.571627
HLA B*4403	1:254-262	9	LVSSGTIFG	0.936013	-0.617838	-4.660596	0.318175	-4.342421	45771.575952
HLA A*0203	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.442893	0.100401	-4.342491	27726.342613
HLA A*2402	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.592841	0.250113	-4.342728	39159.885861
HLA A*1101	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.485569	0.142630	-4.342939	30589.236066
HLA A*0219	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.440935	0.097839	-4.343096	27601.676689
HLA B*0801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.441504	0.097839	-4.343665	27637.836281
HLA B*7301	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.593838	0.250113	-4.343724	39249.813632
HLA B*0803	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.495089	0.151290	-4.343799	31267.182195
HLA B*7301	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.573573	0.229292	-4.344282	37460.475937
HLA B*2705	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.457812	0.113485	-4.344327	28695.369096
HLA A*2602	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.594505	0.250113	-4.344392	39310.163729
HLA A*0301	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.363398	0.019002	-4.344395	23088.608538
HLA A*2602	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.624839	0.280375	-4.344464	42154.025465
HLA B*1503	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.527131	0.182632	-4.344499	33661.310567
HLA B*3801	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.561443	0.216823	-4.344619	36428.635120
HLA A*0216	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.357884	0.013159	-4.344724	22797.305501
HLA A*6901	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.165346	-0.179556	-4.344902	14633.411073
HLA B*1503	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.486273	0.141159	-4.345115	30638.921687
HLA A*2402	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.586970	0.241837	-4.345133	38634.033698
HLA B*5401	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.553922	0.208647	-4.345275	35803.229160
HLA A*0301	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.364960	0.019638	-4.345322	23171.821161
HLA A*0301	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.361243	0.015810	-4.345433	22974.352630
HLA B*3901	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.488078	0.142630	-4.345448	30766.484938
HLA B*4501	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.626712	0.281226	-4.345486	42336.172601
HLA A*2602	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.562561	0.217020	-4.345541	36522.563648
HLA B*7301	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.530145	0.184583	-4.345563	33895.762658
HLA A*3201	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.626820	0.281226	-4.345594	42346.709476
HLA A*3201	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.517533	0.171766	-4.345767	32925.575491
HLA B*3801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.548911	0.203022	-4.345889	35392.459742
HLA A*6901	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.327289	-0.018628	-4.345917	21246.555175
HLA A*2603	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.562806	0.216823	-4.345982	36543.118064
HLA B*5401	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.528280	0.182285	-4.345995	33750.477293
HLA A*2603	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.555287	0.209282	-4.346005	35915.940964
HLA A*0216	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.445294	0.099112	-4.346181	27880.063538
HLA B*0801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.370103	0.023895	-4.346209	23447.858825
HLA A*0101	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.365472	0.019002	-4.346470	23199.165104
HLA A*6901	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.370383	0.023895	-4.346488	23462.958873
HLA A*6802	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.334123	-0.012369	-4.346492	21583.564889
HLA B*1502	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.529504	0.182878	-4.346626	33845.738964
HLA B*3901	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.366426	0.019638	-4.346788	23250.176098
HLA A*2301	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.529119	0.182285	-4.346834	33815.723603
HLA B*1509	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.529485	0.182632	-4.346854	33844.274182
HLA B*3501	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.460387	0.113485	-4.346902	28866.016187
HLA A*8001	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.460584	0.113485	-4.347100	28879.136771
HLA A*0212	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.339901	-0.007282	-4.347182	21872.607563
HLA B*1509	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.565491	0.218302	-4.347189	36769.782623
HLA B*0801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.400522	0.053318	-4.347204	25149.072506
HLA B*0702	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.466775	0.119542	-4.347233	29293.758747
HLA A*0203	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.308206	-0.039278	-4.347484	20333.212913
HLA A*0211	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.530127	0.182632	-4.347495	33894.295711
HLA B*3801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.556434	0.208647	-4.347787	36010.885251
HLA B*0801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.411012	0.063148	-4.347865	25763.948567
HLA A*6801	1:182-190	9	RSRGPVRAS	1.084519	-0.774434	-4.657950	0.310085	-4.347866	45493.604284
HLA B*5301	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.564777	0.216823	-4.347953	36709.360505

HLA B*0803	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.520137	0.171766	-4.348370	33123.529255
HLA B*5401	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.467976	0.119542	-4.348434	29374.852014
HLA B*4601	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.411898	0.063148	-4.348750	25816.548488
HLA A*0216	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.468382	0.119542	-4.348840	29402.357125
HLA A*2403	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.446734	0.097839	-4.348895	27972.674610
HLA B*4001	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.393084	0.044127	-4.348956	24721.994385
HLA A*0203	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.368595	0.019638	-4.348957	23366.562181
HLA B*4801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.441809	0.092742	-4.349068	27657.280409
HLA A*0216	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.462579	0.113485	-4.349094	29012.083606
HLA A*0212	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.449565	0.100401	-4.349164	28155.621799
HLA B*0803	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.515649	0.166065	-4.349584	32783.029730
HLA A*2603	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.604009	0.254408	-4.349601	40179.869282
HLA B*4402	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.365512	0.015810	-4.349702	23201.298786
HLA B*1502	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.534452	0.184583	-4.349869	34233.556185
HLA A*2602	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.618813	0.268910	-4.349902	41573.120540
HLA B*1502	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.394303	0.044127	-4.350175	24791.504669
HLA B*3801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.501684	0.151290	-4.350394	31745.615273
HLA A*3301	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.535143	0.184583	-4.350560	34288.048233
HLA A*0101	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.374600	0.023895	-4.350706	23691.911677
HLA A*0219	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.454034	0.103191	-4.350843	28446.827771
HLA A*3002	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.338517	-0.012369	-4.350886	21803.023068
HLA B*5401	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.108187	-0.242879	-4.351066	12828.837426
HLA B*5801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.370277	0.019002	-4.351275	23457.247628
HLA B*3801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.569697	0.218302	-4.351394	37127.579829
HLA A*0202	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.503004	0.151290	-4.351714	31842.280172
HLA A*6801	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.641462	0.289672	-4.351790	43798.744338
HLA B*7301	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.503892	0.152039	-4.351854	31907.462288
HLA A*2402	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.581263	0.229292	-4.351972	38129.679535
HLA A*0202	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.455366	0.103191	-4.352175	28534.219739
HLA A*3002	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.503545	0.151290	-4.352255	31881.925369
HLA A*6802	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.415439	0.063148	-4.352291	26027.883444
HLA A*2402	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.561596	0.209282	-4.352313	36441.447239
HLA A*2301	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.535232	0.182878	-4.352355	34295.097750
HLA B*1517	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.465861	0.113485	-4.352377	29232.176409
HLA B*1503	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.558175	0.205784	-4.352391	36155.532823
HLA A*0219	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.452871	0.100401	-4.352469	28370.752057
HLA B*4403	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.633025	0.280375	-4.352649	42956.081659
HLA B*4002	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.621569	0.268910	-4.352658	41837.774078
HLA B*3801	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.567446	0.214699	-4.352746	36935.657459
HLA A*8001	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.472301	0.119542	-4.352759	29668.875714
HLA A*2603	1:54-62	9	SQAGHRQPP	0.204349	0.085323	-4.642484	0.289672	-4.352812	43901.937376
HLA A*2602	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.340706	-0.012369	-4.353076	21913.231878
HLA B*0802	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.495707	0.142630	-4.353077	31311.700832
HLA A*0201	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.397298	0.044127	-4.353171	24963.097877
HLA B*1517	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.472905	0.119542	-4.353363	29710.154272
HLA A*2601	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.369300	0.015810	-4.353490	23404.516125
HLA A*6901	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.373362	0.019638	-4.353724	23624.461959
HLA B*1503	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.496668	0.142630	-4.354037	31381.059204
HLA B*3801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.563391	0.209282	-4.354108	36592.377094
HLA A*0201	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.370225	0.015810	-4.354415	23454.455970
HLA A*2403	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.319474	-0.035118	-4.354592	20867.678559
HLA B*1509	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.497419	0.142630	-4.354789	31435.432031
HLA B*3801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.468399	0.113485	-4.354914	29403.470591
HLA A*8001	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.418223	0.063148	-4.355075	26195.276864
HLA B*1517	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.455730	0.100401	-4.355329	28558.156653
HLA B*1501	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.286922	-0.068483	-4.355405	19360.743159

HLA B*4001	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.374541	0.019002	-4.355539	23688.707629
HLA B*1509	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.540166	0.184583	-4.355583	34686.937960
HLA A*0202	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.521805	0.166065	-4.355740	33251.002093
HLA A*2602	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.558769	0.203022	-4.355747	36205.052852
HLA B*0802	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.475781	0.119542	-4.356239	29907.538919
HLA A*0203	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.449083	0.092742	-4.356342	28124.413755
HLA B*1502	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.565085	0.208647	-4.356438	36735.385484
HLA A*0202	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.573585	0.217020	-4.356565	37461.489235
HLA A*3101	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.419717	0.063148	-4.356569	26285.561910
HLA A*0219	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.349599	-0.007282	-4.356881	22366.562098
HLA B*4501	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.637345	0.280375	-4.356970	43385.575457
HLA B*4002	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.637348	0.280375	-4.356972	43385.810169
HLA B*4601	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.373881	0.016895	-4.356987	23652.723914
HLA B*5801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.349785	-0.007282	-4.357066	22376.123190
HLA A*3301	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.626009	0.268910	-4.357099	42267.746791
HLA A*3101	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.372986	0.015810	-4.357176	23604.021891
HLA A*0101	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.376881	0.019638	-4.357243	23816.692796
HLA B*4601	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.373108	0.015810	-4.357298	23610.662972
HLA A*8001	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.460540	0.103191	-4.357349	28876.168498
HLA A*3201	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.540234	0.182878	-4.357357	34692.380309
HLA A*2603	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.638887	0.281226	-4.357661	43539.819509
HLA B*5101	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.509305	0.151290	-4.358016	32307.658085
HLA A*1101	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.471662	0.113485	-4.358177	29625.250369
HLA B*4403	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.612680	0.254408	-4.358273	40990.240710
HLA A*0203	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.411649	0.053318	-4.358331	25801.748278
HLA A*2403	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.411668	0.053318	-4.358350	25802.864979
HLA B*5101	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.510433	0.152039	-4.358395	32391.661913
HLA B*4002	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.639674	0.281226	-4.358448	43618.798830
HLA B*4601	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.411929	0.053318	-4.358611	25818.364193
HLA A*0101	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.375582	0.016895	-4.358688	23745.547616
HLA B*4601	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.378340	0.019638	-4.358702	23896.840510
HLA A*2501	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.459236	0.100401	-4.358834	28789.598164
HLA A*2602	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.530984	0.171766	-4.359218	33961.289832
HLA A*6901	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.376191	0.016895	-4.359296	23778.842278
HLA A*2601	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.379059	0.019638	-4.359421	23936.432725
HLA A*0216	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.459825	0.100401	-4.359424	28828.717599
HLA B*1509	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.541966	0.182285	-4.359681	34830.978010
HLA B*4403	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.324718	-0.035118	-4.359836	21121.180540
HLA B*1501	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.352564	-0.007282	-4.359846	22519.787343
HLA A*2501	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.457753	0.097839	-4.359914	28691.488389
HLA B*5701	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.413425	0.053318	-4.360107	25907.490322
HLA A*0219	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.413449	0.053318	-4.360131	25908.891927
HLA B*0702	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.460594	0.100401	-4.360192	28879.761710
HLA B*4402	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.423366	0.063148	-4.360218	26507.331881
HLA A*0301	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.348168	-0.012369	-4.360538	22292.993976
HLA B*4601	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.404721	0.044127	-4.360593	25393.379470
HLA A*0250	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.512087	0.151290	-4.360798	32515.262786
HLA B*5401	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.543967	0.182878	-4.361090	34991.892404
HLA A*6801	1:18-26	9	ADGLVDRGG	1.009719	-0.685524	-4.685357	0.324195	-4.361163	48457.063042
HLA A*2402	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.564293	0.203022	-4.361271	36668.473017
HLA A*0219	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.454013	0.092742	-4.361271	28445.442757
HLA A*2501	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.474780	0.113485	-4.361295	29838.692985
HLA B*7301	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.543932	0.182632	-4.361300	34989.052985
HLA B*4002	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.636316	0.274750	-4.361566	43282.893674
HLA B*4001	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.385737	0.023895	-4.361842	24307.296797
HLA B*1509	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.544755	0.182878	-4.361877	35055.366160

HLA B*2705	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.465307	0.103191	-4.362116	29194.878515
HLA B*7301	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.545083	0.182878	-4.362206	35081.926607
HLA B*5701	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.381275	0.019002	-4.362273	24058.857056
HLA A*2402	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.580732	0.218302	-4.362430	38083.089343
HLA B*0802	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.475959	0.113485	-4.362475	29919.837979
HLA A*0211	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.375718	0.013159	-4.362559	23752.999511
HLA B*4601	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.350988	-0.011592	-4.362579	22438.187907
HLA B*5101	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.482573	0.119542	-4.363031	30378.969489
HLA A*2603	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.643419	0.280375	-4.363043	43996.566050
HLA A*2601	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.382081	0.019002	-4.363079	24103.541924
HLA B*5801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.351657	-0.011592	-4.363249	22472.810202
HLA B*4002	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.631591	0.268222	-4.363369	42814.558842
HLA A*2301	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.546009	0.182632	-4.363377	35156.783355
HLA B*1501	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.351096	-0.012369	-4.363465	22443.772455
HLA A*6801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.338063	-0.025677	-4.363741	21780.270224
HLA A*0101	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.379600	0.015810	-4.363790	23966.234755
HLA B*1501	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.215841	-0.147950	-4.363791	16437.686918
HLA B*7301	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.581117	0.217020	-4.364097	38116.892484
HLA A*3002	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.578822	0.214699	-4.364123	37915.958591
HLA B*2705	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.377307	0.013159	-4.364148	23840.025284
HLA A*2403	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.427409	0.063148	-4.364262	26755.278707
HLA A*2501	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.463427	0.099112	-4.364315	29068.798698
HLA B*5301	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.606161	0.241837	-4.364323	40379.473111
HLA A*0301	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.357172	-0.007282	-4.364453	22759.966851
HLA A*3101	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.346312	-0.018628	-4.364941	22197.921207
HLA B*1502	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.353455	-0.011592	-4.365046	22566.008112
HLA B*0702	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.380932	0.015810	-4.365122	24039.861819
HLA A*0216	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.462981	0.097839	-4.365141	29038.934843
HLA B*5701	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.381000	0.015810	-4.365190	24043.633652
HLA B*5301	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.583617	0.218302	-4.365315	38336.930645
HLA A*0201	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.389350	0.023895	-4.365456	24510.387186
HLA A*6801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.464809	0.099112	-4.365696	29161.414205
HLA A*3301	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.646085	0.280375	-4.365710	44267.545916
HLA B*0802	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.469002	0.103191	-4.365811	29444.379889
HLA B*3801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.571680	0.205784	-4.365896	37297.489975
HLA B*4001	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.419271	0.053318	-4.365953	26258.557416
HLA B*5101	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.479728	0.113485	-4.366243	30180.595964
HLA B*3901	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.469564	0.103191	-4.366373	29482.475020
HLA B*4002	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.616677	0.250113	-4.366564	41369.182862
HLA B*4501	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.635534	0.268910	-4.366623	43204.990032
HLA A*2301	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.532720	0.166065	-4.366655	34097.335715
HLA A*2403	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.359476	-0.007282	-4.366758	22881.077388
HLA A*1101	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.465436	0.097839	-4.367597	29203.566566
HLA B*0803	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.528797	0.161134	-4.367663	33790.670202
HLA A*3201	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.465622	0.097839	-4.367782	29216.050290
HLA B*5801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.355515	-0.012369	-4.367885	22673.326306
HLA B*2705	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.487784	0.119542	-4.368242	30745.686562
HLA A*6801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.387360	0.019002	-4.368358	24398.333197
HLA B*4501	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.610260	0.241837	-4.368423	40762.470650
HLA A*2501	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.511056	0.142630	-4.368426	32438.132570
HLA B*5701	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.431674	0.063148	-4.368526	27019.281412
HLA B*1801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.529767	0.161134	-4.368633	33866.252568
HLA A*6801	1:294-302	9	GGIEVTLAD	1.217486	-0.948576	-4.637587	0.268910	-4.368677	43409.757442
HLA B*4601	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.259205	-0.109508	-4.368713	18163.734662

HLA B*0801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.361617	-0.007282	-4.368898	22994.123035
HLA B*0702	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.413120	0.044127	-4.368992	25889.276363
HLA A*3002	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.587311	0.218302	-4.369009	38664.351434
HLA B*3501	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.136033	-0.233064	-4.369097	13678.340098
HLA A*1101	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.488780	0.119542	-4.369238	30816.291748
HLA A*0202	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.577948	0.208647	-4.369301	37839.730260
HLA A*3101	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.422828	0.053318	-4.369510	26474.513219
HLA B*4801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.422922	0.053318	-4.369604	26480.242806
HLA B*1501	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.254443	-0.115163	-4.369606	17965.642069
HLA B*5801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.351065	-0.018628	-4.369694	22442.194072
HLA A*2601	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.393788	0.023895	-4.369894	24762.149936
HLA B*7301	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.385706	0.015810	-4.369896	24305.587360
HLA B*3801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.552708	0.182632	-4.370076	35703.230563
HLA B*4501	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.586954	0.216823	-4.370130	38632.570685
HLA B*0803	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.522218	0.152039	-4.370180	33282.676795
HLA B*0802	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.469573	0.099112	-4.370461	29483.113014
HLA B*5801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.359904	-0.010665	-4.370569	22903.617187
HLA B*1509	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.511779	0.141159	-4.370621	32492.227530
HLA A*0206	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.363398	-0.007282	-4.370679	23088.608538
HLA B*5701	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.414936	0.044127	-4.370809	25997.767976
HLA A*3301	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.612880	0.241837	-4.371043	41009.094020
HLA A*2602	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.625610	0.254408	-4.371202	42228.891811
HLA A*3101	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.363957	-0.007282	-4.371239	23118.355506
HLA A*0250	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.577053	0.205784	-4.371269	37761.816552
HLA B*0702	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.424611	0.053318	-4.371293	26583.443860
HLA A*0212	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.434444	0.063148	-4.371296	27192.168167
HLA A*2403	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.336463	-0.034919	-4.371382	21700.176408
HLA B*1503	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.415608	0.044127	-4.371481	26038.023592
HLA A*3002	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.588626	0.217020	-4.371606	38781.664165
HLA A*6801	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.574870	0.203022	-4.371848	37572.509811
HLA A*2601	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.353511	-0.018628	-4.372139	22568.938212
HLA B*4001	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.388027	0.015810	-4.372217	24435.847816
HLA B*7301	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.586935	0.214699	-4.372235	38630.898738
HLA B*1801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.523705	0.151290	-4.372416	33396.847359
HLA A*0212	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.416703	0.044127	-4.372575	26103.748479
HLA A*0202	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.544458	0.171766	-4.372692	35031.478951
HLA B*0801	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.392581	0.019638	-4.372943	24693.389891
HLA A*2501	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.492695	0.119542	-4.373152	31095.290545
HLA A*3002	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.556070	0.182878	-4.373192	35980.701599
HLA B*3901	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.389183	0.015810	-4.373373	24500.974502
HLA B*4801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.436631	0.063148	-4.373483	27329.469903
HLA B*1517	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.417678	0.044127	-4.373550	26162.419946
HLA A*2402	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.590638	0.217020	-4.373617	38961.673298
HLA A*2402	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.545556	0.171766	-4.373789	35120.095012
HLA A*0250	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.590882	0.217020	-4.373862	38983.600412
HLA B*3901	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.227269	-0.146721	-4.373989	16875.964356
HLA A*6802	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.398229	0.023895	-4.374334	25016.634049
HLA B*4403	1:140-148	9	NPAPARPAE	1.010420	-0.729194	-4.655573	0.281226	-4.374347	45245.216103
HLA A*0301	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.362841	-0.011592	-4.374433	23059.024593
HLA B*3501	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.398485	0.023895	-4.374590	25031.390156
HLA B*3901	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.473744	0.099112	-4.374631	29767.589842
HLA B*5801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.349064	-0.025677	-4.374741	22338.990964
HLA A*0101	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.356126	-0.018628	-4.374754	22705.240392

HLA A*0201	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.394524	0.019638	-4.374886	24804.115088
HLA B*5701	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.388138	0.013159	-4.374979	24442.061782
HLA B*3801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.557294	0.182285	-4.375009	36082.258140
HLA B*1801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.467778	0.092742	-4.375037	29361.506212
HLA B*3501	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.438238	0.063148	-4.375090	27430.786232
HLA A*0211	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.536369	0.161134	-4.375235	34385.013231
HLA B*1502	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.584924	0.209282	-4.375641	38452.417836
HLA B*5401	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.536813	0.161134	-4.375679	34420.188823
HLA A*2601	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.363386	-0.012369	-4.375755	23087.984013
HLA B*3801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.541827	0.166065	-4.375762	34819.862312
HLA A*2602	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.584635	0.208647	-4.375988	38426.839479
HLA B*4002	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.579590	0.203022	-4.376568	37983.092565
HLA B*4601	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.389731	0.013159	-4.376572	24531.877555
HLA A*0301	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.365916	-0.010665	-4.376581	23222.897663
HLA B*4601	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.358064	-0.018628	-4.376693	22806.803958
HLA B*5301	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.558997	0.182285	-4.376712	36224.056774
HLA B*4002	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.631272	0.254408	-4.376864	42783.069833
HLA B*1517	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.469656	0.092742	-4.376914	29488.696056
HLA B*1801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.519747	0.142630	-4.377116	33093.796301
HLA A*6801	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.619163	0.241837	-4.377325	41606.645040
HLA B*5701	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.396995	0.019638	-4.377357	24945.682815
HLA B*0702	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.470100	0.092742	-4.377358	29518.862755
HLA A*3201	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.596018	0.218302	-4.377716	39447.357957
HLA A*0250	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.560151	0.182285	-4.377866	36320.405033
HLA A*0216	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.370620	-0.007282	-4.377902	23475.782509
HLA A*3201	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.583833	0.205784	-4.378050	38356.016061
HLA B*3501	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.478562	0.100401	-4.378161	30099.720774
HLA B*4001	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.391606	0.013159	-4.378447	24638.012849
HLA A*0211	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.519639	0.141159	-4.378480	33085.561772
HLA B*1502	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.519730	0.141159	-4.378571	33092.543088
HLA A*2602	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.560865	0.182285	-4.378580	36380.186945
HLA B*0802	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.423202	0.044127	-4.379074	26497.295661
HLA B*4501	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.653848	0.274750	-4.379098	45065.909982
HLA A*2902	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.471881	0.092742	-4.379139	29640.159166
HLA A*3101	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.368581	-0.010665	-4.379246	23365.803731
HLA A*3002	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.520552	0.141159	-4.379394	33155.261894
HLA A*0202	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.588730	0.209282	-4.379447	38790.896662
HLA A*0202	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.594277	0.214699	-4.379577	39289.540769
HLA A*0201	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.398581	0.019002	-4.379579	25036.942870
HLA A*0250	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.597968	0.218302	-4.379666	39624.883063
HLA A*2301	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.540906	0.161134	-4.379772	34746.098888
HLA B*4501	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.532009	0.152039	-4.379970	34041.489269
HLA B*0803	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.521182	0.141159	-4.380023	33203.366924
HLA A*6802	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.433363	0.053318	-4.380045	27124.583253
HLA A*2501	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.233570	-0.146721	-4.380291	17122.608158
HLA A*0101	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.368748	-0.011592	-4.380339	23374.780309
HLA A*3002	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.563029	0.182632	-4.380397	36561.903841
HLA A*3001	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.270962	-0.109508	-4.380470	18662.162728
HLA A*0216	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.424757	0.044127	-4.380629	26592.361792
HLA B*0803	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.494194	0.113485	-4.380709	31202.801660
HLA A*0201	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.397688	0.016895	-4.380794	24985.525846
HLA B*2705	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.481227	0.100401	-4.380825	30284.944547
HLA A*0250	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.595748	0.214699	-4.381048	39422.823919
HLA A*0211	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.480263	0.099112	-4.381151	30217.845330
HLA B*1502	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.374083	-0.007282	-4.381365	23663.730915

HLA B*1509	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.484664	0.103191	-4.381473	30525.590885
HLA B*3501	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.342328	-0.039278	-4.381605	21995.182964
HLA A*2902	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.425882	0.044127	-4.381755	26661.360921
HLA B*0803	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.524403	0.142630	-4.381773	33450.550444
HLA B*1801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.374574	-0.007282	-4.381856	23690.501843
HLA B*4501	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.598908	0.217020	-4.381888	39710.722395
HLA B*4002	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.599037	0.216823	-4.382214	39722.539837
HLA A*0219	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.445409	0.063148	-4.382261	27887.455092
HLA B*5701	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.406297	0.023895	-4.382402	25485.725851
HLA A*2902	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.363776	-0.018628	-4.382404	23108.727295
HLA B*4001	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.370874	-0.011592	-4.382465	23489.502666
HLA B*4801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.406443	0.023895	-4.382548	25494.275531
HLA A*2402	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.597416	0.214699	-4.382716	39574.539008
HLA A*2402	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.565009	0.182285	-4.382725	36729.026535
HLA B*1503	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.375594	-0.007282	-4.382876	23746.189929
HLA A*0219	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.398739	0.015810	-4.382929	25046.019470
HLA A*2601	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.399885	0.016895	-4.382991	25112.228969
HLA A*0202	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.535129	0.152039	-4.383090	34286.935284
HLA B*1509	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.535234	0.152039	-4.383196	34295.283283
HLA A*3002	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.496837	0.113485	-4.383352	31393.284884
HLA B*0702	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.344219	-0.039278	-4.383497	22091.180003
HLA B*4403	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.652065	0.268222	-4.383842	44881.243973
HLA B*1503	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.407737	0.023895	-4.383843	25570.383492
HLA A*6801	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.589639	0.205784	-4.383855	38872.195409
HLA A*0250	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.535902	0.152039	-4.383863	34348.015347
HLA A*2402	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.590140	0.205784	-4.384356	38917.013906
HLA B*3801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.567352	0.182878	-4.384474	36927.665611
HLA A*0250	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.593281	0.208647	-4.384634	39199.521977
HLA B*1801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.482660	0.097839	-4.384821	30385.050931
HLA A*6901	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.372453	-0.012369	-4.384822	23575.052885
HLA A*0203	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.372537	-0.012369	-4.384907	23579.644715
HLA A*0212	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.400726	0.015810	-4.384916	25160.911963
HLA A*3101	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.404605	0.019638	-4.384967	25386.648969
HLA B*5301	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.484166	0.099112	-4.385054	30490.601260
HLA B*4403	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.635529	0.250113	-4.385416	43204.522567
HLA A*3301	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.635564	0.250113	-4.385451	43208.028684
HLA B*0802	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.483320	0.097839	-4.385481	30431.276770
HLA B*5401	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.537565	0.152039	-4.385526	34479.827440
HLA B*3801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.546690	0.161134	-4.385556	35211.982991
HLA B*1501	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.404704	0.019002	-4.385702	25392.417861
HLA B*7301	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.591667	0.205784	-4.385883	39054.103673
HLA B*5801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.276521	-0.109508	-4.386029	18902.569935
HLA A*6801	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.568320	0.182285	-4.386035	37010.064531
HLA B*4403	1:289-297	9	ITDLIGGIE	1.007859	-0.733109	-4.660847	0.274750	-4.386097	45798.078872
HLA A*0203	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.449485	0.063148	-4.386337	28150.443436
HLA A*6801	1:152-160	9	GSRGDSAAG	0.846192	-0.577970	-4.654755	0.268222	-4.386533	45160.115717
HLA B*3901	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.506134	0.119542	-4.386592	32072.563473
HLA B*5801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.351812	-0.034919	-4.386731	22480.835612
HLA A*6801	1:35-43	9	GRIPDAGDP	0.257826	0.022549	-4.667198	0.280375	-4.386823	46472.701448
HLA A*6801	1:260-268	9	IFGGAFLIG	0.843514	-0.589106	-4.641351	0.254408	-4.386944	43787.609275
HLA A*1101	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.431223	0.044127	-4.387095	26991.231089
HLA A*3301	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.603924	0.216823	-4.387100	40172.044773
HLA B*0803	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.506857	0.119542	-4.387315	32126.048797
HLA B*3501	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.264663	-0.122654	-4.387317	18393.441810

HLA B*0802	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.480059	0.092742	-4.387317	30203.626335
HLA A*3001	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.263366	-0.123980	-4.387346	18338.596165
HLA A*2402	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.596281	0.208647	-4.387634	39471.266653
HLA A*0301	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.362005	-0.025677	-4.387682	23014.657482
HLA B*4002	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.629529	0.241837	-4.387691	42611.676925
HLA B*0802	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.488118	0.100401	-4.387716	30769.314603
HLA B*1517	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.406922	0.019002	-4.387920	25522.426988
HLA A*3201	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.597235	0.209282	-4.387953	39558.057214
HLA A*0250	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.597442	0.209282	-4.388159	39576.894111
HLA A*0211	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.501733	0.113485	-4.388248	31749.222023
HLA B*3501	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.405298	0.016895	-4.388404	25427.196308
HLA B*4501	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.539727	0.151290	-4.388437	34651.864688
HLA A*6802	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.208910	-0.179556	-4.388466	16177.437238
HLA A*0206	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.491755	0.103191	-4.388564	31028.074468
HLA B*4601	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.349491	-0.039278	-4.388769	22360.996762
HLA A*3002	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.594787	0.205784	-4.389003	39335.691650
HLA B*4001	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.408877	0.019638	-4.389239	25637.563062
HLA B*3901	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.482044	0.092742	-4.389303	30342.013942
HLA A*3002	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.561098	0.171766	-4.389331	36399.676629
HLA A*0101	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.382175	-0.007282	-4.389456	24108.758388
HLA A*2501	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.482449	0.092742	-4.389707	30370.260354
HLA B*3801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.561567	0.171766	-4.389801	36439.081586
HLA B*0801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.378263	-0.011592	-4.389855	23892.574675
HLA A*0101	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.364258	-0.025677	-4.389935	23134.369721
HLA A*2602	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.599227	0.209282	-4.389945	39739.950108
HLA A*2603	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.378540	-0.011592	-4.390132	23907.831774
HLA A*8001	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.407129	0.016895	-4.390234	25534.580349
HLA B*0802	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.409380	0.019002	-4.390377	25667.261274
HLA A*2902	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.414299	0.023895	-4.390405	25959.681095
HLA B*4403	1:250-258	9	SSAELVSSG	0.787858	-0.571035	-4.607310	0.216823	-4.390486	40486.435833
HLA B*1517	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.406386	0.015810	-4.390576	25490.965637
HLA A*3002	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.312651	-0.077944	-4.390595	20542.402477
HLA A*2602	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.573277	0.182632	-4.390646	37434.949853
HLA B*4801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.211146	-0.179556	-4.390703	16260.969429
HLA A*2403	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.406548	0.015810	-4.390738	25500.482741
HLA B*4001	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.383469	-0.007282	-4.390751	24180.730169
HLA B*4601	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.409758	0.019002	-4.390755	25689.626996
HLA A*2301	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.542882	0.152039	-4.390843	34904.543964
HLA A*0250	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.562660	0.171766	-4.390894	36530.863077
HLA B*3501	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.444272	0.053318	-4.390954	27814.530474
HLA A*2301	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.490178	0.099112	-4.391066	30915.645636
HLA B*4002	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.573397	0.182285	-4.391112	37445.279743
HLA A*2602	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.609473	0.218302	-4.391171	40688.663201
HLA A*3002	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.600562	0.209282	-4.391279	39862.251513
HLA A*0211	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.489215	0.097839	-4.391376	30847.149040
HLA A*0250	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.594580	0.203022	-4.391558	39316.969554
HLA B*5401	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.557724	0.166065	-4.391659	36117.997614
HLA A*3201	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.608740	0.217020	-4.391720	40620.043328
HLA B*0702	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.455018	0.063148	-4.391870	28511.382572
HLA A*0101	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.381282	-0.010665	-4.391947	24059.247526
HLA B*1503	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.489819	0.097839	-4.391980	30890.066941
HLA A*0101	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.269745	-0.122654	-4.392399	18609.938536
HLA B*4501	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.574696	0.182285	-4.392411	37557.471351
HLA B*2705	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.436542	0.044127	-4.392414	27323.852203
HLA B*5801	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.357322	-0.035118	-4.392440	22767.848465

HLA A*2603	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.642662	0.250113	-4.392549	43919.991438
HLA A*3001	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.284307	-0.108442	-4.392749	19244.518382
HLA B*1502	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.405968	0.013159	-4.392809	25466.430665
HLA B*5301	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.485721	0.092742	-4.392980	30599.994442
HLA A*2501	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.496308	0.103191	-4.393117	31355.095439
HLA A*2602	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.545558	0.152039	-4.393519	35120.285008
HLA A*0211	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.437907	0.044127	-4.393780	27409.870161
HLA B*4001	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.410822	0.016895	-4.393928	25752.661252
HLA A*2301	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.545434	0.151290	-4.394144	35110.216619
HLA A*0216	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.457417	0.063148	-4.394269	28669.300831
HLA A*2601	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.387027	-0.007282	-4.394308	24379.597491
HLA B*5101	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.497746	0.103191	-4.394555	31459.079567
HLA B*5101	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.495032	0.100401	-4.394631	31263.122811
HLA A*0201	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.387407	-0.007282	-4.394689	24400.973186
HLA B*0702	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.376315	-0.018628	-4.394943	23785.661224
HLA B*1517	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.419358	0.023895	-4.395463	26263.814010
HLA A*0101	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.383162	-0.012369	-4.395531	24163.599466
HLA A*6801	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.578512	0.182878	-4.395634	37888.892267
HLA B*4002	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.610397	0.214699	-4.395697	40775.262843
HLA A*3002	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.494884	0.099112	-4.395772	31252.469435
HLA B*1502	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.614123	0.218302	-4.395821	41126.623226
HLA B*4801	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.415533	0.019638	-4.395895	26033.516372
HLA A*2403	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.384339	-0.011592	-4.395930	24229.180219
HLA B*5301	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.598999	0.203022	-4.395977	39719.101673
HLA A*3301	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.599068	0.203022	-4.396045	39725.333564
HLA B*5401	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.494074	0.097839	-4.396235	31194.193859
HLA B*4402	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.415958	0.019638	-4.396320	26059.020614
HLA A*0216	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.489128	0.092742	-4.396386	30840.975111
HLA A*0211	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.539221	0.142630	-4.396591	34611.583628
HLA A*0212	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.416299	0.019638	-4.396661	26079.470213
HLA A*1101	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.450059	0.053318	-4.396740	28187.626922
HLA A*3101	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.358215	-0.039278	-4.397492	22814.701792
HLA A*3002	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.495519	0.097839	-4.397680	31298.152337
HLA B*1502	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.600757	0.203022	-4.397735	39880.154512
HLA A*0211	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.517465	0.119542	-4.397923	32920.410308
HLA A*2402	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.580826	0.182878	-4.397949	38091.331247
HLA A*3301	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.627360	0.229292	-4.398069	42399.433202
HLA A*2403	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.422306	0.023895	-4.398412	26442.736536
HLA B*4002	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.627778	0.229292	-4.398487	42440.281836
HLA B*5101	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.496327	0.097839	-4.398488	31356.452489
HLA A*3001	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.237212	-0.161502	-4.398714	17266.790510
HLA A*6801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.541435	0.142630	-4.398805	34788.418461
HLA B*0702	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.388286	-0.010665	-4.398951	24450.393619
HLA B*4801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.443153	0.044127	-4.399026	27742.997218
HLA A*0301	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.359749	-0.039278	-4.399027	22895.440849
HLA A*3002	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.330629	-0.068483	-4.399113	21410.632301
HLA B*3801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.583789	0.184583	-4.399206	38352.073729
HLA B*0803	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.502457	0.103191	-4.399266	31802.168131
HLA A*6901	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.360078	-0.039278	-4.399356	22912.788069
HLA B*4402	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.443492	0.044127	-4.399364	27764.618100
HLA A*0212	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.423375	0.023895	-4.399481	26507.905494
HLA B*5401	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.360313	-0.039278	-4.399591	22925.186987
HLA B*2705	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.497553	0.097839	-4.399714	31445.127071
HLA B*5301	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.609074	0.209282	-4.399792	40651.259807
HLA A*0201	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.387558	-0.012369	-4.399927	24409.423068

HLA A*2603	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.551972	0.152039	-4.399933	35642.825607
HLA A*0101	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.360889	-0.039278	-4.400166	22955.592699
HLA A*2902	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.387800	-0.012369	-4.400169	24423.028243
HLA B*1503	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.322486	-0.077944	-4.400430	21012.908921
HLA B*5301	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.609100	0.208647	-4.400453	40653.678986
HLA A*0250	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.583150	0.182632	-4.400518	38295.680543
HLA A*2501	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.381921	-0.018628	-4.400549	24094.676525
HLA A*2402	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.583281	0.182632	-4.400650	38307.284122
HLA B*4001	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.382447	-0.018628	-4.401076	24123.892518
HLA A*2301	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.544050	0.142630	-4.401420	34998.518610
HLA A*2601	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.362357	-0.039278	-4.401635	23033.341073
HLA A*0219	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.446109	0.044127	-4.401982	27932.450027
HLA B*3801	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.554113	0.152039	-4.402074	35818.921610
HLA A*0250	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.586695	0.184583	-4.402112	38609.587752
HLA B*4501	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.573982	0.171766	-4.402216	37495.754860
HLA A*0250	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.389942	-0.012369	-4.402312	24543.824790
HLA A*0250	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.568571	0.166065	-4.402506	37031.494310
HLA A*0301	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.367601	-0.034919	-4.402520	23313.151670
HLA B*1502	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.574288	0.171766	-4.402521	37522.134359
HLA A*0216	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.455991	0.053318	-4.402673	28575.310910
HLA A*2403	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.415923	0.013159	-4.402764	26056.906054
HLA B*7301	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.574910	0.171766	-4.403144	37575.965442
HLA A*2902	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.456616	0.053318	-4.403298	28616.461256
HLA A*2601	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.392672	-0.010665	-4.403337	24698.600392
HLA A*0219	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.427384	0.023895	-4.403489	26753.686580
HLA B*5301	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.546159	0.142630	-4.403529	35168.957898
HLA B*5301	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.588288	0.184583	-4.403705	38751.464081
HLA A*6802	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.396464	-0.007282	-4.403746	24915.201989
HLA A*3201	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.618495	0.214699	-4.403796	41542.769318
HLA A*2301	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.545053	0.141159	-4.403894	35079.459433
HLA A*6801	1:123-131	9	ASELPDLSG	0.860488	-0.610375	-4.654013	0.250113	-4.403899	45082.979324
HLA A*0301	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.368886	-0.035118	-4.404004	23382.242343
HLA A*6802	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.421122	0.016895	-4.404228	26370.736392
HLA A*3301	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.587290	0.182878	-4.404412	38662.468951
HLA B*1502	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.555705	0.151290	-4.404416	35950.543246
HLA A*6901	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.369365	-0.035118	-4.404483	23408.061637
HLA B*1509	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.524114	0.119542	-4.404572	33428.299304
HLA B*5701	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.421540	0.016895	-4.404646	26396.142594
HLA B*4403	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.634162	0.229292	-4.404870	43068.704658
HLA B*4402	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.428803	0.023895	-4.404908	26841.249186
HLA B*4801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.397696	-0.007282	-4.404977	24985.931356
HLA A*2602	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.393462	-0.011592	-4.405053	24743.536428
HLA A*2602	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.610991	0.205784	-4.405208	40831.110235
HLA B*4002	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.257363	-0.147950	-4.405313	18086.858994
HLA B*2705	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.458813	0.053318	-4.405495	28761.577073
HLA A*2603	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.647382	0.241837	-4.405545	44399.937844
HLA A*2602	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.620283	0.214699	-4.405584	41714.150350
HLA B*1801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.519490	0.113485	-4.406006	33074.287373
HLA B*4601	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.393645	-0.012369	-4.406014	24753.979695
HLA B*2705	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.498890	0.092742	-4.406149	31542.071440
HLA A*8001	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.459635	0.053318	-4.406317	28816.087593
HLA A*0203	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.380685	-0.025677	-4.406363	24026.210133
HLA B*5801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.367145	-0.039278	-4.406423	23288.696922
HLA A*3301	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.558497	0.152039	-4.406458	36182.339602
HLA A*0212	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.419748	0.013159	-4.406589	26287.410601

HLA B*1801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.259943	-0.146721	-4.406664	18194.615714
HLA A*0201	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.396096	-0.010665	-4.406761	24894.049182
HLA B*1502	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.572850	0.166065	-4.406785	37398.109547
HLA B*4601	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.399530	-0.007282	-4.406812	25091.723335
HLA B*4402	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.423768	0.016895	-4.406873	26531.864923
HLA A*3001	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.300518	-0.106651	-4.407169	19976.458313
HLA A*3201	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.616040	0.208647	-4.407393	41308.576770
HLA A*0202	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.506599	0.099112	-4.407486	32106.936664
HLA B*1502	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.613367	0.205784	-4.407583	41055.043657
HLA B*5301	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.590518	0.182878	-4.407640	38950.925085
HLA A*0201	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.382046	-0.025677	-4.407723	24101.586041
HLA A*3002	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.569013	0.161134	-4.407879	37069.176690
HLA A*0101	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.373068	-0.034919	-4.407987	23608.491644
HLA A*0211	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.508638	0.100401	-4.408237	32258.058436
HLA A*2902	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.471568	0.063148	-4.408420	29618.840290
HLA B*0702	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.427698	0.019002	-4.408696	26773.088032
HLA B*1503	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.528400	0.119542	-4.408858	33759.790482
HLA B*5401	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.522390	0.113485	-4.408905	33295.823449
HLA B*3501	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.428561	0.019638	-4.408923	26826.296909
HLA A*6802	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.424844	0.015810	-4.409034	26597.685208
HLA A*6901	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.374375	-0.034919	-4.409294	23679.610493
HLA A*3001	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.286664	-0.122654	-4.409318	19349.225245
HLA A*8001	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.428986	0.019638	-4.409348	26852.577814
HLA A*2402	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.575441	0.166065	-4.409376	37621.935227
HLA B*0702	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.398071	-0.011592	-4.409663	25007.568098
HLA B*0702	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.433643	0.023895	-4.409748	27142.051053
HLA B*3901	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.507611	0.097839	-4.409772	32181.886540
HLA B*5701	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.397658	-0.012369	-4.410027	24983.768712
HLA B*5701	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.402888	-0.007282	-4.410170	25286.452442
HLA A*8001	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.454485	0.044127	-4.410357	28476.390806
HLA A*2402	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.529988	0.119542	-4.410446	33883.478939
HLA B*5301	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.582426	0.171766	-4.410660	38231.923656
HLA A*1101	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.503521	0.092742	-4.410779	31880.200639
HLA B*0702	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.398953	-0.012369	-4.411322	25058.352659
HLA A*0202	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.594042	0.182632	-4.411410	39268.291311
HLA A*0206	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.554056	0.142630	-4.411426	35814.271278
HLA A*2403	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.428408	0.016895	-4.411513	26816.865294
HLA B*1501	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.333790	-0.077944	-4.411734	21566.990670
HLA A*8001	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.404528	-0.007282	-4.411809	25382.117188
HLA A*0212	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.428739	0.016895	-4.411845	26837.328851
HLA B*1517	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.465267	0.053318	-4.411949	29192.193640
HLA A*2501	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.425168	0.013159	-4.412009	26617.549515
HLA B*0801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.296849	-0.115163	-4.412012	19808.363531
HLA A*3001	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.296881	-0.115163	-4.412045	19809.863843
HLA A*6802	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.431686	0.019638	-4.412047	27020.012278
HLA B*3901	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.456393	0.044127	-4.412265	28601.757905
HLA A*0216	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.428262	0.015810	-4.412452	26807.872073
HLA B*1503	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.513076	0.100401	-4.412675	32589.402753
HLA B*0801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.387139	-0.025677	-4.412817	24385.929078
HLA B*0803	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.510682	0.097839	-4.412843	32410.242182
HLA B*4403	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.584809	0.171766	-4.413042	38442.226044
HLA A*3301	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.618836	0.205784	-4.413052	41575.369661
HLA A*8001	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.428927	0.015810	-4.413117	26848.946323

HLA A*2403	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.394533	-0.018628	-4.413161	24804.651844
HLA B*4501	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.627915	0.214699	-4.413215	42453.600564
HLA A*2501	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.400851	-0.012369	-4.413220	25168.127238
HLA B*1501	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.378258	-0.035118	-4.413376	23892.316164
HLA B*5401	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.564789	0.151290	-4.413499	36710.353487
HLA A*0203	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.432515	0.019002	-4.413513	27071.661450
HLA A*3101	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.402103	-0.011592	-4.413695	25240.803530
HLA B*1509	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.511657	0.097839	-4.413818	32483.088289
HLA B*4801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.433100	0.019002	-4.414098	27108.153240
HLA A*6801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.298942	-0.115163	-4.414105	19904.074516
HLA A*1101	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.431608	0.016895	-4.414713	27015.188925
HLA A*2301	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.528266	0.113485	-4.414781	33749.381793
HLA B*1509	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.404248	-0.010665	-4.414913	25365.782028
HLA B*3501	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.459165	0.044127	-4.415038	28784.926087
HLA A*3002	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.557670	0.142630	-4.415039	36113.503824
HLA B*4601	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.404481	-0.010665	-4.415146	25379.371048
HLA B*1517	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.478313	0.063148	-4.415166	30082.465090
HLA B*3901	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.515600	0.100401	-4.415198	32779.305538
HLA A*3201	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.600254	0.184583	-4.415671	39834.011323
HLA A*2601	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.380718	-0.035118	-4.415836	24028.029910
HLA A*0211	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.519324	0.103191	-4.416133	33061.585908
HLA B*0802	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.431977	0.015810	-4.416167	27038.144093
HLA B*7301	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.557740	0.141159	-4.416581	36119.365401
HLA B*4402	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.435762	0.019002	-4.416760	27274.820337
HLA A*8001	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.441046	0.023895	-4.417151	27608.695716
HLA A*0219	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.391566	-0.025677	-4.417243	24635.747042
HLA A*0202	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.560148	0.142630	-4.417518	36320.208544
HLA B*5801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.339583	-0.077944	-4.417527	21856.639063
HLA B*4801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.434679	0.016895	-4.417784	27206.882808
HLA B*4001	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.405421	-0.012369	-4.417790	25434.350346
HLA B*7301	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.600473	0.182285	-4.418188	39854.057641
HLA A*2902	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.434066	0.015810	-4.418255	27168.494313
HLA A*1101	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.518790	0.100401	-4.418389	33021.009718
HLA A*2402	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.561086	0.142630	-4.418456	36398.692051
HLA A*2902	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.437482	0.019002	-4.418479	27383.043828
HLA B*3901	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.471956	0.053318	-4.418638	29645.290809
HLA A*2301	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.538404	0.119542	-4.418862	34546.483726
HLA B*5401	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.522068	0.103191	-4.418877	33271.155232
HLA A*0202	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.580023	0.161134	-4.418889	38020.920504
HLA A*0212	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.438391	0.019002	-4.419389	27440.433767
HLA B*3801	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.562033	0.142630	-4.419402	36478.134514
HLA A*0202	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.443306	0.023895	-4.419411	27752.754559
HLA A*0101	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.384510	-0.035118	-4.419628	24238.750743
HLA A*6801	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.649006	0.229292	-4.419714	44566.225793
HLA B*1517	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.439538	0.019638	-4.419899	27512.972933
HLA A*8001	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.401323	-0.018628	-4.419951	25195.509635
HLA A*2902	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.408477	-0.011592	-4.420069	25613.995517
HLA B*1503	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.311930	-0.108442	-4.420372	20508.313232
HLA A*0203	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.437336	0.016895	-4.420441	27373.860736
HLA A*3301	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.638757	0.218302	-4.420455	43526.866428
HLA A*2501	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.483647	0.063148	-4.420499	30454.168923
HLA B*4403	1:9-17	9	ALSKGDGPN	0.754582	-0.512745	-4.662821	0.241837	-4.420983	46006.672995
HLA B*2705	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.444995	0.023895	-4.421101	27860.914954
HLA B*1502	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.604006	0.182632	-4.421374	40179.651914
HLA B*7301	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.411219	-0.010665	-4.421884	25776.216937
HLA B*2705	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.441577	0.019638	-4.421939	27642.471716

HLA B*4801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.435153	0.013159	-4.421994	27236.630676
HLA B*1801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.525759	0.103191	-4.422568	33555.129676
HLA A*1101	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.446793	0.023895	-4.422898	27976.458093
HLA A*2301	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.523691	0.100401	-4.423290	33395.763337
HLA B*5101	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.314096	-0.109508	-4.423604	20610.862554
HLA A*0101	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.355203	-0.068483	-4.423686	22657.018369
HLA B*0802	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.447716	0.023895	-4.423821	28036.001736
HLA B*4501	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.632491	0.208647	-4.423844	42903.362042
HLA B*4002	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.632531	0.208647	-4.423884	42907.307965
HLA A*0301	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.355468	-0.068483	-4.423951	22670.873235
HLA B*1502	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.537589	0.113485	-4.424104	34481.692811
HLA A*0206	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.537732	0.113485	-4.424247	34493.073759
HLA A*0212	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.346324	-0.077944	-4.424268	22198.521657
HLA A*2402	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.585466	0.161134	-4.424332	38500.501261
HLA A*2603	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.575664	0.151290	-4.424375	37641.275594
HLA B*1502	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.606703	0.182285	-4.424418	40429.966252
HLA A*0219	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.437959	0.013159	-4.424800	27413.132611
HLA B*0803	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.525418	0.100401	-4.425017	33528.818216
HLA B*2705	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.406868	-0.018628	-4.425496	25519.251496
HLA A*0203	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.390398	-0.035118	-4.425516	24569.597510
HLA B*5801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.357226	-0.068483	-4.425709	22762.798992
HLA A*2902	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.386796	-0.039278	-4.426074	24366.675607
HLA B*4601	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.400506	-0.025677	-4.426183	25148.120148
HLA A*6801	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.644612	0.218302	-4.426310	44117.644754
HLA B*0802	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.489626	0.063148	-4.426478	30876.366809
HLA A*0206	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.546319	0.119542	-4.426777	35181.897969
HLA B*5401	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.445846	0.019002	-4.426844	27915.530670
HLA B*5701	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.416217	-0.010665	-4.426881	26074.532634
HLA A*3002	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.440061	0.013159	-4.426902	27546.184758
HLA A*3301	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.644234	0.217020	-4.427214	44079.235361
HLA B*5701	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.408607	-0.018628	-4.427235	25621.617940
HLA B*0801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.318915	-0.108442	-4.427357	20840.827594
HLA A*0212	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.401680	-0.025677	-4.427358	25216.236503
HLA B*5101	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.420091	-0.007282	-4.427372	26308.181752
HLA A*0201	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.392278	-0.035118	-4.427395	24676.162986
HLA B*0802	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.447112	0.019638	-4.427474	27997.049204
HLA B*1503	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.444385	0.016895	-4.427490	27821.754141
HLA B*1801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.547034	0.119542	-4.427491	35239.805945
HLA B*5301	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.593833	0.166065	-4.427768	39249.388960
HLA A*2603	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.636415	0.208647	-4.427768	43292.729328
HLA B*0801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.359585	-0.068483	-4.428068	22886.772165
HLA B*2705	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.415725	-0.012369	-4.428095	26045.067686
HLA B*4402	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.441859	0.013159	-4.428700	27660.422667
HLA A*2603	1:189-197	9	ASMQIRRID	0.826263	-0.623241	-4.631796	0.203022	-4.428774	42834.714700
HLA A*8001	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.417234	-0.011592	-4.428826	26135.683352
HLA B*2705	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.492096	0.063148	-4.428948	31052.423491
HLA A*8001	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.389677	-0.039278	-4.428954	24528.825306
HLA B*1501	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.418488	-0.010665	-4.429153	26211.295390
HLA A*1101	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.492309	0.063148	-4.429161	31067.714360
HLA A*2402	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.581258	0.152039	-4.429220	38129.266982
HLA A*3301	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.612011	0.182632	-4.429379	40927.089898
HLA B*1509	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.529918	0.100401	-4.429516	33877.980209
HLA A*0201	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.390255	-0.039278	-4.429532	24561.490801
HLA B*0803	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.522394	0.092742	-4.429653	33296.183704
HLA A*0219	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.449591	0.019638	-4.429953	28157.297356
HLA A*2403	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.448957	0.019002	-4.429954	28116.198857

HLA A*3001	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.282056	-0.147950	-4.430006	19145.038330
HLA A*3002	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.533360	0.103191	-4.430169	34147.546532
HLA B*4801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.390903	-0.039278	-4.430181	24598.191678
HLA A*3301	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.644890	0.214699	-4.430190	44145.816990
HLA B*1503	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.250660	-0.179556	-4.430216	17809.842224
HLA B*4002	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.647547	0.217020	-4.430527	44416.754940
HLA A*0216	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.321123	-0.109508	-4.430631	20947.079298
HLA B*1801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.493874	0.063148	-4.430726	31179.852800
HLA A*3001	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.284030	-0.146721	-4.430751	19232.237239
HLA A*6901	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.362357	-0.068483	-4.430840	23033.341073
HLA A*0216	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.418611	-0.012369	-4.430980	26218.670038
HLA B*4403	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.648245	0.217020	-4.431224	44488.178351
HLA B*3501	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.444429	0.013159	-4.431270	27824.614028
HLA A*0250	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.592531	0.161134	-4.431397	39131.931559
HLA A*2603	1:49-57	9	AATRQSQAG	0.707385	-0.478093	-4.660706	0.229292	-4.431415	45783.215532
HLA A*2501	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.405771	-0.025677	-4.431448	25454.860567
HLA B*4501	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.637569	0.205784	-4.431785	43407.878747
HLA B*4403	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.646736	0.214699	-4.432037	44333.932301
HLA B*0702	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.449060	0.016895	-4.432165	28122.892297
HLA A*0212	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.421576	-0.010665	-4.432241	26398.284684
HLA A*8001	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.419884	-0.012369	-4.432253	26295.660190
HLA B*0802	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.425039	-0.007282	-4.432320	26609.630804
HLA A*2501	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.485766	0.053318	-4.432448	30603.139913
HLA A*8001	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.451525	0.019002	-4.432522	28282.942682
HLA A*0206	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.485963	0.053318	-4.432645	30617.050079
HLA B*1503	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.451649	0.019002	-4.432647	28291.053247
HLA B*0801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.397780	-0.034919	-4.432699	24990.797991
HLA B*0802	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.446013	0.013159	-4.432854	27926.255145
HLA A*0211	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.448733	0.015810	-4.432923	28101.752545
HLA A*6802	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.422281	-0.010665	-4.432946	26441.163008
HLA B*4801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.421489	-0.011592	-4.433080	26393.001177
HLA A*3301	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.642418	0.209282	-4.433135	43895.287750
HLA A*0203	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.355193	-0.077944	-4.433137	22656.528086
HLA A*3201	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.615859	0.182632	-4.433228	41291.372792
HLA B*5301	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.422619	-0.010665	-4.433284	26461.769335
HLA A*0216	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.457363	0.023895	-4.433468	28665.733805
HLA A*0201	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.398588	-0.034919	-4.433507	25037.349215
HLA A*2601	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.398647	-0.034919	-4.433566	25040.735676
HLA B*1517	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.421524	-0.012369	-4.433893	26395.143012
HLA A*6802	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.398835	-0.035118	-4.433953	25051.575430
HLA A*0211	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.426832	-0.007282	-4.434113	26719.695589
HLA B*0803	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.533258	0.099112	-4.434146	34139.603875
HLA B*2705	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.422628	-0.011592	-4.434220	26462.341962
HLA B*1502	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.595987	0.161134	-4.434853	39444.583779
HLA A*6801	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.600966	0.166065	-4.434901	39899.360637
HLA A*6901	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.357054	-0.077944	-4.434998	22753.811239
HLA B*4601	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.366567	-0.068483	-4.435050	23257.724176
HLA B*1502	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.587158	0.152039	-4.435119	38650.757784
HLA B*4001	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.400076	-0.035118	-4.435193	25123.235585
HLA B*4001	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.424724	-0.010665	-4.435389	26590.347804
HLA A*2301	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.538714	0.103191	-4.435523	34571.162366
HLA B*4601	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.400839	-0.034919	-4.435758	

25167.446463

HLA B*3501	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.423427	-0.012369	-4.435796	26511.060588
HLA A*0203	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.367314	-0.068483	-4.435797	23297.769916
HLA A*0216	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.452993	0.016895	-4.436098	28378.734276
HLA A*0301	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.358180	-0.077944	-4.436124	22812.850492
HLA A*3101	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.410500	-0.025677	-4.436178	25733.581615
HLA A*2501	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.452321	0.015810	-4.436511	28334.859846
HLA B*4001	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.410871	-0.025677	-4.436549	25755.587118
HLA A*3101	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.368264	-0.068483	-4.436747	23348.745096
HLA A*2603	1:296-304	9	IEVTLADRD	1.035610	-0.817308	-4.655093	0.218302	-4.436791	45195.310240
HLA A*3301	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.619304	0.182285	-4.437019	41620.152472
HLA B*4801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.418486	-0.018628	-4.437114	26211.153591
HLA A*0219	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.456170	0.019002	-4.437167	28587.062110
HLA A*2403	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.359260	-0.077944	-4.437204	22869.692085
HLA A*0202	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.556857	0.119542	-4.437315	36045.969012
HLA B*0802	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.490669	0.053318	-4.437351	30950.620700
HLA B*4002	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.643268	0.205784	-4.437485	43981.335628
HLA A*3201	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.603576	0.166065	-4.437511	40139.893353
HLA B*4001	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.398278	-0.039278	-4.437556	25019.476292
HLA A*2902	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.457725	0.019638	-4.438087	28689.625836
HLA B*0702	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.451252	0.013159	-4.438093	28265.199370
HLA A*0202	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.579294	0.141159	-4.438135	37957.210363
HLA A*2902	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.455352	0.016895	-4.438457	28533.293552
HLA B*7301	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.604871	0.166065	-4.438806	40259.722818
HLA A*3301	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.647671	0.208647	-4.439024	44429.492121
HLA A*6802	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.315128	-0.123980	-4.439108	20659.870316
HLA A*6802	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.361166	-0.077944	-4.439110	22970.251469
HLA A*0216	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.413562	-0.025677	-4.439239	25915.620684
HLA B*4501	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.605352	0.166065	-4.439287	40304.396717
HLA B*5301	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.600693	0.161134	-4.439559	39874.329762
HLA B*1517	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.421390	-0.018628	-4.440018	26387.004963
HLA A*2603	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.657429	0.217020	-4.440408	45438.999472
HLA A*6901	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.325472	-0.115163	-4.440636	21157.890908
HLA B*4402	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.430154	-0.010665	-4.440819	26924.873888
HLA B*5701	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.429407	-0.011592	-4.440998	26878.593643
HLA B*4402	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.293049	-0.147950	-4.441000	19635.839813
HLA A*2603	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.646870	0.205784	-4.441087	44347.605384
HLA B*1517	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.457995	0.016895	-4.441101	28707.480275
HLA A*2602	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.607462	0.166065	-4.441397	40500.675100
HLA A*2602	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.592773	0.151290	-4.441484	39153.742675
HLA B*1801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.542031	0.100401	-4.441630	34836.254498
HLA A*0219	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.431194	-0.010665	-4.441859	26989.478911
HLA B*7301	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.584576	0.142630	-4.441946	38421.642707
HLA A*0219	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.364178	-0.077944	-4.442122	23130.114863
HLA A*6801	1:142-150	9	APARPAEGG	0.947554	-0.730534	-4.659165	0.217020	-4.442145	45621.024031
HLA A*2602	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.626737	0.184583	-4.442155	42338.692050
HLA A*2402	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.593459	0.151290	-4.442170	39215.642236
HLA A*0216	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.462001	0.019638	-4.442363	28973.499056
HLA B*4002	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.627048	0.184583	-4.442465	42368.937135
HLA A*0203	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.269019	-0.173733	-4.442752	18578.855113
HLA B*3901	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.505920	0.063148	-4.442772	32056.778039
HLA B*1503	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.403616	-0.039278	-4.442894	25328.895062
HLA B*4402	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.424325	-0.018628	-4.442953	26565.904404
HLA A*0202	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.403948	-0.039278	-4.443225	25348.223172
HLA B*4403	1:17-25	9	NADGLVDRG	0.911402	-0.705618	-4.649020	0.205784	-4.443236	44567.672406
HLA B*4601	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.408188	-0.035118	-4.443306	25596.957215

HLA B*4801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.433189	-0.010665	-4.443854	27113.726593
HLA B*0801	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.409250	-0.035118	-4.444368	25659.625273
HLA B*4402	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.437301	-0.007282	-4.444582	27371.639483
HLA A*3001	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.265459	-0.179556	-4.445016	18427.205458
HLA A*3002	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.419682	-0.025677	-4.445359	26283.428967
HLA A*3101	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.410472	-0.034919	-4.445391	25731.911079
HLA A*3002	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.438180	-0.007282	-4.445461	27427.076545
HLA A*2603	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.628196	0.182632	-4.445565	42481.169825
HLA B*5701	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.406457	-0.039278	-4.445734	25495.103072
HLA A*2902	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.438934	-0.007282	-4.446215	27474.747084
HLA B*1801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.406938	-0.039278	-4.446216	25523.393521
HLA B*0803	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.466272	0.019638	-4.446634	29259.864509
HLA A*2501	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.465718	0.019002	-4.446716	29222.531288
HLA A*2301	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.544604	0.097839	-4.446765	35043.230940
HLA A*2403	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.421129	-0.025677	-4.446807	26371.164384
HLA B*5701	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.412103	-0.034919	-4.447022	25828.702174
HLA B*1801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.500453	0.053318	-4.447134	31655.750810
HLA B*3901	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.436540	-0.010665	-4.447205	27323.704384
HLA A*3201	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.608416	0.161134	-4.447282	40589.729154
HLA A*2403	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.434963	-0.012369	-4.447332	27224.698171
HLA A*0219	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.434989	-0.012369	-4.447358	27226.318328
HLA A*0250	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.590050	0.142630	-4.447420	38909.014332
HLA A*2501	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.491689	0.044127	-4.447562	31023.374787
HLA B*0802	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.435337	-0.012369	-4.447706	27248.126179
HLA A*0201	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.369854	-0.077944	-4.447798	23434.416546
HLA A*2402	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.561323	0.113485	-4.447838	36418.585687
HLA B*5101	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.511185	0.063148	-4.448037	32447.785775
HLA A*0202	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.545899	0.097839	-4.448060	35147.845359
HLA A*0206	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.546646	0.097839	-4.448807	35208.363812
HLA A*1101	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.430212	-0.018628	-4.448841	26928.515649
HLA A*2403	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.339694	-0.109508	-4.449202	21862.197144
HLA A*0212	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.414342	-0.034919	-4.449261	25962.209120
HLA A*2501	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.442047	-0.007282	-4.449328	27672.396444
HLA A*2601	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.334205	-0.115163	-4.449369	21587.652040
HLA A*2602	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.547276	0.097839	-4.449436	35259.447691
HLA A*0250	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.590816	0.141159	-4.449657	38977.695745
HLA A*0212	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.340342	-0.109508	-4.449850	21894.864615
HLA B*7301	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.414873	-0.035118	-4.449990	25993.970837
HLA A*0219	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.340652	-0.109508	-4.450160	21910.505440
HLA A*0101	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.372291	-0.077944	-4.450235	23566.254376
HLA B*3801	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.549465	0.099112	-4.450353	35437.675351
HLA B*3801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.569915	0.119542	-4.450373	37146.264145
HLA A*2501	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.439801	-0.010665	-4.450466	27529.648303
HLA B*4403	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.659259	0.208647	-4.450612	45630.897287
HLA A*8001	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.440348	-0.010665	-4.451013	27564.371420
HLA B*4801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.438675	-0.012369	-4.451045	27458.402061
HLA B*1503	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.335913	-0.115163	-4.451077	21672.723230
HLA B*1801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.464496	0.013159	-4.451337	29140.439669
HLA B*5101	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.504778	0.053318	-4.451460	31972.604865
HLA A*2603	1:15-23	9	GPNADGLVD	1.314613	-1.099914	-4.666253	0.214699	-4.451554	46371.743578
HLA A*2402	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.592806	0.141159	-4.451647	39156.708231
HLA A*0203	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.416729	-0.034919	-4.451648	26105.301927

HLA A*1101	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.471429	0.019638	-4.451791	29609.387955
HLA A*2501	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.468876	0.016895	-4.451981	29435.779440
HLA B*4403	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.603306	0.151290	-4.452016	40114.928596
HLA A*0219	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.468998	0.016895	-4.452103	29444.061309
HLA A*0212	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.417069	-0.035118	-4.452187	26125.787845
HLA B*1503	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.439871	-0.012369	-4.452240	27534.116636
HLA A*3002	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.496531	0.044127	-4.452404	31371.214201
HLA B*5401	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.552858	0.100401	-4.452456	35715.594337
HLA B*4801	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.417412	-0.035118	-4.452530	26146.431289
HLA B*2705	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.471603	0.019002	-4.452601	29621.243907
HLA B*4402	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.440311	-0.012369	-4.452680	27561.985600
HLA B*7301	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.472541	0.019638	-4.452903	29685.251775
HLA B*5701	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.427367	-0.025677	-4.453045	26752.673458
HLA A*0203	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.442564	-0.010665	-4.453229	27705.351062
HLA B*0802	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.470295	0.016895	-4.453400	29532.120314
HLA A*0206	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.546451	0.092742	-4.453709	35192.558073
HLA B*4402	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.428251	-0.025677	-4.453928	26807.146945
HLA B*4002	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.625765	0.171766	-4.453998	42243.972442
HLA B*1502	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.596958	0.142630	-4.454328	39532.812717
HLA B*3801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.552419	0.097839	-4.454579	35679.480952
HLA B*5301	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.606720	0.152039	-4.454681	40431.497332
HLA A*2301	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.547468	0.092742	-4.454726	35275.092637
HLA B*1503	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.547485	0.092742	-4.454743	35276.428503
HLA A*6801	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.606800	0.152039	-4.454761	40438.934834
HLA B*5701	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.419915	-0.035118	-4.455032	26297.509591
HLA B*1509	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.447984	-0.007282	-4.455266	28053.297638
HLA B*4001	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.377377	-0.077944	-4.455321	23843.894754
HLA B*4801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.429841	-0.025677	-4.455519	26905.507999
HLA B*1509	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.548352	0.092742	-4.455610	35346.919376
HLA A*3301	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.627463	0.171766	-4.455697	42409.526957
HLA A*3301	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.553687	0.097839	-4.455848	35783.865248
HLA A*3101	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.420793	-0.035118	-4.455911	26350.771168
HLA B*4002	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.569751	0.113485	-4.456266	37132.199806
HLA B*0803	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.509698	0.053318	-4.456380	32336.859676
HLA A*0250	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.575927	0.119542	-4.456385	37664.089639
HLA B*3801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.559627	0.103191	-4.456436	36276.614325
HLA A*0101	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.348046	-0.108442	-4.456488	22286.723521
HLA B*4403	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.638969	0.182285	-4.456684	43548.064386
HLA B*0803	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.472910	0.015810	-4.457099	29710.475731
HLA B*4402	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.445590	-0.011592	-4.457181	27899.074351
HLA B*5301	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.608487	0.151290	-4.457197	40596.317267
HLA B*7301	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.555153	0.097839	-4.457314	35904.867500
HLA B*4501	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.640287	0.182878	-4.457409	43680.431250
HLA A*1101	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.476927	0.019002	-4.457925	29986.599912
HLA A*0211	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.550809	0.092742	-4.458067	35547.505543
HLA A*2403	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.389851	-0.068483	-4.458334	24538.646941
HLA B*7301	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.557547	0.099112	-4.458435	36103.346010
HLA A*2902	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.447930	-0.010665	-4.458595	28049.807255
HLA A*2902	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.433276	-0.025677	-4.458953	27119.154380
HLA B*4002	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.625535	0.166065	-4.459469	42221.581928
HLA B*1502	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.433845	-0.025677	-4.459522	27154.681842
HLA A*3002	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.560068	0.100401	-4.459667	36313.528556
HLA A*0206	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.503812	0.044127	-4.459685	31901.593889
HLA A*2603	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.631472	0.171766	-4.459705	42802.747749
HLA A*0250	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.558828	0.099112	-4.459715	

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36209.949816
HLA A*3201	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.560393	0.100401	-4.459991	36340.649077
HLA A*3101	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.382170	-0.077944	-4.460114	24108.497538
HLA B*1509	1:46-54 9	WQRAATRQS	1.013661	-0.997851	-4.475931	0.015810	-4.460121	29917.895686
HLA A*2603	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.644866	0.184583	-4.460283	44143.428815
HLA B*3801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.560961	0.100401	-4.460560	36388.257164
HLA A*3201	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.611987	0.151290	-4.460698	40924.875848
HLA B*4002	1:43-51 9	PPPWQRAAT	0.896839	-0.714207	-4.643583	0.182632	-4.460952	44013.230363
HLA B*4501	1:57-65 9	GHRQPPPVS	1.076955	-0.963470	-4.574692	0.113485	-4.461207	37557.064989
HLA A*2403	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.451029	-0.010665	-4.461694	28250.676501
HLA B*1501	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.337770	-0.123980	-4.461750	21765.546597
HLA A*0250	1:57-65 9	GHRQPPPVS	1.076955	-0.963470	-4.575326	0.113485	-4.461841	37611.963555
HLA B*5701	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.384040	-0.077944	-4.461984	24212.539135
HLA B*7301	1:25-33 9	GGAHRAATG	0.837696	-0.734505	-4.565317	0.103191	-4.462126	36755.065456
HLA B*4403	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.647039	0.184583	-4.462457	44364.882674
HLA B*3901	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.486614	0.023895	-4.462720	30662.965326
HLA A*0201	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.394244	-0.068483	-4.462727	24788.151913
HLA B*2705	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.353232	-0.109508	-4.462739	22554.413529
HLA A*2501	1:5-13  9	NEPGALSKG	0.682258	-0.717376	-4.427799	-0.035118	-4.462917	26779.316852
HLA A*2602	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.624426	0.161134	-4.463292	42113.908013
HLA A*2501	1:27-35 9	AHRAATGPG	0.551366	-0.531728	-4.483106	0.019638	-4.463468	30416.299142
HLA B*5101	1:79-87 9	DARLNRFIS	1.021930	-1.002928	-4.482566	0.019002	-4.463564	30378.476452
HLA B*1517	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.354066	-0.109508	-4.463573	22597.771141
HLA B*5301	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.583154	0.119542	-4.463612	38296.094896
HLA B*4501	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.648207	0.184583	-4.463624	44484.327700
HLA B*1517	1:82-90 9	LNRFISGAS	0.922756	-0.962034	-4.424515	-0.039278	-4.463793	26577.548161
HLA B*1503	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.517336	0.053318	-4.464018	32910.616498
HLA B*3901	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.354524	-0.109508	-4.464032	22621.622750
HLA B*4601	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.386098	-0.077944	-4.464043	24327.556202
HLA A*0206	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.564645	0.100401	-4.464244	36698.240950
HLA B*5301	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.457018	-0.007282	-4.464299	28642.946336
HLA A*0211	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.517728	0.053318	-4.464410	32940.363079
HLA A*0202	1:46-54 9	WQRAATRQS	1.013661	-0.997851	-4.480235	0.015810	-4.464425	30215.883692
HLA B*3901	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.438783	-0.025677	-4.464461	27465.236069
HLA A*2402	1:25-33 9	GGAHRAATG	0.837696	-0.734505	-4.567704	0.103191	-4.464513	36957.643959
HLA A*2601	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.290937	-0.173733	-4.464670	19540.572948
HLA B*3801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.457847	-0.007282	-4.465129	28697.697772
HLA A*0212	1:82-90 9	LNRFISGAS	0.922756	-0.962034	-4.425871	-0.039278	-4.465148	26660.639756
HLA A*6801	1:15-23 9	GPNADGLVD	1.314613	-1.099914	-4.679866	0.214699	-4.465167	47848.281207
HLA B*1509	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.564300	0.099112	-4.465187
36669.068139
HLA A*6801	1:98-106	9	AAVRTPQPD	0.774386	-0.602620	-4.637028	0.171766	-4.465262	43353.901019
HLA A*6802	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.350198	-0.115163	-4.465362	22397.438549
HLA A*2602	1:37-45 9	IPDAGDPPP	0.238307	-0.097148	-4.606999	0.141159	-4.465840	40457.534573
HLA B*5101	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.510229	0.044127	-4.466101	32376.420029
HLA B*4002	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.649046	0.182878	-4.466168	44570.324653
HLA A*8001	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.440515	-0.025677	-4.466192	27574.960987
HLA A*0212	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.453905	-0.012369	-4.466274	28438.364850
HLA A*2601	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.397926	-0.068483	-4.466409	24999.181638
HLA A*0203	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.342544	-0.123980	-4.466524	22006.132907
HLA A*0202	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.454175	-0.012369	-4.466544	28456.062921
HLA B*3901	1:79-87 9	DARLNRFIS	1.021930	-1.002928	-4.485677	0.019002	-4.466674	30596.849295
HLA B*1509	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.529988	0.063148	-4.466840	33883.478939
HLA B*5701	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.398469	-0.068483	-4.466952	25030.442254
HLA B*4002	1:31-39 9	ATGPGRIPD	0.891200	-0.739161	-4.619224	0.152039	-4.467185	41612.497722
HLA B*3901	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.305232	-0.162047	-4.467279	20194.428177
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HLA A*0211	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.455211	-0.012369	-4.467580	28524.033338
HLA A*2603	1:249-257	9	GSSAELVSS	1.197912	-1.015627	-4.649929	0.182285	-4.467644	44661.078237
HLA B*0702	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.442068	-0.025677	-4.467745	27673.743818
HLA A*3001	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.294041	-0.173733	-4.467774	19680.719119
HLA B*4402	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.428577	-0.039278	-4.467855	26827.312820
HLA A*6901	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.306068	-0.162047	-4.468115	20233.358517
HLA B*3501	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.390236	-0.077944	-4.468180	24560.427825
HLA B*5801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.361718	-0.106651	-4.468368	22999.472670
HLA B*1501	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.359070	-0.109508	-4.468578	22859.672758
HLA A*0202	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.522082	0.053318	-4.468764	33272.235209
HLA B*5101	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.362174	-0.106651	-4.468824	23023.623713
HLA B*5401	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.484716	0.015810	-4.468906	30529.224182
HLA A*6801	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.620391	0.151290	-4.469102	41724.532412
HLA A*3002	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.429834	-0.039278	-4.469112	26905.071335
HLA B*5801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.360684	-0.108442	-4.469126	22944.790954
HLA A*0301	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.359695	-0.109508	-4.469203	22892.592205
HLA A*2403	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.345469	-0.123980	-4.469449	22154.851348
HLA B*1502	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.572798	0.103191	-4.469607	37393.658780
HLA B*5401	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.489513	0.019638	-4.469875	30868.350039
HLA A*0250	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.567895	0.097839	-4.470055	36973.842385
HLA B*4402	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.392292	-0.077944	-4.470236	24676.963971
HLA A*0206	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.346474	-0.123980	-4.470455	22206.208846
HLA B*4801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.435609	-0.034919	-4.470528	27265.231029
HLA A*2603	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.533883	0.063148	-4.470736	34188.767172
HLA B*5801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.355621	-0.115163	-4.470784	22678.846686
HLA B*4501	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.653451	0.182632	-4.470819	45024.726345
HLA A*0211	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.494788	0.023895	-4.470893	31245.538235
HLA B*0803	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.534172	0.063148	-4.471025	34211.524508
HLA B*3901	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.228222	-0.242879	-4.471101	16913.071713
HLA B*3901	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.484272	0.013159	-4.471113	30498.024948
HLA A*2602	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.584663	0.113485	-4.471178	38429.334179
HLA A*3301	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.484518	0.013159	-4.471359	30515.353918
HLA A*6901	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.364871	-0.106651	-4.471521	23167.058085
HLA A*2602	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.614607	0.142630	-4.471977	41172.481811
HLA A*3201	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.613308	0.141159	-4.472149	41049.491451
HLA B*1517	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.460791	-0.011592	-4.472383	28892.888542
HLA B*4403	1:287-295	9	NLITDLIGG	0.755550	-0.572672	-4.655291	0.182878	-4.472413	45215.853043
HLA A*3001	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.310607	-0.162047	-4.472654	20445.944705
HLA A*6901	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.350588	-0.122654	-4.473242	22417.561415
HLA B*2705	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.395386	-0.077944	-4.473330	24853.410826
HLA A*3002	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.592877	0.119542	-4.473335	39163.063750
HLA A*2501	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.497246	0.023895	-4.473351	31422.849946
HLA B*2705	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.490279	0.016895	-4.473385	30922.838232
HLA B*5101	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.493214	0.019638	-4.473576	31132.489857
HLA B*4002	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.634716	0.161134	-4.473582	43123.727047
HLA A*3101	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.364084	-0.109508	-4.473592	23125.110151
HLA B*5101	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.462198	-0.011592	-4.473790	28986.668495
HLA A*6802	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.438884	-0.034919	-4.473803	27471.625920
HLA A*3201	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.455230	-0.018628	-4.473858	28525.267859
HLA B*1801	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.493510	0.019638	-4.473872	31153.718429
HLA B*1503	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.405503	-0.068483	-4.473986	25439.166698
HLA B*1502	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.571865	0.097839	-4.474026	37313.433629
HLA A*0203	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.358985	-0.115163	-4.474149	22855.221133
HLA B*1801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.359164	-0.115163	-4.474327	22864.620025

HLA A*6801	1:223-231	9	LYLVLGGMG	0.710677	-0.526094	-4.658914	0.184583	-4.474331	45594.623572
HLA A*0301	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.365905	-0.108442	-4.474347	23222.269505
HLA A*2403	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.435073	-0.039278	-4.474351	27231.621333
HLA B*3901	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.491456	0.016895	-4.474562	31006.763767
HLA B*0801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.367984	-0.106651	-4.474634	23333.718552
HLA A*3301	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.640703	0.166065	-4.474638	43722.277495
HLA B*5101	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.498871	0.023895	-4.474977	31540.706356
HLA B*1801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.498888	0.023895	-4.474993	31541.900801
HLA A*3201	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.617683	0.142630	-4.475052	41465.081395
HLA A*2402	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.574285	0.099112	-4.475173	37521.931369
HLA A*0216	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.494234	0.019002	-4.475231	31205.671455
HLA A*6801	1:67-75	9	PEGRPTNPP	0.513566	-0.304284	-4.684579	0.209282	-4.475297	48370.369916
HLA B*5101	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.488588	0.013159	-4.475429	30802.624336
HLA B*0802	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.450007	-0.025677	-4.475684	28184.272299
HLA A*0219	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.440780	-0.034919	-4.475699	27591.823196
HLA A*2601	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.397782	-0.077944	-4.475727	24990.933188
HLA B*1801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.492659	0.016895	-4.475765	31092.767316
HLA A*0301	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.369131	-0.106651	-4.475781	23395.401560
HLA A*0206	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.500291	0.023895	-4.476396	31643.936482
HLA A*0216	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.441499	-0.034919	-4.476418	27637.537247
HLA A*0301	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.361260	-0.115163	-4.476423	22975.222667
HLA A*1101	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.469345	-0.007282	-4.476627	29467.645537
HLA A*3002	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.354148	-0.122654	-4.476802	22602.050347
HLA A*3301	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.638339	0.161134	-4.477205	43484.971960
HLA A*2603	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.493033	0.015810	-4.477223	31119.523962
HLA A*6801	1:144-152	9	ARPAEGGAG	0.731172	-0.522525	-4.685933	0.208647	-4.477286	48521.331723
HLA A*2301	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.490665	0.013159	-4.477506	30950.285823
HLA B*1801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.451844	-0.025677	-4.477521	28303.759371
HLA B*1502	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.497184	0.019638	-4.477546	31418.430410
HLA A*2301	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.501684	0.023895	-4.477789	31745.615273
HLA B*1503	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.452368	-0.025677	-4.478045	28337.925781
HLA A*0250	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.578625	0.100401	-4.478223	37898.732331
HLA A*6901	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.354249	-0.123980	-4.478229	22607.308766
HLA A*6801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.465887	-0.012369	-4.478256	29233.916032
HLA B*3501	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.409786	-0.068483	-4.478269	25691.294786
HLA B*1801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.466839	-0.011592	-4.478430	29298.037911
HLA A*1101	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.400503	-0.077944	-4.478447	25147.984100
HLA B*1509	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.531915	0.053318	-4.478596	34034.123639
HLA B*0803	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.502769	0.023895	-4.478875	31825.058510
HLA A*0211	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.542083	0.063148	-4.478935	34840.400870
HLA A*1101	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.466589	-0.012369	-4.478959	29281.241819
HLA B*5401	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.317014	-0.162047	-4.479061	20749.814930
HLA B*4001	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.411008	-0.068483	-4.479491	25763.669809
HLA B*2705	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.440759	-0.039278	-4.480037	27590.479810
HLA A*2602	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.469712	-0.010665	-4.480377	29492.525038
HLA B*5101	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.496355	0.015810	-4.480545	31358.488174
HLA B*5401	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.534144	0.053318	-4.480826	34209.303613
HLA A*0202	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.594354	0.113485	-4.480870	39296.555613
HLA B*0702	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.446008	-0.034919	-4.480927	27925.952990
HLA B*4002	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.622104	0.141159	-4.480945	41889.410917
HLA B*0803	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.500161	0.019002	-4.481159	31634.522422
HLA B*4801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.371710	-0.109508	-4.481218	23534.785172

HLA A*6802	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.413045	-0.068483	-4.481528	25884.794892
HLA A*2403	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.319744	-0.162047	-4.481792	20880.665159
HLA A*2402	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.579670	0.097839	-4.481831	37990.079675
HLA B*0802	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.470419	-0.011592	-4.482011	29540.589100
HLA A*0219	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.447133	-0.035118	-4.482251	27998.412386
HLA B*1801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.526429	0.044127	-4.482301	33606.905497
HLA B*3801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.575211	0.092742	-4.482469	37601.994525
HLA A*0250	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.585661	0.103191	-4.482470	38517.792668
HLA B*0702	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.414259	-0.068483	-4.482743	25957.293742
HLA B*4001	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.360120	-0.122654	-4.482774	22915.019379
HLA B*5801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.360261	-0.122654	-4.482915	22922.458650
HLA A*2301	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.546178	0.063148	-4.483030	35170.480012
HLA B*3901	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.471502	-0.011592	-4.483094	29614.354060
HLA B*1503	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.546272	0.063148	-4.483124	35178.091572
HLA B*4501	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.644598	0.161134	-4.483464	44116.212748
HLA B*4402	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.415032	-0.068483	-4.483516	26003.535062
HLA A*0216	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.448989	-0.035118	-4.484107	28118.328415
HLA B*1801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.471848	-0.012369	-4.484217	29637.914351
HLA B*1509	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.503225	0.019002	-4.484223	31858.477031
HLA A*2301	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.537645	0.053318	-4.484327	34486.170113
HLA B*7301	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.604206	0.119542	-4.484664	40198.132397
HLA B*0702	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.369683	-0.115163	-4.484846	23425.163609
HLA A*0202	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.360889	-0.123980	-4.484869	22955.592699
HLA B*4002	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.636241	0.151290	-4.484951	43275.401341
HLA B*4403	1:31-39	9	ATGPGRIPD	0.891200	-0.739161	-4.637127	0.152039	-4.485088	43363.752810
HLA A*6801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.498648	0.013159	-4.485489	31524.500507
HLA A*0301	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.361558	-0.123980	-4.485538	22991.013354
HLA A*3301	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.628243	0.142630	-4.485613	42485.766442
HLA B*7301	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.586639	0.100401	-4.486237	38604.575111
HLA B*1502	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.585448	0.099112	-4.486335	38498.835029
HLA B*4801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.408423	-0.077944	-4.486367	25610.808631
HLA B*0802	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.475724	-0.010665	-4.486389	29903.656055
HLA A*2601	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.339710	-0.146721	-4.486431	21863.025064
HLA A*2403	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.380112	-0.106651	-4.486763	23994.516147
HLA A*8001	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.451861	-0.034919	-4.486780	28304.831232
HLA A*2902	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.408891	-0.077944	-4.486835	25638.395254
HLA A*6901	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.378404	-0.108442	-4.486846	23900.331305
HLA B*1502	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.550137	0.063148	-4.486989	35492.547964
HLA A*2501	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.448069	-0.039278	-4.487346	28058.761719
HLA A*3301	1:153-161	9	SRGDSAAGS	1.099233	-0.947943	-4.638807	0.151290	-4.487517	43531.811695
HLA B*7301	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.540864	0.053318	-4.487546	34742.715547
HLA A*1101	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.503577	0.015810	-4.487767	31884.340148
HLA A*0211	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.505133	0.016895	-4.488238	31998.733741
HLA A*2603	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.588713	0.100401	-4.488312	38789.427709
HLA A*0301	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.366196	-0.122654	-4.488850	23237.852840
HLA A*3201	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.592113	0.103191	-4.488922	39094.267201
HLA A*0206	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.552226	0.063148	-4.489078	35663.656655
HLA A*0211	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.411186	-0.077944	-4.489130	25774.264760
HLA A*0202	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.589785	0.100401	-4.489383	38885.235841
HLA B*5101	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.470800	-0.018628	-4.489428	29566.489880
HLA B*5801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.365498	-0.123980	-4.489479	23200.545699
HLA B*0802	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.470903	-0.018628	-4.489531	29573.528581
HLA B*1517	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.479054	-0.010665	-4.489718	30133.772777
HLA B*4403	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.655949	0.166065	-4.489883	45284.396514

HLA A*0206	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.509665	0.019638	-4.490027	32334.410625
HLA A*6801	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.672710	0.182632	-4.490078	47066.273101
HLA B*0802	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.455194	-0.034919	-4.490113	28522.953175
HLA A*3201	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.609737	0.119542	-4.490194	40713.324241
HLA B*7301	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.477954	-0.012369	-4.490323	30057.575744
HLA A*3101	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.382222	-0.108442	-4.490664	24111.367043
HLA B*1801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.455787	-0.034919	-4.490706	28561.864809
HLA A*0216	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.382339	-0.108442	-4.490781	24117.889916
HLA B*4403	1:43-51	9	PPPWQRAAT	0.896839	-0.714207	-4.673452	0.182632	-4.490821	47146.802885
HLA B*5401	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.472266	-0.018628	-4.490894	29666.468231
HLA B*4403	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.652450	0.161134	-4.491316	44921.081262
HLA B*0702	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.456245	-0.035118	-4.491363	28592.011429
HLA A*2402	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.504545	0.013159	-4.491386	31955.485593
HLA A*2603	1:248-256	9	SGSSAELVS	1.170460	-1.004395	-4.657755	0.166065	-4.491690	45473.181295
HLA B*1502	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.611487	0.119542	-4.491945	40877.745012
HLA B*5301	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.605604	0.113485	-4.492119	40327.733998
HLA B*3801	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.480005	-0.012369	-4.492374	30199.868409
HLA A*0206	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.509388	0.016895	-4.492493	32313.775994
HLA B*5701	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.383047	-0.109508	-4.492554	24157.194918
HLA B*5401	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.556152	0.063148	-4.493004	35987.515050
HLA B*5101	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.509966	0.016895	-4.493071	32356.808853
HLA B*3501	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.458402	-0.034919	-4.493321	28734.360493
HLA A*8001	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.415453	-0.077944	-4.493397	26028.728306
HLA A*2902	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.425370	-0.068483	-4.493853	26629.936224
HLA A*0201	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.370047	-0.123980	-4.494027	23444.814615
HLA A*0101	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.387388	-0.106651	-4.494039	24399.917156
HLA A*0216	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.483412	-0.010665	-4.494077	30437.698010
HLA A*3301	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.613782	0.119542	-4.494240	41094.374757
HLA A*3301	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.635515	0.141159	-4.494356	43203.120199
HLA A*6801	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.592280	0.097839	-4.494441	39109.286277
HLA A*3002	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.511418	0.016895	-4.494523	32465.168783
HLA B*5101	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.347839	-0.146721	-4.494560	22276.116000
HLA A*3301	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.538735	0.044127	-4.494608	34572.845643
HLA B*4601	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.379513	-0.115163	-4.494676	23961.438012
HLA B*1509	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.469007	-0.025677	-4.494684	29444.698472
HLA A*2601	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.385234	-0.109508	-4.494742	24279.172127
HLA A*0206	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.482528	-0.012369	-4.494898	30375.847059
HLA A*3002	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.513953	0.019002	-4.494950	32655.230934
HLA A*0212	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.371074	-0.123980	-4.495054	23500.306576
HLA A*2902	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.379903	-0.115163	-4.495066	23982.966045
HLA A*6802	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.321467	-0.173733	-4.495200	20963.630755
HLA B*0702	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.417394	-0.077944	-4.495338	26145.299719
HLA B*1801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.477230	-0.018628	-4.495859	30007.534135
HLA A*0101	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.380744	-0.115163	-4.495907	24029.459831
HLA A*2902	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.461103	-0.034919	-4.496022	28913.684897
HLA B*3501	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.372128	-0.123980	-4.496109	23557.459151
HLA A*0201	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.387708	-0.108442	-4.496150	24417.875877
HLA A*2301	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.540375	0.044127	-4.496248	34703.643053
HLA A*0219	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.457267	-0.039278	-4.496544	28659.376294
HLA B*1509	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.540723	0.044127	-4.496595	34731.440123
HLA B*7301	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.589808	0.092742	-4.497067	38887.339546
HLA B*4403	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.596417	0.099112	-4.497305	39483.653636
HLA A*2602	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.616895	0.119542	-4.497353	41390.001749

HLA B*2705	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.462511	-0.034919	-4.497430	29007.532351
HLA B*4001	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.387955	-0.109508	-4.497462	24431.750107
HLA B*0803	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.486086	-0.011592	-4.497677	30625.664303
HLA B*4402	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.382673	-0.115163	-4.497836	24136.424500
HLA B*5301	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.601255	0.103191	-4.498064	39925.919160
HLA B*0803	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.515038	0.016895	-4.498144	32736.950480
HLA B*1502	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.590931	0.092742	-4.498190	38988.029500
HLA B*4501	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.597310	0.099112	-4.498198	39564.905957
HLA A*8001	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.429858	-0.068483	-4.498341	26906.526909
HLA A*2601	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.390081	-0.108442	-4.498523	24551.660023
HLA A*0201	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.383404	-0.115163	-4.498567	24177.067625
HLA B*3501	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.464115	-0.035118	-4.499233	29114.912116
HLA A*1101	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.488698	-0.010665	-4.499363	30810.457355
HLA A*2603	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.597322	0.097839	-4.499483	39565.976180
HLA A*0101	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.375801	-0.123980	-4.499781	23757.497475
HLA B*1517	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.464874	-0.034919	-4.499793	29165.831820
HLA A*0216	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.422243	-0.077944	-4.500187	26438.874407
HLA A*3001	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.305255	-0.194957	-4.500212	20195.520703
HLA A*3002	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.376553	-0.123980	-4.500533	23798.661232
HLA B*2705	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.489903	-0.010665	-4.500568	30896.083553
HLA A*2603	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.614118	0.113485	-4.500634	41126.178247
HLA A*6801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.489340	-0.011592	-4.500931	30855.994930
HLA B*1509	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.517832	0.016895	-4.500937	32948.204975
HLA B*5801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.353250	-0.147950	-4.501200	22555.389685
HLA A*8001	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.391881	-0.109508	-4.501388	24653.612589
HLA A*2602	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.594181	0.092742	-4.501439	39280.827101
HLA B*5301	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.391937	-0.109508	-4.501445	24656.813757
HLA B*2705	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.476088	-0.025677	-4.501766	29928.741769
HLA B*0803	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.489549	-0.012369	-4.501918	30870.855056
HLA A*2402	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.594923	0.092742	-4.502181	39348.036087
HLA A*2902	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.378228	-0.123980	-4.502208	23890.635911
HLA A*3201	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.615754	0.113485	-4.502269	41281.321837
HLA B*0803	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.483966	-0.018628	-4.502595	30476.583667
HLA B*5301	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.600712	0.097839	-4.502873	39876.055525
HLA B*0801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.393384	-0.109508	-4.502892	24739.119449
HLA B*1509	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.526964	0.023895	-4.503070	33648.383669
HLA A*2603	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.664242	0.161134	-4.503108	46157.498741
HLA A*0201	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.396662	-0.106651	-4.503312	24926.526794
HLA B*5801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.356793	-0.146721	-4.503514	22740.151729
HLA B*4402	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.395144	-0.108442	-4.503586	24839.565901
HLA A*8001	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.468786	-0.035118	-4.503904	29429.728779
HLA B*3801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.548222	0.044127	-4.504095	35336.403680
HLA A*1101	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.464872	-0.039278	-4.504150	29165.674036
HLA A*0201	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.381637	-0.122654	-4.504291	24078.909393
HLA A*2301	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.520456	0.015810	-4.504646	33147.908691
HLA A*0202	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.426707	-0.077944	-4.504651	26712.035506
HLA B*1503	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.395186	-0.109508	-4.504694	24841.984846
HLA A*2601	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.380784	-0.123980	-4.504764	24031.669877
HLA B*4501	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.469822	-0.035118	-4.504940	29500.024903
HLA A*2601	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.398649	-0.106651	-4.505300	25040.871144
HLA B*5101	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.493162	-0.012369	-4.505531	31128.784764
HLA A*1101	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.493980	-0.011592	-4.505571	31187.444304
HLA B*3901	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.487063	-0.018628	-4.505691	30694.665400

HLA A*1101	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.470833	-0.034919	-4.505752	29568.729285
HLA A*0301	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.359049	-0.146721	-4.505770	22858.559771
HLA B*3801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.529744	0.023895	-4.505849	33864.420491
HLA A*0202	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.599281	0.092742	-4.506540	39744.895157
HLA B*4801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.382664	-0.123980	-4.506644	24135.902204
HLA B*5101	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.467644	-0.039278	-4.506922	29352.453586
HLA B*4002	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.649673	0.142630	-4.507043	44634.750349
HLA A*0206	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.496585	-0.010665	-4.507250	31375.117884
HLA A*3101	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.392108	-0.115163	-4.507272	24666.553195
HLA A*2902	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.472543	-0.035118	-4.507661	29685.412369
HLA B*4501	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.650451	0.142630	-4.507821	44714.748209
HLA B*1502	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.608343	0.100401	-4.507942	40582.922561
HLA A*0212	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.439575	-0.068483	-4.508058	27515.354510
HLA A*3201	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.496604	-0.011592	-4.508196	31376.475801
HLA B*1501	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.361476	-0.146721	-4.508197	22986.660507
HLA B*0803	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.501305	-0.007282	-4.508587	31717.977129
HLA B*4501	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.649852	0.141159	-4.508693	44653.105770
HLA B*1517	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.384802	-0.123980	-4.508782	24255.016188
HLA B*4001	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.400459	-0.108442	-4.508900	25145.399324
HLA A*3201	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.608097	0.099112	-4.508984	40559.876450
HLA A*0250	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.602089	0.092742	-4.509347	40002.670991
HLA B*5301	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.609831	0.100401	-4.509429	40722.135377
HLA A*0216	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.470205	-0.039278	-4.509483	29526.049849
HLA A*2403	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.401175	-0.108442	-4.509617	25186.923889
HLA B*5401	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.533533	0.023895	-4.509639	34161.219617
HLA B*5301	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.362998	-0.146721	-4.509719	23067.384141
HLA A*0203	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.401734	-0.108442	-4.510176	25219.374290
HLA B*3801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.573421	0.063148	-4.510273	37447.305546
HLA B*4801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.395301	-0.115163	-4.510465	24848.570946
HLA B*4801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.442040	-0.068483	-4.510523	27671.947334
HLA A*1101	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.485042	-0.025677	-4.510720	30552.190017
HLA B*3901	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.498437	-0.012369	-4.510806	31509.155278
HLA B*1501	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.331257	-0.179556	-4.510813	21441.581030
HLA B*0802	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.471862	-0.039278	-4.511139	29638.876394
HLA B*0801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.433429	-0.077944	-4.511373	27128.692312
HLA A*0206	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.476305	-0.035118	-4.511422	29943.641304
HLA B*0801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.332063	-0.179556	-4.511619	21481.404793
HLA A*2602	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.485961	-0.025677	-4.511638	30616.884445
HLA B*1501	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.389007	-0.122654	-4.511661	24491.035452
HLA A*0211	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.531381	0.019638	-4.511743	33992.353862
HLA B*5801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.350478	-0.161502	-4.511980	22411.862143
HLA A*3002	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.532439	0.019638	-4.512800	34075.207362
HLA B*4601	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.390187	-0.122654	-4.512841	24557.637730
HLA A*3002	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.501360	-0.011592	-4.512951	31721.923962
HLA B*3501	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.205376	-0.307784	-4.513160	16046.343994
HLA A*1101	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.389287	-0.123980	-4.513267	24506.807289
HLA A*2603	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.655058	0.141159	-4.513899	45191.642864
HLA A*3101	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.390081	-0.123980	-4.514061	24551.660023
HLA A*0301	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.366414	-0.147950	-4.514365	23249.547203
HLA B*1503	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.502908	-0.011592	-4.514500	31835.218164
HLA B*0802	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.479798	-0.035118	-4.514916	30185.494572
HLA B*4601	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.390983	-0.123980	-4.514963	24602.716593
HLA B*4001	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.353518	-0.161502	-4.515021	22569.304502
HLA A*0301	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.353563	-0.161502	-4.515065	22571.624472
HLA A*3201	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.559230	0.044127	-4.515102	36243.462816

HLA A*6801	1:100-108	9	VRTPQPDPD	0.782151	-0.621017	-4.676255	0.161134	-4.515121	47452.072289
HLA A*6802	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.368430	-0.146721	-4.515151	23357.715121
HLA A*0216	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.446786	-0.068483	-4.515269	27976.004048
HLA A*2501	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.480416	-0.034919	-4.515335	30228.473087
HLA B*4601	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.407173	-0.108442	-4.515615	25537.205130
HLA B*1501	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.407296	-0.108442	-4.515737	25544.390120
HLA A*1101	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.480715	-0.035118	-4.515832	30249.248874
HLA B*5801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.354336	-0.162047	-4.516383	22611.834431
HLA A*2601	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.394047	-0.122654	-4.516701	24776.889975
HLA A*2603	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.609513	0.092742	-4.516772	40692.405433
HLA B*5801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.337563	-0.179556	-4.517119	21755.187134
HLA A*6901	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.369248	-0.147950	-4.517198	23401.730743
HLA A*2603	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.659966	0.142630	-4.517336	45705.262104
HLA A*1101	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.449098	-0.068483	-4.517581	28125.326670
HLA A*6901	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.356526	-0.161502	-4.518028	22726.131579
HLA A*0219	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.449551	-0.068483	-4.518034	28154.707901
HLA B*4403	1:75-83	9	PAAADARLN	0.953438	-0.810808	-4.660739	0.142630	-4.518109	45786.683213
HLA B*0801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.344595	-0.173733	-4.518328	22110.310014
HLA A*3301	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.617706	0.099112	-4.518594	41467.324671
HLA B*7301	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.582043	0.063148	-4.518895	38198.225150
HLA B*4001	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.403950	-0.115163	-4.519113	25348.360303
HLA A*6802	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.396953	-0.122654	-4.519607	24943.253772
HLA B*7301	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.563844	0.044127	-4.519717	36630.603462
HLA B*7301	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.538730	0.019002	-4.519728	34572.471574
HLA A*0202	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.494212	-0.025677	-4.519890	31204.152119
HLA B*5401	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.564570	0.044127	-4.520443	36691.888430
HLA B*0801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.397968	-0.122654	-4.520622	25001.616127
HLA B*4002	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.619898	0.099112	-4.520786	41677.157058
HLA A*0212	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.405862	-0.115163	-4.521026	25460.231744
HLA A*0212	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.398607	-0.122654	-4.521261	25038.432832
HLA A*2301	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.538221	0.016895	-4.521326	34531.909175
HLA A*2603	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.620507	0.099112	-4.521394	41735.594408
HLA B*1502	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.482127	-0.039278	-4.521404	30347.759628
HLA B*4002	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.486506	-0.035118	-4.521624	30655.335646
HLA A*2603	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.641217	0.119542	-4.521675	43774.108849
HLA A*3301	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.622212	0.100401	-4.521811	41899.836600
HLA A*2301	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.541148	0.019002	-4.522146	34765.465455
HLA B*5101	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.496675	-0.025677	-4.522352	31381.568512
HLA A*3101	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.415824	-0.106651	-4.522475	26050.986197
HLA A*2602	1:230-238	9	MGVWAKLNS	1.150403	-1.051291	-4.621623	0.099112	-4.522510	41842.980169
HLA A*0206	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.496839	-0.025677	-4.522516	31393.454719
HLA B*5701	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.414219	-0.108442	-4.522661	25954.906608
HLA A*3002	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.615422	0.092742	-4.522681	41249.844684
HLA B*1501	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.416101	-0.106651	-4.522752	26067.621594
HLA B*3901	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.488233	-0.034919	-4.523152	30777.472155
HLA B*0803	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.483983	-0.039278	-4.523260	30477.737814
HLA A*0202	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.516197	-0.007282	-4.523478	32824.378931
HLA B*2705	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.455035	-0.068483	-4.523518	28512.462296
HLA B*5301	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.361960	-0.162047	-4.524007	23012.291975
HLA A*2301	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.513513	-0.010665	-4.524178	32622.211998

HLA A*2603	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.498817	-0.025677	-4.524495	31536.782071
HLA A*0206	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.543540	0.019002	-4.524537	34957.456348
HLA B*0801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.363069	-0.161502	-4.524571	23071.128205
HLA B*1509	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.538068	0.013159	-4.524909	34519.768413
HLA A*2301	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.544548	0.019638	-4.524910	35038.681315
HLA A*3101	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.402272	-0.122654	-4.524926	25250.637042
HLA B*4601	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.418406	-0.106651	-4.525057	26206.332853
HLA A*6802	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.416710	-0.108442	-4.525152	26104.172137
HLA A*1101	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.415690	-0.109508	-4.525198	26042.954258
HLA A*2501	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.447368	-0.077944	-4.525312	28013.563314
HLA A*0101	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.377701	-0.147950	-4.525652	23861.702411
HLA B*1501	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.364648	-0.161502	-4.526150	23155.154679
HLA A*0206	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.403499	-0.122654	-4.526153	25322.044663
HLA B*0802	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.457734	-0.068483	-4.526217	28690.246674
HLA A*0301	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.352487	-0.173733	-4.526220	22515.767326
HLA A*3002	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.589376	0.063148	-4.526228	38848.649585
HLA B*3801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.542060	0.015810	-4.526249	34838.516094
HLA B*7301	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.417997	-0.108442	-4.526439	26181.675896
HLA B*4501	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.619191	0.092742	-4.526449	41609.346176
HLA B*1517	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.491454	-0.035118	-4.526572	31006.596024
HLA A*3301	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.640287	0.113485	-4.526802	43680.431250
HLA A*0203	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.379236	-0.147950	-4.527186	23946.146704
HLA A*6801	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.668420	0.141159	-4.527261	46603.619832
HLA B*1503	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.403550	-0.123980	-4.527531	25325.058610
HLA A*0301	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.348063	-0.179556	-4.527619	22287.567518
HLA B*2705	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.492629	-0.035118	-4.527747	31090.580684
HLA A*2602	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.450054	-0.077944	-4.527998	28187.321940
HLA B*1502	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.544989	0.016895	-4.528095	35074.335855
HLA A*0212	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.381402	-0.146721	-4.528123	24065.886493
HLA B*3901	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.493063	-0.035118	-4.528181	31121.712630
HLA A*0202	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.591396	0.063148	-4.528249	39029.814216
HLA B*4801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.420016	-0.108442	-4.528458	26303.627767
HLA B*5801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.354731	-0.173733	-4.528464	22632.394796
HLA A*2402	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.572657	0.044127	-4.528530	37381.523017
HLA A*0203	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.405999	-0.122654	-4.528653	25468.221746
HLA A*8001	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.420283	-0.108442	-4.528725	26319.854937
HLA A*2403	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.367303	-0.161502	-4.528805	23297.139733
HLA A*6901	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.268519	-0.260368	-4.528887	18557.458910
HLA A*2403	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.413886	-0.115163	-4.529049	25934.975595
HLA A*3201	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.622074	0.092742	-4.529332	41886.464999
HLA A*2601	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.349938	-0.179556	-4.529494	22383.992976
HLA A*0301	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.367733	-0.162047	-4.529780	23320.215548
HLA B*3801	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.549562	0.019638	-4.529923	35445.536492
HLA B*4402	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.420577	-0.109508	-4.530085	26337.659394
HLA B*4403	1:37-45	9	IPDAGDPPP	0.238307	-0.097148	-4.671321	0.141159	-4.530162	46916.031028
HLA B*4001	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.406243	-0.123980	-4.530223	25482.554924
HLA B*4501	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.550558	0.019638	-4.530920	35526.934535
HLA A*2902	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.408266	-0.122654	-4.530920	25601.527354
HLA A*2403	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.382995	-0.147950	-4.530945	24154.319958
HLA A*2902	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.422516	-0.108442	-4.530957	26455.471254
HLA B*0802	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.453214	-0.077944	-4.531158	28393.169372
HLA A*3001	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.298115	-0.233064	-4.531179	19866.207631
HLA B*4402	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.407274	-0.123980	-4.531255	25543.146419
HLA B*4403	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.645458	0.113485	-4.531973	44203.650242
HLA B*5701	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.425565	-0.106651	-4.532216	26641.896304
HLA A*3301	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.635722	0.103191	-4.532531	43223.692816

HLA B*4403	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.625281	0.092742	-4.532539	42196.920413
HLA B*4002	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.652138	0.119542	-4.532596	44888.771484
HLA B*0702	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.424228	-0.108442	-4.532670	26560.012595
HLA A*3002	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.417528	-0.115163	-4.532691	26153.363223
HLA A*3301	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.521145	-0.011592	-4.532736	33200.493024
HLA A*0212	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.424311	-0.108442	-4.532752	26565.042106
HLA A*3002	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.586298	0.053318	-4.532980	38574.304247
HLA A*0203	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.386293	-0.146721	-4.533014	24338.482233
HLA B*1503	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.498160	-0.034919	-4.533079	31489.047295
HLA A*0211	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.552221	0.019002	-4.533219	35663.270784
HLA B*3801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.586578	0.053318	-4.533260	38599.145485
HLA B*5101	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.498211	-0.035118	-4.533329	31492.795268
HLA A*8001	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.418178	-0.115163	-4.533342	26192.584445
HLA B*5701	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.410113	-0.123980	-4.534093	25710.621253
HLA A*2601	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.386197	-0.147950	-4.534147	24333.084424
HLA A*2402	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.597329	0.063148	-4.534181	39566.618328
HLA B*0803	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.508650	-0.025677	-4.534327	32258.931011
HLA B*1517	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.372840	-0.161502	-4.534343	23596.106120
HLA A*0211	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.466345	-0.068483	-4.534828	29264.771992
HLA B*7301	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.499997	-0.034919	-4.534916	31622.544942
HLA A*2602	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.638490	0.103191	-4.535299	43500.030495
HLA A*6801	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.654863	0.119542	-4.535321	45171.355432
HLA A*2402	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.588845	0.053318	-4.535527	38801.180893
HLA A*0250	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.599051	0.063148	-4.535903	39723.829225
HLA A*3301	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.523821	-0.012369	-4.536190	33405.701522
HLA A*0101	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.374894	-0.161502	-4.536396	23707.938423
HLA B*0803	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.525754	-0.010665	-4.536419	33554.766619
HLA A*3101	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.389867	-0.146721	-4.536588	24539.576218
HLA B*1502	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.560578	0.023895	-4.536684	36356.183708
HLA A*0202	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.556610	0.019638	-4.536972	36025.499333
HLA A*6801	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.640285	0.103191	-4.537094	43680.194944
HLA B*7301	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.497838	-0.039278	-4.537115	31465.717682
HLA A*0101	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.390605	-0.146721	-4.537326	24581.297149
HLA A*2602	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.581493	0.044127	-4.537366	38149.900074
HLA A*0206	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.498124	-0.039278	-4.537402	31486.492115
HLA B*1509	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.429505	-0.108442	-4.537947	26884.701566
HLA B*5401	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.554935	0.016895	-4.538040	35886.807597
HLA B*1501	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.364591	-0.173733	-4.538324	23152.148470
HLA A*0212	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.390497	-0.147950	-4.538447	24575.180734
HLA A*3301	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.631302	0.092742	-4.538561	42786.078811
HLA B*4501	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.591951	0.053318	-4.538633	39079.676725
HLA A*0211	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.528017	-0.010665	-4.538682	33730.033817
HLA B*3901	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.499651	-0.039278	-4.538929	31597.406993
HLA A*0219	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.424334	-0.115163	-4.539497	26566.479284
HLA A*0250	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.563471	0.023895	-4.539576	36599.108377
HLA B*3801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.556626	0.016895	-4.539732	36026.863616
HLA A*0211	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.504813	-0.034919	-4.539732	31975.199494
HLA A*6801	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.584162	0.044127	-4.540035	38385.077316
HLA B*0801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.378192	-0.162047	-4.540240	23888.697305
HLA B*5701	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.417828	-0.122654	-4.540482	26171.479805
HLA B*4501	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.462802	-0.077944	-4.540746	29026.997893
HLA B*4501	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.660730	0.119542	-4.541188	45785.692420
HLA B*5401	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.554369	0.013159	-4.541210	35840.049466
HLA B*4501	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.644685	0.103191	-4.541494	44125.044193

HLA A*0250	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.594972	0.053318	-4.541654	39352.506579
HLA A*2602	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.534490	-0.007282	-4.541771	34236.519509
HLA A*2602	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.560825	0.019002	-4.541823	36376.841282
HLA A*0201	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.395196	-0.146721	-4.541916	24842.522422
HLA B*4001	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.394136	-0.147950	-4.542086	24781.984027
HLA A*6802	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.435576	-0.106651	-4.542227	27263.166081
HLA B*1502	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.529981	-0.012369	-4.542350	33882.929026
HLA B*4001	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.435858	-0.106651	-4.542509	27280.870712
HLA A*2501	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.427536	-0.115163	-4.542700	26763.095975
HLA A*0203	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.381404	-0.161502	-4.542907	24066.016687
HLA B*5301	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.606363	0.063148	-4.543215	40398.264051
HLA A*0201	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.395597	-0.147950	-4.543548	24865.514650
HLA B*0801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.419722	-0.123980	-4.543702	26285.846316
HLA A*3201	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.597188	0.053318	-4.543870	39553.777351
HLA A*0212	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.437576	-0.106651	-4.544226	27388.970039
HLA B*0803	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.509362	-0.034919	-4.544281	32311.853097
HLA B*3501	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.382917	-0.161502	-4.544420	24150.008161
HLA A*6802	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.349536	-0.194957	-4.544493	22363.295320
HLA A*2301	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.532142	-0.012369	-4.544512	34051.988047
HLA A*8001	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.422215	-0.122654	-4.544869	26437.158086
HLA B*1509	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.435525	-0.109508	-4.545032	27259.921479
HLA A*2601	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.383512	-0.162047	-4.545559	24183.084955
HLA B*4002	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.638386	0.092742	-4.545644	43489.677192
HLA B*4801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.423051	-0.122654	-4.545705	26488.123013
HLA B*1502	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.599072	0.053318	-4.545754	39725.763385
HLA B*4002	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.649231	0.103191	-4.546040	44589.377245
HLA B*4601	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.398182	-0.147950	-4.546132	25013.927451
HLA B*4501	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.644105	0.097839	-4.546266	44066.121805
HLA B*5101	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.511540	-0.034919	-4.546459	32474.302982
HLA A*3001	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.286133	-0.260368	-4.546501	19325.582662
HLA A*0250	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.562324	0.015810	-4.546514	36502.613214
HLA B*3801	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.565545	0.019002	-4.546543	36774.358078
HLA B*4403	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.600169	0.053318	-4.546851	39826.254166
HLA A*6801	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.647528	0.100401	-4.547127	44414.832664
HLA A*2402	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.566490	0.019002	-4.547487	36854.421076
HLA A*0202	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.564396	0.016895	-4.547502	36677.202441
HLA B*3501	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.352583	-0.194957	-4.547540	22520.762000
HLA B*1509	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.508537	-0.039278	-4.547815	32250.555271
HLA A*0206	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.513051	-0.034919	-4.547970	32587.463455
HLA B*4001	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.401286	-0.146721	-4.548006	25193.328851
HLA A*2402	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.563863	0.015810	-4.548053	36632.188837
HLA A*0101	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.368513	-0.179556	-4.548069	23362.138232
HLA A*0201	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.387069	-0.161502	-4.548571	24381.971644
HLA B*4801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.442026	-0.106651	-4.548676	27671.049135
HLA B*4601	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.402289	-0.146721	-4.549010	25251.593282
HLA B*0801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.401116	-0.147950	-4.549067	25183.517657
HLA B*5701	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.434204	-0.115163	-4.549367	27177.167431
HLA A*2403	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.402832	-0.146721	-4.549552	25283.169530
HLA A*0101	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.375888	-0.173733	-4.549621	23762.253391
HLA A*0211	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.524373	-0.025677	-4.550050	33448.197998
HLA B*4002	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.650514	0.100401	-4.550113	44721.280035
HLA B*5301	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.603576	0.053318	-4.550258	40139.893353
HLA A*0101	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.388380	-0.162047	-4.550427	24455.685148

HLA A*3101	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.389033	-0.161502	-4.550535	24492.492927
HLA B*4402	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.444124	-0.106651	-4.550774	27805.052257
HLA B*2705	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.428222	-0.122654	-4.550876	26805.406717
HLA B*5801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.356039	-0.194957	-4.550996	22700.696032
HLA A*3101	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.403048	-0.147950	-4.550998	25295.756343
HLA A*0250	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.567989	0.016895	-4.551094	36981.844227
HLA B*4002	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.649100	0.097839	-4.551261	44575.870770
HLA A*2403	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.428692	-0.122654	-4.551346	26834.425269
HLA B*3901	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.427872	-0.123980	-4.551853	26783.808296
HLA B*2705	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.427879	-0.123980	-4.551860	26784.242992
HLA B*3901	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.429355	-0.122654	-4.552009	26875.394809
HLA B*4001	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.389996	-0.162047	-4.552043	24546.878906
HLA A*2301	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.544834	-0.007282	-4.552116	35061.814705
HLA A*0203	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.445545	-0.106651	-4.552196	27896.206811
HLA A*3001	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.309378	-0.242879	-4.552257	20388.177282
HLA A*0202	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.437204	-0.115163	-4.552368	27365.568977
HLA B*4403	1:71-79	9	PTNPPAAAD	1.087869	-0.990030	-4.650369	0.097839	-4.552529	44706.282446
HLA A*2501	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.443341	-0.109508	-4.552849	27755.006740
HLA A*0219	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.428953	-0.123980	-4.552933	26850.544119
HLA B*0802	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.443452	-0.109508	-4.552960	27762.064758
HLA A*3201	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.475353	-0.077944	-4.553297	29878.106453
HLA B*5301	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.597543	0.044127	-4.553415	39586.101766
HLA B*4801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.406043	-0.147950	-4.553993	25470.839705
HLA B*4403	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.657262	0.103191	-4.554071	45421.549607
HLA A*8001	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.447502	-0.106651	-4.554153	28022.203012
HLA B*5401	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.476272	-0.077944	-4.554216	29941.373505
HLA A*6901	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.359387	-0.194957	-4.554344	22876.374076
HLA A*1101	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.445935	-0.108442	-4.554377	27921.270017
HLA B*3801	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.567584	0.013159	-4.554425	36947.448591
HLA B*3801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.543843	-0.010665	-4.554508	34981.860822
HLA A*0219	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.446238	-0.108442	-4.554680	27940.762394
HLA A*2902	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.381007	-0.173733	-4.554740	24044.023875
HLA A*2601	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.393323	-0.161502	-4.554825	24735.639961
HLA B*5401	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.543237	-0.011592	-4.554828	34933.068900
HLA A*2602	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.618439	0.063148	-4.555291	41537.375866
HLA B*4601	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.375937	-0.179556	-4.555493	23764.953119
HLA A*0216	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.431862	-0.123980	-4.555842	27030.977648
HLA B*3501	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.382299	-0.173733	-4.556032	24115.671941
HLA A*0201	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.394019	-0.162047	-4.556066	24775.281545
HLA A*2301	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.537511	-0.018628	-4.556139	34475.537470
HLA B*5701	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.408259	-0.147950	-4.556209	25601.111853
HLA A*0216	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.441220	-0.115163	-4.556383	27619.750568
HLA B*1509	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.544195	-0.012369	-4.556565	35010.259542
HLA B*7301	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.530925	-0.025677	-4.556603	33956.696973
HLA B*5401	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.377215	-0.179556	-4.556771	23834.995910
HLA B*4402	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.410216	-0.146721	-4.556937	25716.742012
HLA B*1503	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.383455	-0.173733	-4.557188	24179.945291
HLA A*8001	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.410665	-0.146721	-4.557386	25743.328568
HLA A*2603	1:25-33	9	GGAHRAATG	0.837696	-0.734505	-4.660859	0.103191	-4.557668	45799.317701
HLA A*2301	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.546545	-0.011592	-4.558136	35200.174411
HLA B*1509	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.546690	-0.011592	-4.558282	35211.982991
HLA B*4403	1:141-149	9	PAPARPAEG	0.855639	-0.736097	-4.678102	0.119542	-4.558560	47654.276301
HLA B*1502	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.548037	-0.010665	-4.558702	35321.304791
HLA B*3901	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.490651	-0.068483	-4.559134	30949.281214

HLA A*0202	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.578277	0.019002	-4.559275	37868.400340
HLA A*3002	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.548662	-0.010665	-4.559327	35372.169816
HLA A*6801	1:6-14	9	EPGALSKGD	1.111689	-1.018947	-4.652128	0.092742	-4.559387	44887.800121
HLA A*3002	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.575488	0.015810	-4.559678	37626.006057
HLA B*4801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.413075	-0.146721	-4.559796	25886.615396
HLA A*3201	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.623305	0.063148	-4.560157	42005.372451
HLA B*4501	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.660610	0.100401	-4.560209	45773.061691
HLA A*0211	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.451799	-0.108442	-4.560241	28300.850236
HLA B*4501	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.623474	0.063148	-4.560326	42021.737235
HLA B*0702	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.437674	-0.122654	-4.560328	27395.193940
HLA B*4001	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.387111	-0.173733	-4.560844	24384.346027
HLA A*0206	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.492387	-0.068483	-4.560870	31073.261260
HLA B*4002	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.580577	0.019638	-4.560939	38069.494101
HLA A*2902	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.398969	-0.162047	-4.561016	25059.301617
HLA B*5701	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.414370	-0.146721	-4.561091	25963.894607
HLA B*4601	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.399733	-0.161502	-4.561235	25103.399987
HLA A*2603	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.580934	0.019638	-4.561296	38100.811641
HLA B*5101	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.492819	-0.068483	-4.561302	31104.207593
HLA B*5701	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.382048	-0.179556	-4.561604	24101.716428
HLA B*1517	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.453298	-0.108442	-4.561740	28398.699650
HLA B*1503	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.526729	-0.035118	-4.561847	33630.185190
HLA B*0702	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.253094	-0.308836	-4.561930	17909.940315
HLA A*0201	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.388227	-0.173733	-4.561960	24447.086994
HLA A*0301	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.367025	-0.194957	-4.561983	23282.272355
HLA A*0211	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.522909	-0.039278	-4.562187	33335.655259
HLA A*2402	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.586206	0.023895	-4.562312	38566.166480
HLA A*2402	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.582085	0.019638	-4.562447	38201.944998
HLA B*3901	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.484582	-0.077944	-4.562526	30519.811530
HLA B*5701	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.401025	-0.161502	-4.562527	25178.204856
HLA B*5401	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.550614	-0.012369	-4.562983	35531.547557
HLA A*2602	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.582682	0.019638	-4.563044	38254.474826
HLA B*0803	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.528108	-0.035118	-4.563226	33737.151122
HLA B*5301	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.582694	0.019002	-4.563692	38255.509602
HLA A*3001	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.300596	-0.263155	-4.563751	19980.024956
HLA A*2501	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.495561	-0.068483	-4.564044	31301.200237
HLA B*4402	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.442044	-0.122654	-4.564698	27672.246740
HLA A*0211	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.530047	-0.035118	-4.565165	33888.061895
HLA B*5101	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.403160	-0.162047	-4.565208	25302.325863
HLA A*0219	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.418691	-0.146721	-4.565411	26223.493045
HLA B*4601	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.391765	-0.173733	-4.565498	24647.078163
HLA B*1801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.456195	-0.109508	-4.565703	28588.763342
HLA A*1101	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.443151	-0.122654	-4.565805	27742.847132
HLA B*4403	1:132-140	9	PTPRAPQRN	0.907048	-0.806647	-4.667118	0.100401	-4.566717	46464.154220
HLA B*0702	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.405219	-0.161502	-4.566721	25422.519755
HLA A*3301	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.556448	-0.010665	-4.567113	36012.054159
HLA B*1509	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.531997	-0.035118	-4.567115	34040.568478
HLA B*4001	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.387628	-0.179556	-4.567184	24413.384958
HLA A*0250	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.586979	0.019002	-4.567977	38634.869730
HLA B*7301	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.591991	0.023895	-4.568096	39083.270974
HLA A*6801	1:57-65	9	GHRQPPPVS	1.076955	-0.963470	-4.681708	0.113485	-4.568224	48051.653644
HLA A*3101	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.389009	-0.179556	-4.568566	24491.167946
HLA A*3101	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.406671	-0.162047	-4.568718	25507.657399
HLA A*2402	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.557270	-0.011592	-4.568862	36080.306183
HLA A*6801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.550628	-0.018628	-4.569256	35532.700906
HLA A*0250	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.460173	-0.109508	-4.569681	28851.808947

HLA B*2705	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.408296	-0.161502	-4.569799	25603.327936
HLA A*2301	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.530688	-0.039278	-4.569966	33938.148142
HLA A*2602	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.585786	0.015810	-4.569976	38528.838232
HLA B*1509	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.535631	-0.034919	-4.570550	34326.652813
HLA B*3801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.462189	-0.108442	-4.570631	28986.041244
HLA B*4601	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.408762	-0.162047	-4.570809	25630.767840
HLA B*0702	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.464461	-0.106651	-4.571111	29138.075067
HLA A*2602	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.584444	0.013159	-4.571285	38410.004488
HLA A*6901	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.262532	-0.308836	-4.571368	18303.410494
HLA A*2902	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.464776	-0.106651	-4.571426	29159.205648
HLA A*3201	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.559089	-0.012369	-4.571458	36231.700338
HLA A*0202	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.448896	-0.122654	-4.571549	28112.244392
HLA A*0219	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.465140	-0.106651	-4.571790	29183.666853
HLA A*8001	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.448090	-0.123980	-4.572070	28060.127905
HLA A*0216	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.449436	-0.122654	-4.572090	28147.245512
HLA A*0201	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.392769	-0.179556	-4.572325	24704.079284
HLA B*5401	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.546843	-0.025677	-4.572521	35224.367209
HLA A*2301	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.537459	-0.035118	-4.572577	34471.434519
HLA B*4403	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.494856	-0.077944	-4.572800	31250.440632
HLA B*0803	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.464374	-0.108442	-4.572816	29132.243201
HLA A*0216	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.426263	-0.146721	-4.572984	26684.737235
HLA A*2402	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.589999	0.016895	-4.573104	38904.383752
HLA A*0250	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.592820	0.019638	-4.573182	39157.979252
HLA B*7301	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.458117	-0.115163	-4.573280	28715.557234
HLA A*2301	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.547607	-0.025677	-4.573284	35286.353660
HLA A*2902	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.427038	-0.146721	-4.573759	26732.419069
HLA B*3901	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.412272	-0.161502	-4.573774	25838.764724
HLA A*0212	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.411837	-0.162047	-4.573884	25812.917462
HLA A*2603	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.561671	-0.012369	-4.574040	36447.756400
HLA B*3501	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.426221	-0.147950	-4.574171	26682.138855
HLA B*0801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.341190	-0.233064	-4.574255	21937.666410
HLA B*1801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.400762	-0.173733	-4.574495	25162.953812
HLA A*0219	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.451842	-0.122654	-4.574496	28303.606251
HLA B*4801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.413411	-0.161502	-4.574914	25906.649396
HLA B*1801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.497022	-0.077944	-4.574966	31406.704653
HLA A*3201	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.588352	0.013159	-4.575192	38757.124805
HLA B*1501	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.413146	-0.162047	-4.575193	25890.817048
HLA A*3301	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.638483	0.063148	-4.575335	43499.324510
HLA A*0250	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.568209	-0.007282	-4.575491	37000.655371
HLA A*0202	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.540502	-0.035118	-4.575620	34713.782648
HLA A*0206	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.414288	-0.161502	-4.575790	25958.978910
HLA A*0212	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.414673	-0.161502	-4.576175	25982.020502
HLA B*1502	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.541571	-0.034919	-4.576490	34799.335860
HLA A*3201	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.594042	0.016895	-4.577147	39268.291311
HLA B*0802	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.462304	-0.115163	-4.577467	28993.726014
HLA A*2301	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.542616	-0.034919	-4.577535	34883.212727
HLA B*1509	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.558983	-0.018628	-4.577611	36222.880985
HLA B*7301	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.570366	-0.007282	-4.577648	37184.867967
HLA B*3501	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.469409	-0.108442	-4.577851	29471.950102
HLA A*0206	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.404206	-0.173733	-4.577939	25363.312079
HLA B*5301	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.601934	0.023895	-4.578039	39988.390479
HLA A*2602	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.595482	0.016895	-4.578588	39398.731422
HLA A*6801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.432320	-0.146721	-4.579041	27059.508440

HLA A*2602	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.632491	0.053318	-4.579173	42903.362042
HLA A*3201	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.603120	0.023895	-4.579226	40097.787891
HLA A*2603	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.572020	-0.007282	-4.579302	37326.758869
HLA A*3201	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.599432	0.019638	-4.579794	39758.658530
HLA A*2601	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.384975	-0.194957	-4.579933	24264.728186
HLA B*1502	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.599093	0.019002	-4.580091	39727.697640
HLA B*0702	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.418101	-0.162047	-4.580148	26187.908796
HLA B*0702	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.470814	-0.109508	-4.580322	29567.449604
HLA B*0802	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.434037	-0.146721	-4.580758	27166.730628
HLA B*7301	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.597954	0.016895	-4.581059	39623.596886
HLA B*3901	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.433173	-0.147950	-4.581123	27112.699837
HLA B*5101	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.503241	-0.077944	-4.581186	31859.683510
HLA B*5701	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.419586	-0.162047	-4.581633	26277.599806
HLA B*3801	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.570799	-0.011592	-4.582390	37221.900942
HLA A*6802	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.434660	-0.147950	-4.582610	27205.705344
HLA A*1101	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.467656	-0.115163	-4.582819	29353.247565
HLA A*3201	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.598915	0.015810	-4.583105	39711.366892
HLA B*0702	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.459315	-0.123980	-4.583296	28794.894101
HLA B*0702	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.340511	-0.242879	-4.583390	21903.394589
HLA B*4002	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.646602	0.063148	-4.583454	44320.263434
HLA A*2403	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.409734	-0.173733	-4.583467	25688.237253
HLA B*7301	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.596857	0.013159	-4.583698	39523.617457
HLA A*6901	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.275926	-0.307784	-4.583710	18876.715648
HLA A*3301	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.637195	0.053318	-4.583877	43370.556543
HLA A*2501	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.461240	-0.122654	-4.583894	28922.758671
HLA B*1801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.461244	-0.122654	-4.583898	28923.071610
HLA B*1503	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.437641	-0.146721	-4.584362	27393.119149
HLA B*3801	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.565949	-0.018628	-4.584577	36808.592577
HLA B*3901	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.405136	-0.179556	-4.584693	25417.706555
HLA A*6802	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.422821	-0.162047	-4.584868	26474.083550
HLA A*1101	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.437273	-0.147950	-4.585223	27369.862610
HLA B*4001	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.390412	-0.194957	-4.585369	24570.395036
HLA B*4501	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.601213	0.015810	-4.585402	39922.031443
HLA B*1503	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.437524	-0.147950	-4.585474	27385.710464
HLA A*0101	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.390607	-0.194957	-4.585564	24581.430132
HLA B*4403	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.601445	0.015810	-4.585635	39943.418572
HLA A*2603	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.629919	0.044127	-4.585791	42649.961172
HLA A*2403	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.342981	-0.242879	-4.585859	22028.287489
HLA B*5801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.352820	-0.233064	-4.585884	22533.070680
HLA A*2402	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.578728	-0.007282	-4.586010	37907.754634
HLA B*5301	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.603332	0.016895	-4.586437	40117.315858
HLA A*3101	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.412960	-0.173733	-4.586693	25879.754163
HLA B*5401	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.551911	-0.035118	-4.587029	35637.812542
HLA B*1501	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.392087	-0.194957	-4.587045	24665.352235
HLA B*7301	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.575643	-0.011592	-4.587235	37639.442923
HLA B*5301	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.603182	0.015810	-4.587371	40103.428327
HLA B*1517	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.480773	-0.106651	-4.587424	30253.340278
HLA B*0702	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.407881	-0.179556	-4.587437	25578.823194
HLA B*0802	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.479136	-0.108442	-4.587578	30139.479030
HLA A*2402	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.575469	-0.012369	-4.587839	37624.377673
HLA B*5301	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.601055	0.013159	-4.587896	39907.563823
HLA A*3002	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.478974	-0.109508	-4.588481	30128.230594

HLA A*8001	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.414866	-0.173733	-4.588599	25993.548967
HLA A*6802	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.427097	-0.161502	-4.588599	26736.034799
HLA A*6901	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.346075	-0.242879	-4.588954	22185.795603
HLA B*1517	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.473840	-0.115163	-4.589003	29774.193189
HLA A*0216	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.482437	-0.106651	-4.589087	30369.438866
HLA A*2402	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.570507	-0.018628	-4.589135	37196.939887
HLA A*0211	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.465302	-0.123980	-4.589282	29194.562635
HLA B*5301	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.608954	0.019638	-4.589316	40640.045495
HLA A*3001	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.279425	-0.310152	-4.589577	19029.387813
HLA B*1517	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.443146	-0.146721	-4.589867	27742.546962
HLA A*6801	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.613952	0.023895	-4.590057	41110.384628
HLA A*0219	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.442195	-0.147950	-4.590145	27681.829441
HLA A*2501	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.481983	-0.108442	-4.590425	30337.746422
HLA A*1101	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.429367	-0.161502	-4.590869	26876.121784
HLA A*2902	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.429381	-0.161502	-4.590883	26876.994179
HLA A*2402	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.580321	-0.010665	-4.590986	38047.051979
HLA A*3301	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.565439	-0.025677	-4.591117	36765.406633
HLA B*0803	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.444396	-0.146721	-4.591117	27822.506715
HLA B*0801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.396479	-0.194957	-4.591436	24916.010733
HLA B*0702	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.417727	-0.173733	-4.591460	26165.392366
HLA B*5401	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.556718	-0.034919	-4.591637	36034.465571
HLA B*4402	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.412244	-0.179556	-4.591800	25837.087360
HLA A*6901	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.358765	-0.233064	-4.591829	22843.601532
HLA A*0201	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.396899	-0.194957	-4.591856	24940.150340
HLA B*4403	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.655556	0.063148	-4.592408	45243.502734
HLA B*4501	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.609835	0.016895	-4.592941	40722.575984
HLA B*4501	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.606327	0.013159	-4.593168	40394.985932
HLA B*1502	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.558198	-0.035118	-4.593316	36157.488850
HLA A*3301	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.617913	0.023895	-4.594018	41487.070730
HLA B*1502	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.525764	-0.068483	-4.594247	33555.492738
HLA A*6801	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.611144	0.016895	-4.594249	40845.470725
HLA A*0219	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.432867	-0.161502	-4.594370	27093.638569
HLA A*3301	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.575927	-0.018628	-4.594556	37664.089639
HLA A*2501	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.488226	-0.106651	-4.594876	30776.972651
HLA A*3001	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.251868	-0.343296	-4.595164	17859.434668
HLA A*8001	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.433925	-0.161502	-4.595427	27159.677032
HLA A*0203	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.433412	-0.162047	-4.595460	27127.664989
HLA A*0206	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.487204	-0.108442	-4.595646	30704.630302
HLA A*2603	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.649046	0.053318	-4.595728	44570.324653
HLA A*3201	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.614781	0.019002	-4.595779	41188.967765
HLA B*0802	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.489130	-0.106651	-4.595781	30841.141958
HLA B*0702	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.448134	-0.147950	-4.596084	28063.012295
HLA A*2603	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.615305	0.019002	-4.596303	41238.688338
HLA A*6801	1:148-156	9	EGGAGSRGD	1.060267	-0.997119	-4.660528	0.063148	-4.597380	45764.395560
HLA A*8001	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.417993	-0.179556	-4.597549	26181.392618
HLA B*5801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.354747	-0.242879	-4.597626	22633.251883
HLA A*0202	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.562775	-0.034919	-4.597694	36540.548129
HLA B*5101	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.337474	-0.260368	-4.597842	21750.715254
HLA A*2501	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.424195	-0.173733	-4.597928	26558.001057
HLA A*1101	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.451219	-0.146721	-4.597940	28263.058689
HLA A*2602	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.622090	0.023895	-4.598196	41888.051237
HLA B*0803	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.489036	-0.109508	-4.598544	30834.468793

HLA B*4002	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.622675	0.023895	-4.598781	41944.515077
HLA B*4002	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.611964	0.013159	-4.598805	40922.661917
HLA B*1509	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.356363	-0.242879	-4.599242	22717.649898
HLA A*2902	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.451560	-0.147950	-4.599510	28285.237889
HLA A*2501	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.420446	-0.179556	-4.600002	26329.681508
HLA B*3801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.561377	-0.039278	-4.600655	36423.117441
HLA B*2705	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.426982	-0.173733	-4.600715	26728.948429
HLA A*3201	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.593692	-0.007282	-4.600974	39236.650937
HLA B*4501	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.624893	0.023895	-4.600998	42159.270909
HLA B*4801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.427311	-0.173733	-4.601044	26749.200187
HLA A*0212	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.368076	-0.233064	-4.601140	23338.642152
HLA A*0216	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.453266	-0.147950	-4.601216	28396.548858
HLA A*0301	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.368278	-0.233064	-4.601342	23349.502993
HLA B*4501	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.620565	0.019002	-4.601563	41741.239413
HLA B*1517	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.478988	-0.122654	-4.601642	30129.208553
HLA B*3801	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.576003	-0.025677	-4.601680	37670.610477
HLA A*1101	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.495288	-0.106651	-4.601939	31281.563421
HLA A*0203	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.422478	-0.179556	-4.602034	26453.181415
HLA A*2501	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.478109	-0.123980	-4.602089	30068.309798
HLA B*2705	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.495697	-0.106651	-4.602348	31311.023268
HLA B*3901	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.496870	-0.106651	-4.603520	31395.662653
HLA A*2603	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.620742	0.016895	-4.603847	41758.179010
HLA B*1509	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.457196	-0.146721	-4.603917	28654.725350
HLA B*7301	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.424661	-0.179556	-4.604217	26586.464115
HLA B*5701	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.430523	-0.173733	-4.604256	26947.752315
HLA B*4002	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.648390	0.044127	-4.604263	44503.102773
HLA B*4601	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.409438	-0.194957	-4.604396	25670.732934
HLA A*3002	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.569492	-0.034919	-4.604411	37110.109460
HLA B*4402	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.442947	-0.161502	-4.604449	27729.792746
HLA A*0206	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.489361	-0.115163	-4.604524	30857.497314
HLA B*1509	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.526616	-0.077944	-4.604561	33621.453416
HLA B*4801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.442594	-0.162047	-4.604641	27707.299608
HLA A*0101	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.371640	-0.233064	-4.604704	23530.965865
HLA B*4501	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.648996	0.044127	-4.604869	44565.261410
HLA B*0802	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.482477	-0.122654	-4.605131	30372.232015
HLA B*4002	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.565933	-0.039278	-4.605210	36807.198691
HLA A*3001	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.297690	-0.307784	-4.605473	19846.764361
HLA B*1801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.537234	-0.068483	-4.605717	34453.536450
HLA B*0803	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.537614	-0.068483	-4.606098	34483.744835
HLA B*5301	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.594665	-0.011592	-4.606256	39324.627516
HLA A*2603	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.619898	0.013159	-4.606739	41677.157058
HLA A*0250	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.596121	-0.010665	-4.606786	39456.748931
HLA B*1517	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.459085	-0.147950	-4.607035	28779.631983
HLA A*0301	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.364241	-0.242879	-4.607120	23133.493657
HLA A*0202	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.433549	-0.173733	-4.607282	27136.178268
HLA A*0219	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.445362	-0.162047	-4.607409	27884.437894
HLA A*2402	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.581754	-0.025677	-4.607432	38172.815881
HLA A*1101	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.427971	-0.179556	-4.607527	26789.894679
HLA A*0202	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.597162	-0.010665	-4.607827	39551.423624
HLA A*3101	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.347755	-0.260368	-4.608123	22271.778015
HLA B*5101	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.428612	-0.179556	-4.608169	26829.489900
HLA A*2402	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.573425	-0.035118	-4.608543	37447.710720
HLA B*5301	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.590128	-0.018628	-4.608756	38915.961236
HLA A*0206	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.462151	-0.146721	-4.608872	28983.532372
HLA B*3801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.573980	-0.034919	-4.608899	

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37495.552013
HLA B*0803	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.531362	-0.077944	-4.609307	33990.882735
HLA A*3301	1:46-54 9	WQRAATRQS	1.013661	-0.997851	-4.625260	0.015810	-4.609449	42194.865937
HLA A*3301	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.626824	0.016895	-4.609930	42347.167661
HLA A*2301	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.541479	-0.068483	-4.609962	34791.994473
HLA B*2705	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.495014	-0.115163	-4.610177	31261.769800
HLA B*1517	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.436551	-0.173733	-4.610284	27324.443485
HLA B*0803	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.495164	-0.115163	-4.610327	31272.595528
HLA B*5801	1:3-11  9	APNEPGALS	0.822079	-1.082447	-4.350043	-0.260368	-4.610412	22389.442911
HLA B*5401	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.542015	-0.068483	-4.610498	34834.935301
HLA B*4402	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.448562	-0.162047	-4.610609	28090.656739
HLA A*6802	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.367925	-0.242879	-4.610804	23330.562945
HLA B*5101	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.495824	-0.115163	-4.610987	31320.171619
HLA A*0216	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.449577	-0.161502	-4.611079	28156.383403
HLA B*4402	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.437463	-0.173733	-4.611196	27381.858740
HLA A*0212	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.431827	-0.179556	-4.611383	27028.784218
HLA B*4501	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.599434	-0.012369	-4.611803	39758.873620
HLA A*0250	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.576964	-0.034919	-4.611883	37754.054434
HLA A*2603	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.636145	0.023895	-4.612250	43265.803685
HLA B*3801	1:5-13  9	NEPGALSKG	0.682258	-0.717376	-4.577960	-0.035118	-4.613078	37840.753817
HLA A*3001	1:60-68 9	QPPPVSHPE	0.444789	-0.753625	-4.304748	-0.308836	-4.613583	20171.935291
HLA A*2902	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.434627	-0.179556	-4.614183	27203.644904
HLA B*0802	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.490282	-0.123980	-4.614262	30923.005522
HLA B*2705	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.466359	-0.147950	-4.614309	29265.721923
HLA A*3201	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.588730	-0.025677	-4.614407	38790.896662
HLA A*2403	1:33-41 9	GPGRIPDAG	0.649005	-0.882069	-4.381383	-0.233064	-4.614447	24064.844965
HLA B*4002	1:79-87 9	DARLNRFIS	1.021930	-1.002928	-4.633534	0.019002	-4.614532	43006.539388
HLA B*4002	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.631610	0.016895	-4.614716	42816.411858
HLA B*4501	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.607852	-0.007282	-4.615134	40537.062728
HLA B*5801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.352160	-0.263155	-4.615315	22498.842406
HLA B*5101	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.507008	-0.108442	-4.615450	32137.173818
HLA B*0803	1:61-69 9	PPPVSHPEG	0.867067	-0.973718	-4.509092	-0.106651	-4.615742	32291.756942
HLA B*5301	1:61-69 9	PPPVSHPEG	0.867067	-0.973718	-4.509247	-0.106651	-4.615897	32303.288859
HLA A*2403	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.436478	-0.179556	-4.616035	27319.861381
HLA B*5101	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.493468	-0.122654	-4.616122	31150.684890
HLA B*5401	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.493698	-0.122654	-4.616352	31167.204400
HLA B*1509	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.547879	-0.068483	-4.616362	35308.504460
HLA B*1509	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.493773	-0.122654	-4.616427	31172.600423
HLA A*2402	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.507010	-0.109508	-4.616518	32137.347677
HLA A*0250	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.548119	-0.068483	-4.616602	35327.993376
HLA B*5301	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.604584	-0.012369	-4.616953	40233.159907
HLA A*3301	1:27-35 9	AHRAATGPG	0.551366	-0.531728	-4.636781	0.019638	-4.617143	43329.281333
HLA A*0250	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.591568	-0.025677	-4.617245	39045.230989
HLA B*7301	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.598880	-0.018628	-4.617508	39708.144512
HLA B*1509	1:61-69 9	PPPVSHPEG	0.867067	-0.973718	-4.511028	-0.106651	-4.617678	32436.026798
HLA B*4402	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.354634	-0.263155	-4.617789	22627.375364
HLA A*2902	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.423387	-0.194957	-4.618344
26508.622528
HLA A*3101	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.423404	-0.194957	-4.618361
26509.626408
HLA B*4403	1:27-35 9	AHRAATGPG	0.551366	-0.531728	-4.638325	0.019638	-4.618687	43483.560490
HLA A*2403	1:60-68 9	QPPPVSHPE	0.444789	-0.753625	-4.310353	-0.308836	-4.619189	20434.002282
HLA B*4002	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.541468	-0.077944	-4.619412	34791.053382
HLA B*5101	1:60-68 9	QPPPVSHPE	0.444789	-0.753625	-4.311274	-0.308836	-4.620110	20477.382173
HLA A*2602	1:5-13  9	NEPGALSKG	0.682258	-0.717376	-4.585412	-0.035118	-4.620530	38495.711040
HLA A*6901	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.357425	-0.263155	-4.620580	22773.268657
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HLA A*0216	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.458604	-0.162047	-4.620651	28747.732278
HLA A*0219	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.441217	-0.179556	-4.620774	27619.601148
HLA A*8001	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.458921	-0.162047	-4.620968	28768.735423
HLA A*3201	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.610531	-0.010665	-4.621196	40787.838392
HLA A*2301	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.543333	-0.077944	-4.621277	34940.818104
HLA A*3301	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.582346	-0.039278	-4.621624	38224.892067
HLA A*0301	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.361664	-0.260368	-4.622032	22996.611083
HLA A*2402	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.582828	-0.039278	-4.622106	38267.308031
HLA B*5101	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.379400	-0.242879	-4.622279	23955.216641
HLA A*6801	1:241-249	9	GDLLNNASG	0.842099	-0.788781	-4.675609	0.053318	-4.622291	47381.529402
HLA A*0202	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.554091	-0.068483	-4.622575	35817.177665
HLA B*1503	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.516119	-0.106651	-4.622769	32818.519437
HLA A*2402	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.588298	-0.034919	-4.623216	38752.302655
HLA B*5701	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.428831	-0.194957	-4.623788	26842.991741
HLA A*0250	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.588864	-0.035118	-4.623982	38802.860210
HLA B*4402	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.429324	-0.194957	-4.624282	26873.504768
HLA A*8001	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.476544	-0.147950	-4.624494	29960.169025
HLA A*2602	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.605900	-0.018628	-4.624528	40355.232609
HLA B*5301	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.381940	-0.242879	-4.624818	24095.719344
HLA B*1517	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.462809	-0.162047	-4.624856	29027.468995
HLA A*0206	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.462941	-0.162047	-4.624988	29036.264310
HLA A*0216	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.445475	-0.179556	-4.625031	27891.679717
HLA A*0101	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.382725	-0.242879	-4.625603	24139.297330
HLA A*0202	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.517508	-0.108442	-4.625949	32923.616188
HLA B*5301	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.600752	-0.025677	-4.626429	39879.723020
HLA A*1101	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.464719	-0.162047	-4.626766	29155.419940
HLA B*0802	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.464755	-0.162047	-4.626802	29157.785950
HLA B*0802	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.465687	-0.161502	-4.627190	29220.476181
HLA A*0101	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.366873	-0.260368	-4.627241	23274.086751
HLA B*1801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.448599	-0.179556	-4.628156	28093.088321
HLA A*0201	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.395123	-0.233064	-4.628187	24838.356517
HLA A*3002	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.454814	-0.173733	-4.628547	28497.966552
HLA B*4601	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.385995	-0.242879	-4.628874	24321.766078
HLA A*0301	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.366377	-0.263155	-4.629532	23247.534850
HLA B*1501	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.396699	-0.233064	-4.629763	24928.684483
HLA A*0211	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.507271	-0.122654	-4.629925	32156.651875
HLA B*4403	1:163-171	9	GGRSITAES	1.149832	-1.125937	-4.654269	0.023895	-4.630374	45109.571601
HLA B*5101	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.506394	-0.123980	-4.630375	32091.828757
HLA A*3201	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.591422	-0.039278	-4.630700	39032.136902
HLA A*2602	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.596563	-0.034919	-4.631482	39496.899193
HLA A*0101	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.368369	-0.263155	-4.631524	23354.429923
HLA A*3101	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.398877	-0.233064	-4.631941	25054.015021
HLA B*2705	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.469916	-0.162047	-4.631964	29506.409268
HLA A*0212	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.389472	-0.242879	-4.632351	24517.283277
HLA B*0802	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.452944	-0.179556	-4.632500	28375.510417
HLA B*4403	1:177-185	9	QLSARRSRG	0.616799	-0.572672	-4.676636	0.044127	-4.632508	47493.677610
HLA B*3801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.564187	-0.068483	-4.632670	36659.547347
HLA A*0250	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.593443	-0.039278	-4.632721	39214.157198
HLA B*1801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.526109	-0.106651	-4.632759	33582.188481
HLA A*3301	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.523412	-0.109508	-4.632920	33374.270838
HLA A*6801	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.593894	-0.039278	-4.633172	39254.910054
HLA A*0203	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.372859	-0.260368	-4.633227	23597.127360

HLA A*2602	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.564821	-0.068483	-4.633305	36713.133977
HLA B*0802	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.485836	-0.147950	-4.633787	30608.107104
HLA B*4002	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.622325	-0.011592	-4.633917	41910.718339
HLA A*0203	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.438974	-0.194957	-4.633931	27477.274001
HLA B*1801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.525531	-0.108442	-4.633973	33537.525931
HLA B*0801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.391951	-0.242879	-4.634830	24657.614113
HLA A*3002	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.599937	-0.035118	-4.635055	39804.929770
HLA A*3301	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.627999	-0.007282	-4.635281	42461.869463
HLA B*3801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.557359	-0.077944	-4.635304	36087.724182
HLA A*2301	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.526391	-0.109508	-4.635899	33603.996669
HLA A*0212	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.440973	-0.194957	-4.635930	27604.065945
HLA B*4403	1:162-170	9	SGGRSITAE	0.835506	-0.818611	-4.653042	0.016895	-4.636148	44982.363579
HLA B*3801	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.521579	-0.115163	-4.636742	33233.737690
HLA B*4801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.442019	-0.194957	-4.636976	27670.600047
HLA A*2602	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.598020	-0.039278	-4.637297	39629.599400
HLA B*1503	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.475987	-0.161502	-4.637490	29921.780398
HLA A*2601	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.404469	-0.233064	-4.637533	25378.684559
HLA A*2603	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.627231	-0.010665	-4.637896	42386.819385
HLA A*6802	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.329415	-0.308836	-4.638251	21350.832299
HLA B*4601	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.405874	-0.233064	-4.638938	25460.920439
HLA B*0803	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.516584	-0.122654	-4.639238	32853.692093
HLA B*0801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.331929	-0.307784	-4.639712	21474.781729
HLA B*5301	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.605026	-0.034919	-4.639945	40274.100227
HLA A*3101	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.397209	-0.242879	-4.640088	24957.966596
HLA B*5101	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.492140	-0.147950	-4.640090	31055.615468
HLA A*0201	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.397350	-0.242879	-4.640229	24966.069101
HLA B*5301	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.601095	-0.039278	-4.640373	39911.234215
HLA B*1801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.516446	-0.123980	-4.640426	32843.207411
HLA A*0206	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.533813	-0.106651	-4.640463	34183.218899
HLA B*4501	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.572523	-0.068483	-4.641006	37369.997690
HLA A*6801	1:46-54	9	WQRAATRQS	1.013661	-0.997851	-4.657285	0.015810	-4.641475	45424.006929
HLA A*2301	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.534875	-0.106651	-4.641525	34266.908375
HLA A*2403	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.446591	-0.194957	-4.641548	27963.445060
HLA A*3301	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.462511	-0.179556	-4.642067	29007.532351
HLA B*5301	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.607256	-0.035118	-4.642373	40481.398523
HLA A*0250	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.564483	-0.077944	-4.642427	36684.544701
HLA B*4001	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.409530	-0.233064	-4.642594	25676.149663
HLA B*3901	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.468861	-0.173733	-4.642594	29434.823990
HLA B*4002	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.635475	-0.007282	-4.642757	43199.147072
HLA B*1502	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.564847	-0.077944	-4.642791	36715.318796
HLA B*4403	1:79-87	9	DARLNRFIS	1.021930	-1.002928	-4.662191	0.019002	-4.643189	45940.018538
HLA B*2705	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.496844	-0.146721	-4.643565	31393.794391
HLA A*0206	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.495805	-0.147950	-4.643755	31318.816139
HLA A*2501	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.481826	-0.162047	-4.643873	30326.752117
HLA B*4403	1:201-209	9	TLKVSLLLS	0.967877	-0.954718	-4.657351	0.013159	-4.644192	45430.888138
HLA B*5401	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.520282	-0.123980	-4.644263	33134.641185
HLA B*4501	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.632682	-0.011592	-4.644273	42922.166459
HLA A*6801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.471025	-0.173733	-4.644758	29581.849206
HLA A*6801	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.638067	-0.007282	-4.645348	43457.691651
HLA B*0802	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.471925	-0.173733	-4.645658	29643.205972
HLA B*4002	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.627080	-0.018628	-4.645709	42372.146214

HLA A*2403	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.385626	-0.260368	-4.645995	24301.117093
HLA B*1801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.498181	-0.147950	-4.646131	31490.580503
HLA A*2603	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.611090	-0.035118	-4.646208	40840.388744
HLA B*5701	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.413353	-0.233064	-4.646417	25903.145831
HLA A*0211	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.485000	-0.161502	-4.646502	30549.215050
HLA A*2602	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.500060	-0.146721	-4.646781	31627.164290
HLA B*2705	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.467283	-0.179556	-4.646839	29328.009568
HLA A*2501	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.499633	-0.147950	-4.647583	31596.039515
HLA B*4402	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.387231	-0.260368	-4.647599	24391.074702
HLA A*2601	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.387271	-0.260368	-4.647639	24393.318006
HLA B*5101	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.414635	-0.233064	-4.647699	25979.771642
HLA B*1501	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.387562	-0.260368	-4.647931	24409.687174
HLA A*0211	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.532932	-0.115163	-4.648095	34113.941410
HLA A*0219	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.387889	-0.260368	-4.648257	24428.049542
HLA A*3001	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.284565	-0.364035	-4.648601	19255.973969
HLA A*2501	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.487136	-0.161502	-4.648638	30699.813529
HLA B*5301	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.388330	-0.260368	-4.648699	24452.906952
HLA A*0211	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.502353	-0.146721	-4.649074	31794.598999
HLA B*0803	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.487284	-0.162047	-4.649331	30710.278515
HLA B*0803	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.501472	-0.147950	-4.649422	31730.162412
HLA A*0219	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.454478	-0.194957	-4.649435	28475.928647
HLA A*6801	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.639117	-0.010665	-4.649782	43562.909098
HLA A*2603	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.572067	-0.077944	-4.650011	37330.797760
HLA A*2501	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.341183	-0.308836	-4.650019	21937.310372
HLA B*4002	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.639380	-0.010665	-4.650045	43589.312193
HLA B*1501	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.407237	-0.242879	-4.650115	25540.935545
HLA A*2301	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.534983	-0.115163	-4.650146	34275.436924
HLA B*7301	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.543552	-0.106651	-4.650202	34958.401941
HLA B*0803	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.526234	-0.123980	-4.650214	33591.818685
HLA A*3201	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.615317	-0.034919	-4.650236	41239.803837
HLA B*5301	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.581928	-0.068483	-4.650411	38188.100732
HLA B*4501	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.611315	-0.039278	-4.650593	40861.604682
HLA B*5801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.340481	-0.310152	-4.650633	21901.854209
HLA A*2601	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.407768	-0.242879	-4.650646	25572.181883
HLA A*2603	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.632851	-0.018628	-4.651479	42938.888415
HLA A*0202	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.503542	-0.147950	-4.651492	31881.752892
HLA B*4002	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.639359	-0.012369	-4.651728	43587.189924
HLA B*5401	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.537168	-0.115163	-4.652331	34448.317931
HLA B*1503	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.529718	-0.122654	-4.652372	33862.405320
HLA A*0211	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.545819	-0.106651	-4.652469	35141.380992
HLA B*3801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.491165	-0.161502	-4.652667	30985.970591
HLA A*2601	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.389832	-0.263155	-4.652987	24537.584953
HLA A*3002	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.506437	-0.146721	-4.653158	32094.953948
HLA A*6802	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.392842	-0.260368	-4.653210	24708.222668
HLA A*2301	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.545838	-0.108442	-4.654279	35142.901912
HLA B*0801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.345542	-0.308836	-4.654378	22158.567173
HLA A*0201	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.391462	-0.263155	-4.654617	24629.883567
HLA A*2402	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.586141	-0.068483	-4.654624	38560.325039
HLA B*4001	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.412533	-0.242879	-4.655411	25854.285502
HLA B*0702	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.422931	-0.233064	-4.655995	26480.815833
HLA B*7301	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.578089	-0.077944	-4.656033	37852.014778
HLA A*3201	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.620977	-0.035118	-4.656094	41780.775834
HLA A*2602	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.541054	-0.115163	-4.656217	34757.943177

HLA A*0201	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.395922	-0.260368	-4.656290	24884.085297
HLA B*1502	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.509907	-0.146721	-4.656628	32352.432980
HLA B*5801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.348526	-0.308836	-4.657361	22311.333114
HLA A*0212	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.397627	-0.260368	-4.657996	24982.011701
HLA A*2501	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.416301	-0.242879	-4.659180	26079.611301
HLA A*6801	1:27-35	9	AHRAATGPG	0.551366	-0.531728	-4.679065	0.019638	-4.659427	47760.093396
HLA B*4501	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.648926	-0.010665	-4.659591	44558.029203
HLA B*1517	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.399246	-0.260368	-4.659615	25075.303753
HLA A*3002	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.551251	-0.108442	-4.659693	35583.677851
HLA B*4501	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.641203	-0.018628	-4.659831	43772.687993
HLA B*4402	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.426808	-0.233064	-4.659872	26718.250122
HLA B*1509	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.480682	-0.179556	-4.660238	30246.957930
HLA B*1503	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.399904	-0.260368	-4.660272	25113.315827
HLA A*2603	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.625765	-0.034919	-4.660684	42243.972442
HLA B*4403	1:197-205	9	DPWSTLKVS	1.156556	-1.167221	-4.650430	-0.010665	-4.661095	44712.571145
HLA A*0203	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.418432	-0.242879	-4.661311	26207.892406
HLA A*6802	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.428471	-0.233064	-4.661536	26820.782639
HLA B*5701	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.418705	-0.242879	-4.661583	26224.344256
HLA A*0250	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.553762	-0.108442	-4.662204	35790.060561
HLA B*4601	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.401915	-0.260368	-4.662284	25229.881898
HLA B*4403	1:192-200	9	QIRRIDPWS	0.866028	-0.878397	-4.650073	-0.012369	-4.662442	44675.818970
HLA A*2301	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.539926	-0.122654	-4.662580	34667.802686
HLA B*3801	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.553163	-0.109508	-4.662671	35740.721434
HLA A*2402	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.584985	-0.077944	-4.662929	38457.826823
HLA B*1801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.501681	-0.161502	-4.663184	31745.443533
HLA B*4403	1:145-153	9	RPAEGGAGS	0.920876	-0.928158	-4.656317	-0.007282	-4.663599	45322.875273
HLA B*0801	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.403452	-0.260368	-4.663820	25319.305022
HLA A*2301	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.540063	-0.123980	-4.664043	34678.682233
HLA A*6901	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.354357	-0.310152	-4.664509	22612.935405
HLA B*0803	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.503136	-0.161502	-4.664638	31851.928373
HLA B*5301	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.586709	-0.077944	-4.664653	38610.841014
HLA B*4801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.431686	-0.233064	-4.664750	27020.012278
HLA A*8001	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.470102	-0.194957	-4.665059	29519.022449
HLA B*4501	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.639486	-0.025677	-4.665163	43599.925085
HLA A*2602	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.491713	-0.173733	-4.665446	31025.053163
HLA B*3901	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.356805	-0.308836	-4.665641	22740.766846
HLA B*3801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.503996	-0.162047	-4.666043	31915.058288
HLA B*5801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.358487	-0.307784	-4.666271	22829.023586
HLA B*1502	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.557042	-0.109508	-4.666550	36061.377675
HLA A*0219	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.424597	-0.242879	-4.667476	26582.580993
HLA B*2705	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.407582	-0.260368	-4.667950	25561.255148
HLA B*4002	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.642596	-0.025677	-4.668274	43913.339077
HLA A*2501	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.473807	-0.194957	-4.668764	29771.938223
HLA A*2603	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.495211	-0.173733	-4.668944	31275.979336
HLA A*0219	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.436201	-0.233064	-4.669265	27302.426851
HLA A*0203	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.436432	-0.233064	-4.669496	27316.905593
HLA B*1501	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.359843	-0.310152	-4.669995	22900.395857
HLA A*3301	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.634902	-0.035118	-4.670020	43142.161258
HLA B*4801	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.409758	-0.260368	-4.670126	25689.626996
HLA B*1501	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.407206	-0.263155	-4.670361	25539.139351
HLA B*5101	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.475978	-0.194957	-4.670935	29921.132911
HLA B*1801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.509040	-0.162047	-4.671087	32287.913884
HLA B*5401	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.363367	-0.307784	-4.671151	23086.984807

HLA B*5101	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.497751	-0.173733	-4.671484	31459.419949
HLA B*5101	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.510875	-0.161502	-4.672377	32424.622908
HLA A*8001	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.439772	-0.233064	-4.672837	27527.861173
HLA B*3901	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.412819	-0.260368	-4.673187	25871.355130
HLA B*3801	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.526544	-0.146721	-4.673264	33615.815350
HLA B*7301	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.604828	-0.068483	-4.673312	40255.802598
HLA B*5401	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.565045	-0.108442	-4.673487	36732.007155
HLA A*3201	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.563987	-0.109508	-4.673495	36642.693675
HLA A*2402	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.566875	-0.106651	-4.673525	36887.133632
HLA B*4402	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.430727	-0.242879	-4.673606	26960.438538
HLA B*4801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.430772	-0.242879	-4.673650	26963.209888
HLA B*5701	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.413338	-0.260368	-4.673707	25902.305045
HLA A*3101	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.410745	-0.263155	-4.673900	25748.064134
HLA A*2402	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.565731	-0.108442	-4.674173	36790.078107
HLA A*0206	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.494748	-0.179556	-4.674304	31242.664774
HLA B*4403	1:125-133	9	ELPDLSGPT	0.358371	-0.369963	-4.662715	-0.011592	-4.674307	45995.474264
HLA B*0802	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.479533	-0.194957	-4.674490	30167.047291
HLA B*1801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.479972	-0.194957	-4.674929	30197.581204
HLA A*2902	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.414941	-0.260368	-4.675309	25998.049267
HLA A*0301	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.365482	-0.310152	-4.675634	23199.667129
HLA A*0301	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.368146	-0.307784	-4.675930	23342.430244
HLA A*1101	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.502638	-0.173733	-4.676371	31815.418448
HLA B*3801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.552482	-0.123980	-4.676462	35684.692928
HLA A*0301	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.368017	-0.308836	-4.676853	23335.485879
HLA A*0211	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.528954	-0.147950	-4.676904	33802.920275
HLA B*1517	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.482007	-0.194957	-4.676964	30339.387705
HLA B*3801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.570460	-0.106651	-4.677111	37192.915479
HLA B*1509	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.515292	-0.162047	-4.677339	32756.083222
HLA A*2403	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.414595	-0.263155	-4.677750	25977.382441
HLA B*3801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.555149	-0.122654	-4.677803	35904.479019
HLA B*0702	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.482968	-0.194957	-4.677925	30406.592311
HLA B*5401	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.530265	-0.147950	-4.678215	33905.115936
HLA A*2902	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.435586	-0.242879	-4.678464	27263.756050
HLA B*4601	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.415411	-0.263155	-4.678566	26026.193803
HLA B*0802	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.435990	-0.242879	-4.678868	27289.136807
HLA A*0202	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.532241	-0.146721	-4.678962	34059.726060
HLA B*4403	1:243-251	9	LLNNASGSS	1.048167	-1.066795	-4.660370	-0.018628	-4.678999	45747.810686
HLA A*3301	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.644171	-0.034919	-4.679090	44072.797310
HLA A*6801	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.610752	-0.068483	-4.679235	40808.585489
HLA B*4001	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.419508	-0.260368	-4.679876	26272.908981
HLA A*0203	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.416724	-0.263155	-4.679879	26105.019475
HLA A*8001	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.437822	-0.242879	-4.680701	27404.532444
HLA B*0803	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.501336	-0.179556	-4.680892	31720.207887
HLA A*3201	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.507207	-0.173733	-4.680940	32151.955192
HLA A*2301	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.534377	-0.146721	-4.681098	34227.630306
HLA B*4403	1:156-164	9	DSAAGSSGG	0.705434	-0.731111	-4.656599	-0.025677	-4.682277	45352.307833
HLA A*2603	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.644467	-0.039278	-4.683744	44102.849598
HLA A*0211	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.504670	-0.179556	-4.684226	31964.649315
HLA B*5701	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.421136	-0.263155	-4.684291	26371.592383
HLA A*3201	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.615895	-0.068483	-4.684378	41294.723654
HLA A*2402	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.560743	-0.123980	-4.684723	36369.954120
HLA B*1503	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.522914	-0.162047	-4.684961	33336.015945

HLA A*0216	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.490390	-0.194957	-4.685347	30930.701821
HLA A*2603	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.570352	-0.115163	-4.685515	37183.660991
HLA B*1502	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.538047	-0.147950	-4.685997	34518.087721
HLA A*2601	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.378035	-0.308836	-4.686871	23880.040115
HLA B*1509	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.538947	-0.147950	-4.686897	34589.682915
HLA B*0803	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.513941	-0.173733	-4.687674	32654.347640
HLA B*1502	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.579285	-0.108442	-4.687727	37956.388995
HLA A*2602	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.508786	-0.179556	-4.688342	32269.054599
HLA B*1509	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.565059	-0.123980	-4.689039	36733.199471
HLA A*1101	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.428690	-0.260368	-4.689058	26834.280098
HLA A*2402	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.574078	-0.115163	-4.689242	37504.072546
HLA A*1101	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.494600	-0.194957	-4.689557	31232.018370
HLA A*2902	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.457140	-0.233064	-4.690204	28651.005138
HLA B*5301	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.510992	-0.179556	-4.690549	32433.394776
HLA B*4001	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.381787	-0.308836	-4.690623	24087.247747
HLA A*2602	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.581134	-0.109508	-4.690642	38118.335969
HLA B*1801	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.430804	-0.260368	-4.691173	26965.252117
HLA B*4403	1:82-90	9	LNRFISGAS	0.922756	-0.962034	-4.652157	-0.039278	-4.691434	44890.714272
HLA A*0211	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.529676	-0.162047	-4.691723	33859.108027
HLA A*2301	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.544153	-0.147950	-4.692103	35006.850478
HLA A*2603	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.513469	-0.179556	-4.693025	32618.859002
HLA A*0101	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.384783	-0.308836	-4.693619	24253.966475
HLA B*3901	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.460960	-0.233064	-4.694024	28904.144862
HLA A*6802	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.431014	-0.263155	-4.694169	26978.238476
HLA A*2402	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.547553	-0.146721	-4.694274	35281.963342
HLA A*0211	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.434371	-0.260368	-4.694739	27187.608244
HLA A*0206	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.452601	-0.242879	-4.695479	28353.107044
HLA B*4403	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.627196	-0.068483	-4.695679	42383.379905
HLA A*3101	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.388509	-0.307784	-4.696293	24462.962870
HLA B*1502	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.518548	-0.179556	-4.698105	33002.614923
HLA A*0212	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.435123	-0.263155	-4.698278	27234.715230
HLA A*6801	1:5-13	9	NEPGALSKG	0.682258	-0.717376	-4.663387	-0.035118	-4.698505	46066.694846
HLA B*5801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.355264	-0.343296	-4.698560	22660.205464
HLA A*0101	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.391032	-0.307784	-4.698816	24605.511809
HLA A*0101	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.388725	-0.310152	-4.698877	24475.141357
HLA A*3201	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.590962	-0.108442	-4.699404	38990.771568
HLA B*1502	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.439096	-0.260368	-4.699464	27485.004837
HLA A*2602	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.575552	-0.123980	-4.699532	37631.502377
HLA A*0201	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.390924	-0.308836	-4.699760	24599.389369
HLA A*3101	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.391406	-0.308836	-4.700242	24626.685896
HLA A*0201	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.392642	-0.307784	-4.700425	24696.863436
HLA A*3301	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.526896	-0.173733	-4.700629	33643.105096
HLA B*4001	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.390567	-0.310152	-4.700719	24579.169528
HLA B*3901	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.505852	-0.194957	-4.700809	32051.749149
HLA B*5301	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.585889	-0.115163	-4.701053	38538.010541
HLA A*2603	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.632726	-0.068483	-4.701209	42926.578565
HLA B*7301	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.591718	-0.109508	-4.701226	39058.752074
HLA A*2601	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.393577	-0.307784	-4.701361	24750.096427
HLA B*0801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.438454	-0.263155	-4.701609	27444.442201
HLA B*4601	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.393535	-0.308836	-4.702370	24747.686430
HLA A*0250	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.595809	-0.106651	-4.702459	39428.369409
HLA A*3301	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.634131	-0.068483	-4.702614	43065.675804
HLA A*0201	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.392639	-0.310152	-4.702791	24696.729829
HLA A*0202	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.541738	-0.161502	-4.703240	34812.704927

HLA A*6801	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.625466	-0.077944	-4.703410	42214.958439
HLA A*3101	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.393730	-0.310152	-4.703881	24758.801151
HLA B*7301	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.579954	-0.123980	-4.703935	38014.955992
HLA A*1101	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.461101	-0.242879	-4.703980	28913.528478
HLA B*5301	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.471530	-0.233064	-4.704595	29616.276647
HLA B*2705	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.509829	-0.194957	-4.704787	32346.657734
HLA B*4801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.441647	-0.263155	-4.704802	27646.958361
HLA A*2301	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.543439	-0.161502	-4.704941	34949.325308
HLA B*0802	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.472238	-0.233064	-4.705302	29664.542386
HLA A*0212	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.396493	-0.308836	-4.705328	24916.819503
HLA A*0212	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.395407	-0.310152	-4.705559	24854.620943
HLA B*4002	1:158-166	9	AAGSSGGRS	0.869841	-0.938324	-4.637103	-0.068483	-4.705587	43361.406942
HLA A*0202	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.599124	-0.106651	-4.705774	39730.491730
HLA A*8001	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.445977	-0.260368	-4.706346	27923.989067
HLA A*0250	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.582546	-0.123980	-4.706526	38242.473465
HLA A*0216	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.464703	-0.242879	-4.707581	29154.315868
HLA A*2301	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.533975	-0.173733	-4.707708	34195.981273
HLA B*4001	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.444648	-0.263155	-4.707803	27838.616661
HLA A*0219	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.445054	-0.263155	-4.708209	27864.683320
HLA A*3201	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.586035	-0.122654	-4.708689	38550.938863
HLA A*3002	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.560844	-0.147950	-4.708794	36378.415673
HLA A*3002	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.602251	-0.106651	-4.708902	40017.606069
HLA A*3301	1:109-117	9	ASLGCGDGS	0.870761	-0.948705	-4.631018	-0.077944	-4.708962	42758.080354
HLA A*0250	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.593845	-0.115163	-4.709008	39250.450648
HLA A*2301	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.547315	-0.162047	-4.709363	35262.690585
HLA A*8001	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.446311	-0.263155	-4.709466	27945.448636
HLA B*1801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.400740	-0.308836	-4.709576	25161.728683
HLA B*5301	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.586237	-0.123980	-4.710217	38568.878878
HLA A*2402	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.588267	-0.122654	-4.710921	38749.577357
HLA B*1502	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.586947	-0.123980	-4.710927	38631.943696
HLA B*1502	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.588330	-0.122654	-4.710984	38755.237805
HLA A*0301	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.368454	-0.343296	-4.711750	23358.978782
HLA B*1503	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.469357	-0.242879	-4.712236	29468.442631
HLA A*3301	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.597249	-0.115163	-4.712412	39559.341263
HLA B*1501	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.404784	-0.308836	-4.713620	25397.088876
HLA A*0216	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.481596	-0.233064	-4.714660	30310.678070
HLA B*4501	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.599582	-0.115163	-4.714745	39772.426669
HLA B*5301	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.606311	-0.108442	-4.714753	40393.456234
HLA B*0803	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.520061	-0.194957	-4.715019	33117.795524
HLA A*0250	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.592567	-0.122654	-4.715220	39135.107179
HLA B*1502	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.608668	-0.106651	-4.715318	40613.231651
HLA A*0216	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.455700	-0.260368	-4.716068	28556.148270
HLA B*5801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.352184	-0.364035	-4.716219	22500.059601
HLA A*2601	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.406574	-0.310152	-4.716726	25502.000289
HLA A*6801	1:147-155	9	AEGGAGSRG	0.700440	-0.735359	-4.682000	-0.034919	-4.716919	48083.898769
HLA B*1509	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.556175	-0.161502	-4.717678	35989.461987
HLA A*1101	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.484883	-0.233064	-4.717947	30540.952775
HLA B*1509	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.544550	-0.173733	-4.718283	35038.870871
HLA B*5701	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.408369	-0.310152	-4.718521	25607.622142
HLA B*0802	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.458742	-0.260368	-4.719111	28756.909543
HLA A*2603	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.611109	-0.108442	-4.719551	40842.156318
HLA A*0250	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.573270	-0.146721	-4.719991	37434.342301
HLA A*2602	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.611637	-0.108442	-4.720079	40891.900683

HLA A*2301	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.540664	-0.179556	-4.720220	34726.743109
HLA A*2403	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.410113	-0.310152	-4.720264	25710.621253
HLA B*4501	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.540812	-0.179556	-4.720368	34738.580800
HLA A*8001	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.411673	-0.308836	-4.720508	25803.144162
HLA B*3501	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.457506	-0.263155	-4.720661	28675.195151
HLA B*4601	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.412906	-0.307784	-4.720690	25876.534212
HLA A*3201	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.605935	-0.115163	-4.721098	40358.507502
HLA B*5701	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.412399	-0.308836	-4.721234	25846.314208
HLA B*3801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.573559	-0.147950	-4.721509	37459.260014
HLA B*1801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.478882	-0.242879	-4.721761	30121.874640
HLA B*4501	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.613449	-0.108442	-4.721891	41062.818006
HLA B*4002	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.612847	-0.109508	-4.722355	41005.988173
HLA A*3201	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.560910	-0.161502	-4.722412	36383.926580
HLA A*0212	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.414950	-0.307784	-4.722734	25998.611860
HLA B*5301	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.600130	-0.122654	-4.722783	39822.591589
HLA B*5401	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.561582	-0.161502	-4.723084	36440.264393
HLA B*7301	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.576649	-0.146721	-4.723370	37726.695489
HLA A*3301	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.529098	-0.194957	-4.724055	33814.077189
HLA B*4001	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.416280	-0.307784	-4.724064	26078.341542
HLA B*2705	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.481408	-0.242879	-4.724286	30297.562716
HLA A*0301	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.360292	-0.364035	-4.724327	22924.070810
HLA B*2705	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.491485	-0.233064	-4.724549	31008.776750
HLA B*4601	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.415507	-0.310152	-4.725659	26031.967195
HLA A*2602	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.619015	-0.106651	-4.725665	41592.466954
HLA B*4501	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.577840	-0.147950	-4.725790	37830.314829
HLA A*0202	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.546648	-0.179556	-4.726204	35208.554286
HLA A*2902	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.463119	-0.263155	-4.726274	29048.205070
HLA B*1517	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.416303	-0.310152	-4.726455	26079.752389
HLA A*6801	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.602902	-0.123980	-4.726882	40077.618979
HLA B*5401	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.531994	-0.194957	-4.726952	34040.384323
HLA A*2501	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.467149	-0.260368	-4.727517	29318.967269
HLA A*2902	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.419252	-0.308836	-4.728088	26257.420994
HLA A*0203	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.419388	-0.308836	-4.728224	26265.661171
HLA B*1501	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.421371	-0.307784	-4.729155	26385.862982
HLA B*1501	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.365331	-0.364035	-4.729367	23191.636032
HLA A*3002	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.567507	-0.162047	-4.729554	36940.853087
HLA A*0206	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.535009	-0.194957	-4.729966	34277.476674
HLA B*0702	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.466886	-0.263155	-4.730041	29301.208065
HLA A*0219	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.419943	-0.310152	-4.730095	26299.216846
HLA A*2501	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.497328	-0.233064	-4.730392	31428.800305
HLA B*7301	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.582774	-0.147950	-4.730724	38262.546823
HLA A*0101	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.388074	-0.343296	-4.731370	24438.491863
HLA A*2603	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.609894	-0.122654	-4.732548	40728.083972
HLA A*6802	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.424797	-0.307784	-4.732581	26594.807554
HLA A*6901	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.389404	-0.343296	-4.732700	24513.437141
HLA A*3201	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.553600	-0.179556	-4.733157	35776.703256
HLA B*4002	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.625335	-0.108442	-4.733777	42202.171194
HLA B*4002	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.610183	-0.123980	-4.734163	40755.194125
HLA B*5701	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.427179	-0.307784	-4.734963	26741.097643
HLA A*0216	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.471965	-0.263155	-4.735120	29645.932327
HLA B*3801	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.561471	-0.173733	-4.735204	36431.000095

HLA B*1502	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.573357	-0.162047	-4.735404	37441.836130
HLA A*0206	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.475224	-0.260368	-4.735592	29869.217727
HLA B*1509	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.502762	-0.233064	-4.735826	31824.542004
HLA A*0202	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.574078	-0.162047	-4.736126	37504.072546
HLA B*4801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.426315	-0.310152	-4.736467	26687.913376
HLA B*4403	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.588563	-0.147950	-4.736513	38775.999857
HLA B*5401	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.562829	-0.173733	-4.736562	36545.095059
HLA A*2603	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.590212	-0.146721	-4.736933	38923.541092
HLA A*3201	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.630553	-0.106651	-4.737204	42712.304213
HLA A*6802	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.427522	-0.310152	-4.737674	26762.227277
HLA B*1517	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.505805	-0.233064	-4.738869	32048.281408
HLA A*0203	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.374976	-0.364035	-4.739011	23712.427854
HLA B*4801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.430447	-0.308836	-4.739283	26943.087619
HLA A*3301	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.592806	-0.146721	-4.739527	39156.708231
HLA A*6901	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.375505	-0.364035	-4.739540	23741.308789
HLA A*0250	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.591650	-0.147950	-4.739600	39052.624752
HLA A*2601	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.396852	-0.343296	-4.740148	24937.452017
HLA A*0203	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.431333	-0.310152	-4.741485	26998.094882
HLA B*0801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.431345	-0.310152	-4.741497	26998.825175
HLA A*2902	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.431733	-0.310152	-4.741884	27022.935942
HLA A*0201	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.398821	-0.343296	-4.742117	25050.762285
HLA A*2603	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.632637	-0.109508	-4.742145	42917.754807
HLA A*2402	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.594249	-0.147950	-4.742199	39286.990227
HLA B*3901	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.434728	-0.307784	-4.742512	27209.973894
HLA B*4002	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.619954	-0.122654	-4.742608	41682.568661
HLA B*0702	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.433048	-0.310152	-4.743200	27104.927086
HLA A*2301	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.548316	-0.194957	-4.743274	35344.051149
HLA B*0802	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.434669	-0.308836	-4.743505	27206.294070
HLA B*7301	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.548777	-0.194957	-4.743734	35381.547675
HLA A*2602	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.621399	-0.122654	-4.744053	41821.480936
HLA B*4403	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.634547	-0.109508	-4.744055	43106.933108
HLA A*3301	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.635762	-0.108442	-4.744204	43227.668200
HLA B*7301	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.621707	-0.122654	-4.744361	41851.130135
HLA A*3301	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.637733	-0.106651	-4.744384	43424.320087
HLA B*1502	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.583180	-0.161502	-4.744683	38298.373918
HLA B*7301	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.571212	-0.173733	-4.744945	37257.358299
HLA B*4402	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.434907	-0.310152	-4.745059	27221.163618
HLA B*4002	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.631349	-0.115163	-4.746513	42790.708420
HLA B*1517	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.504118	-0.242879	-4.746996	31924.037712
HLA B*4403	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.638588	-0.108442	-4.747030	43509.915492
HLA B*1501	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.403745	-0.343296	-4.747041	25336.432642
HLA A*1101	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.436892	-0.310152	-4.747044	27345.886115
HLA B*1503	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.552346	-0.194957	-4.747303	35673.497770
HLA A*2403	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.440113	-0.307784	-4.747897	27549.463433
HLA B*5301	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.600118	-0.147950	-4.748068	39821.514424
HLA A*2402	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.586902	-0.161502	-4.748404	38627.973004
HLA A*3201	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.602030	-0.146721	-4.748751	39997.261106
HLA A*0250	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.587865	-0.161502	-4.749368	38713.747046
HLA B*4501	1:122-130	9	YASELPDLS	0.787644	-0.897152	-4.640050	-0.109508	-4.749557	43656.570834
HLA A*0250	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.587821	-0.162047	-4.749868	38709.767946
HLA B*1509	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.555205	-0.194957	-4.750162	35909.141064
HLA A*0101	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.386575	-0.364035	-4.750611	24354.287582

HLA A*3002	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.555670	-0.194957	-4.750627	35947.626037
HLA B*0702	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.386763	-0.364035	-4.750799	24364.830183
HLA A*2402	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.577370	-0.173733	-4.751103	37789.405403
HLA B*5401	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.488007	-0.263155	-4.751162	30761.492045
HLA B*4402	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.442486	-0.308836	-4.751322	27700.405369
HLA A*1101	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.488421	-0.263155	-4.751576	30790.795255
HLA A*2402	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.589651	-0.162047	-4.751698	38873.246895
HLA A*3301	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.627734	-0.123980	-4.751714	42435.919713
HLA A*3301	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.629162	-0.122654	-4.751816	42575.730282
HLA B*4002	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.645571	-0.106651	-4.752221	44215.130301
HLA B*0801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.388213	-0.364035	-4.752248	24446.293471
HLA B*4501	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.628279	-0.123980	-4.752259	42489.214231
HLA B*4501	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.606182	-0.146721	-4.752903	40381.439195
HLA A*0211	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.558450	-0.194957	-4.753407	36178.424965
HLA B*0802	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.490472	-0.263155	-4.753627	30936.558983
HLA A*0203	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.445912	-0.307784	-4.753695	27919.759549
HLA A*6802	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.389705	-0.364035	-4.753740	24530.417737
HLA B*4403	1:245-253	9	NNASGSSAE	0.584464	-0.699627	-4.638729	-0.115163	-4.753892	43524.040814
HLA B*5101	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.446269	-0.307784	-4.754052	27942.727497
HLA B*1502	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.513044	-0.242879	-4.755922	32586.934576
HLA B*0803	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.514214	-0.242879	-4.757092	32674.846214
HLA B*1503	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.524171	-0.233064	-4.757235	33432.639827
HLA B*3801	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.578491	-0.179556	-4.758047	37887.047540
HLA B*1801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.450345	-0.307784	-4.758129	28206.237079
HLA B*4402	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.450380	-0.307784	-4.758164	28208.526061
HLA B*4801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.450451	-0.307784	-4.758235	28213.104583
HLA A*0211	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.525315	-0.233064	-4.758379	33520.838129
HLA A*3101	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.415138	-0.343296	-4.758434	26009.866264
HLA A*2603	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.634632	-0.123980	-4.758612	43115.329260
HLA A*0201	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.394601	-0.364035	-4.758637	24808.543671
HLA B*1517	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.496261	-0.263155	-4.759416	31351.703070
HLA B*0702	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.416513	-0.343296	-4.759809	26092.312295
HLA A*2601	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.396006	-0.364035	-4.760042	24888.932094
HLA B*1801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.527873	-0.233064	-4.760938	33718.904633
HLA B*0803	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.528045	-0.233064	-4.761109	33732.223597
HLA B*1509	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.500890	-0.260368	-4.761258	31687.620105
HLA A*2402	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.582114	-0.179556	-4.761670	38204.425098
HLA A*0211	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.518927	-0.242879	-4.761805	33031.372464
HLA A*0216	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.452037	-0.310152	-4.762189	28316.318013
HLA A*3002	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.583234	-0.179556	-4.762791	38303.139583
HLA A*0250	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.583711	-0.179556	-4.763268	38345.227485
HLA A*0219	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.455641	-0.307784	-4.763425	28552.286391
HLA B*4501	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.641718	-0.122654	-4.764372	43824.579107
HLA B*0803	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.504057	-0.260368	-4.764425	31919.547684
HLA B*4501	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.658115	-0.106651	-4.764765	45510.835622
HLA B*5701	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.421470	-0.343296	-4.764766	26391.858936
HLA A*2301	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.521955	-0.242879	-4.764834	33262.516677
HLA B*4601	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.421583	-0.343296	-4.764879	26398.713123
HLA B*4601	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.400928	-0.364035	-4.764964	25172.620813

HLA A*3101	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.401427	-0.364035	-4.765462	25201.507765
HLA B*3501	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.455436	-0.310152	-4.765588	28538.851124
HLA A*0216	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.457859	-0.308836	-4.766695	28698.474039
HLA B*5301	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.605538	-0.161502	-4.767040	40321.625741
HLA B*4001	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.403454	-0.364035	-4.767489	25319.441997
HLA B*1801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.505008	-0.263155	-4.768163	31989.560247
HLA B*3801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.525890	-0.242879	-4.768769	33565.296870
HLA A*6801	1:171-179	9	SRDARVQLS	0.904720	-1.013162	-4.660476	-0.108442	-4.768918	45758.949118
HLA A*0219	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.460187	-0.308836	-4.769023	28852.745473
HLA A*3201	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.621277	-0.147950	-4.769227	41809.717612
HLA B*5101	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.506136	-0.263155	-4.769291	32072.736983
HLA A*2301	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.536318	-0.233064	-4.769382	34380.921054
HLA A*3002	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.509576	-0.260368	-4.769944	32327.764136
HLA A*8001	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.462295	-0.307784	-4.770078	28993.098610
HLA B*4403	1:116-124	9	GSPAEAYAS	0.979742	-1.103722	-4.646544	-0.123980	-4.770524	44314.269647
HLA B*7301	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.608508	-0.162047	-4.770555	40598.293909
HLA A*2902	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.463079	-0.307784	-4.770863	29045.533684
HLA A*0206	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.538117	-0.233064	-4.771181	34523.690346
HLA B*1509	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.509780	-0.263155	-4.772935	32342.983114
HLA A*8001	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.462809	-0.310152	-4.772961	29027.468995
HLA A*2602	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.625274	-0.147950	-4.773224	42196.235576
HLA B*5701	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.409866	-0.364035	-4.773901	25696.020781
HLA B*4801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.430666	-0.343296	-4.773962	26956.646628
HLA A*2501	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.511744	-0.263155	-4.774899	32489.590946
HLA A*2603	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.668250	-0.106651	-4.774901	46585.470697
HLA B*0702	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.467266	-0.307784	-4.775050	29326.898960
HLA A*2501	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.467529	-0.307784	-4.775313	29344.673735
HLA B*2705	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.512724	-0.263155	-4.775879	32562.967722
HLA B*1517	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.468918	-0.307784	-4.776702	29438.645977
HLA B*3901	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.514402	-0.263155	-4.777557	32688.990658
HLA B*4001	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.434554	-0.343296	-4.777850	27199.083057
HLA B*5301	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.604218	-0.173733	-4.777951	40199.219749
HLA A*6801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.583573	-0.194957	-4.778530	38332.990275
HLA A*0206	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.468906	-0.310152	-4.779058	29437.849689
HLA B*1517	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.471093	-0.308836	-4.779929	29586.490571
HLA B*2705	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.470837	-0.310152	-4.780989	29569.049214
HLA A*2602	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.619642	-0.161502	-4.781144	41652.588204
HLA A*0216	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.473485	-0.307784	-4.781269	29749.880782
HLA A*6802	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.438217	-0.343296	-4.781513	27429.450687
HLA B*4403	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.675008	-0.106651	-4.781658	47315.954642
HLA B*4402	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.438711	-0.343296	-4.782007	27460.630355
HLA B*4002	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.603367	-0.179556	-4.782923	40120.571443
HLA A*6801	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.661439	-0.122654	-4.784093	45860.557608
HLA A*1101	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.476410	-0.307784	-4.784194	29950.931822
HLA A*3002	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.420354	-0.364035	-4.784389	26324.126909
HLA B*4801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.420448	-0.364035	-4.784483	26329.823949
HLA B*4002	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.637808	-0.146721	-4.784529	43431.838202
HLA A*2402	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.589928	-0.194957	-4.784885	38898.070212
HLA A*0202	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.590205	-0.194957	-4.785163	

									38922.909381
HLA B*7301	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.623721	-0.161502	-4.785223	42045.613975
HLA B*3801	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.590377	-0.194957	-4.785334	38938.283926
HLA A*3201	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.623730	-0.162047	-4.785777	42046.523833
HLA A*0206	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.523015	-0.263155	-4.786170	33343.771646
HLA A*2902	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.422960	-0.364035	-4.786995	26482.534988
HLA A*0212	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.443703	-0.343296	-4.786999	27778.139707
HLA B*4403	1:240-248	9	VGDLLNNAS	0.957632	-1.080286	-4.664470	-0.122654	-4.787124	46181.726672
HLA A*1101	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.478905	-0.308836	-4.787741	30123.504244
HLA B*3801	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.527375	-0.260368	-4.787744	33680.254708
HLA B*0802	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.480177	-0.307784	-4.787960	30211.797354
HLA A*6801	1:61-69	9	PPPVSHPEG	0.867067	-0.973718	-4.682070	-0.106651	-4.788721	48091.703260
HLA A*0203	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.447068	-0.343296	-4.790364	27994.171594
HLA A*0206	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.481572	-0.308836	-4.790408	30309.038340
HLA B*2705	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.482265	-0.308836	-4.791101	30357.447677
HLA A*8001	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.447845	-0.343296	-4.791141	28044.344919
HLA A*2501	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.481184	-0.310152	-4.791336	30281.995603
HLA A*2602	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.629308	-0.162047	-4.791355	42590.013136
HLA B*4403	1:117-125	9	SPAEAYASE	0.646594	-0.793315	-4.645320	-0.146721	-4.792040	44189.543419
HLA B*5301	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.597162	-0.194957	-4.792119	39551.423624
HLA B*0802	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.481983	-0.310152	-4.792135	30337.746422
HLA A*2603	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.644457	-0.147950	-4.792407	44101.895243
HLA B*0803	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.529553	-0.263155	-4.792708	33849.584318
HLA A*2603	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.631246	-0.161502	-4.792748	42780.523941
HLA A*1101	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.428786	-0.364035	-4.792822	26840.232748
HLA B*1503	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.529713	-0.263155	-4.792868	33862.038939
HLA A*3301	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.645287	-0.147950	-4.793237	44186.196698
HLA A*0250	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.598346	-0.194957	-4.793304	39659.411059
HLA A*2403	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.432186	-0.364035	-4.796221	27051.165557
HLA A*3002	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.486398	-0.310152	-4.796550	30647.707865
HLA B*3901	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.486553	-0.310152	-4.796705	30658.652665
HLA B*5301	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.488134	-0.308836	-4.796970	30770.479835
HLA B*1517	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.453743	-0.343296	-4.797039	28427.751292
HLA A*0212	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.433384	-0.364035	-4.797420	27125.903954
HLA B*1509	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.488599	-0.308836	-4.797435	30803.457542
HLA A*2403	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.454633	-0.343296	-4.797929	28486.097869
HLA B*4002	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.637237	-0.161502	-4.798740	43374.780087
HLA B*2705	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.491048	-0.307784	-4.798831	30977.590191
HLA B*3801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.565954	-0.233064	-4.799018	36808.990840
HLA B*1502	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.491301	-0.308836	-4.800137	30995.694695
HLA B*3501	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.456992	-0.343296	-4.800288	28641.241880
HLA A*8001	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.436281	-0.364035	-4.800316	27307.449218
HLA B*1503	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.491729	-0.308836	-4.800565	31026.228080
HLA B*0801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.457328	-0.343296	-4.800624	28663.407723
HLA A*3301	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.639328	-0.162047	-4.801376	43584.124608
HLA B*4403	1:120-128	9	EAYASELPD	0.526970	-0.706526	-4.622259	-0.179556	-4.801816	41904.370314
HLA A*0211	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.493794	-0.310152	-4.803946	31174.118223
HLA B*4402	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.441577	-0.364035	-4.805612	27642.471716
HLA A*0211	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.543277	-0.263155	-4.806432	34936.281776
HLA A*2301	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.546164	-0.260368	-4.806533	35169.338420

HLA A*0216	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.443738	-0.364035	-4.807774	27780.393949
HLA A*3301	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.646468	-0.161502	-4.807971	44306.598782
HLA B*7301	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.574931	-0.233064	-4.807995	37577.795023
HLA B*1502	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.613096	-0.194957	-4.808054	41029.509728
HLA A*0202	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.548234	-0.260368	-4.808602	35337.359524
HLA B*4501	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.647105	-0.161502	-4.808607	44371.603438
HLA A*3001	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.300946	-0.508110	-4.809056	19996.136817
HLA A*3002	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.567103	-0.242879	-4.809981	36906.495576
HLA A*2301	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.547435	-0.263155	-4.810590	35272.421057
HLA B*0803	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.501063	-0.310152	-4.811215	31700.308206
HLA B*4002	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.649626	-0.162047	-4.811673	44629.921229
HLA A*0202	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.578726	-0.233064	-4.811790	37907.549558
HLA A*0219	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.448416	-0.364035	-4.812452	28081.236344
HLA B*4501	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.650463	-0.162047	-4.812510	44715.957734
HLA B*0803	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.503744	-0.308836	-4.812580	31896.589343
HLA B*3501	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.450049	-0.364035	-4.814084	28187.016961
HLA A*3002	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.505257	-0.308836	-4.814093	32007.909865
HLA A*2602	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.619590	-0.194957	-4.814548	41647.631109
HLA B*4002	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.641485	-0.173733	-4.815218	43801.113866
HLA B*4501	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.555614	-0.260368	-4.815982	35942.958996
HLA A*2902	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.472971	-0.343296	-4.816267	29714.655015
HLA A*0219	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.473036	-0.343296	-4.816333	29719.156439
HLA A*0206	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.452690	-0.364035	-4.816725	28358.936356
HLA A*6801	1:155-163	9	GDSAAGSSG	0.613438	-0.761388	-4.669623	-0.147950	-4.817573	46732.884425
HLA A*2402	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.585081	-0.233064	-4.818145	38466.357925
HLA A*6801	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.656712	-0.162047	-4.818759	45364.086208
HLA A*0250	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.558903	-0.260368	-4.819271	36216.218897
HLA A*2603	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.657347	-0.162047	-4.819394	45430.396588
HLA A*3201	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.624978	-0.194957	-4.819935	42167.482480
HLA A*2602	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.577238	-0.242879	-4.820117	37777.958693
HLA B*4403	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.659790	-0.161502	-4.821292	45686.721336
HLA A*2602	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.561152	-0.260368	-4.821520	36404.206030
HLA B*4501	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.648026	-0.173733	-4.821759	44465.801102
HLA B*3801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.513683	-0.308836	-4.822518	32634.921217
HLA A*0206	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.516119	-0.307784	-4.823903	32818.519437
HLA A*3002	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.590866	-0.233064	-4.823930	38982.124161
HLA B*4403	1:104-112	9	QPDPDASLG	0.709269	-0.871316	-4.662480	-0.162047	-4.824527	45970.597951
HLA B*5101	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.514932	-0.310152	-4.825084	32728.981802
HLA B*4403	1:242-250	9	DLLNNASGS	0.936466	-1.110199	-4.651525	-0.173733	-4.825258	44825.434114
HLA B*0803	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.517602	-0.307784	-4.825385	32930.741484
HLA A*6801	1:154-162	9	RGDSAAGSS	0.877673	-1.039175	-4.664762	-0.161502	-4.826264	46212.716980
HLA A*0202	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.583465	-0.242879	-4.826343	38323.452110
HLA A*2402	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.584045	-0.242879	-4.826924	38374.695769
HLA A*0216	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.484798	-0.343296	-4.828094	30535.005320
HLA A*3201	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.595926	-0.233064	-4.828990	39439.036007
HLA A*0202	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.567093	-0.263155	-4.830248	36905.696945
HLA A*0250	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.588229	-0.242879	-4.831108	38746.223408
HLA A*0250	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.598161	-0.233064	-4.831225	39642.464993
HLA A*0202	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.521314	-0.310152	-4.831466	33213.427534
HLA B*1517	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.469322	-0.364035	-4.833357	

									29466.051413
HLA B*1502	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.601300	-0.233064	-4.834364	39930.023272
HLA B*0802	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.491823	-0.343296	-4.835119	31032.942744
HLA B*5301	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.527394	-0.307784	-4.835178	33681.712391
HLA A*0211	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.529450	-0.308836	-4.838286	33841.527887
HLA B*1801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.528628	-0.310152	-4.838780	33777.510893
HLA A*2301	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.532643	-0.308836	-4.841479	34091.248986
HLA B*2705	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.477641	-0.364035	-4.841677	30035.956638
HLA A*2501	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.498735	-0.343296	-4.842031	31530.811269
HLA B*4002	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.579158	-0.263155	-4.842313	37945.302262
HLA A*1101	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.499029	-0.343296	-4.842325	31552.140754
HLA A*2603	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.648691	-0.194957	-4.843648	44533.930322
HLA B*3801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.580608	-0.263155	-4.843763	38072.171568
HLA B*0802	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.479848	-0.364035	-4.843883	30188.924070
HLA B*4002	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.649744	-0.194957	-4.844701	44641.995008
HLA B*4501	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.651146	-0.194957	-4.846103	44786.408511
HLA B*1503	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.539106	-0.310152	-4.849258	34602.409848
HLA B*2705	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.506124	-0.343296	-4.849420	32071.869445
HLA A*2602	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.617520	-0.233064	-4.850585	41449.606101
HLA A*3201	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.607782	-0.242879	-4.850660	40530.484231
HLA A*2402	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.590309	-0.260368	-4.850677	38932.175503
HLA A*2402	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.543108	-0.308836	-4.851943	34922.676324
HLA B*1509	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.542027	-0.310152	-4.852179	34835.877579
HLA B*7301	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.591974	-0.260368	-4.852343	39081.790949
HLA A*2301	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.542349	-0.310152	-4.852501	34861.705928
HLA B*7301	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.610347	-0.242879	-4.853226	40770.630723
HLA B*5101	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.510464	-0.343296	-4.853760	32393.940052
HLA A*0211	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.546228	-0.307784	-4.854011	35174.475875
HLA B*3901	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.491743	-0.364035	-4.855778	31027.235187
HLA A*2301	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.548690	-0.307784	-4.856474	35374.466205
HLA A*2402	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.594752	-0.263155	-4.857907	39332.499753
HLA B*1503	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.551880	-0.307784	-4.859664	35635.306274
HLA B*1801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.516382	-0.343296	-4.859678	32838.410453
HLA A*2501	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.497130	-0.364035	-4.861166	31414.521338
HLA B*5301	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.598454	-0.263155	-4.861609	39669.281726
HLA A*0250	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.598468	-0.263155	-4.861623	39670.569386
HLA B*3801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.552254	-0.310152	-4.862406	35665.971967
HLA B*3901	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.519643	-0.343296	-4.862939	33085.919752
HLA B*0803	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.519890	-0.343296	-4.863186	33104.719163
HLA B*5401	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.553852	-0.310152	-4.864004	35797.418887
HLA B*5801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.357839	-0.508110	-4.865949	22794.962335
HLA B*4501	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.623688	-0.242879	-4.866566	42042.429626
HLA B*4501	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.634209	-0.233064	-4.867273	43073.364848
HLA B*4403	1:108-116	9	DASLGCGDG	0.589830	-0.784787	-4.673043	-0.194957	-4.868001	47102.443504
HLA B*1509	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.560541	-0.307784	-4.868324	36353.036918
HLA A*3201	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.609290	-0.260368	-4.869658	40671.497373
HLA B*4403	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.606884	-0.263155	-4.870039	40446.811326
HLA A*6801	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.561610	-0.308836	-4.870446	36442.630124
HLA A*3201	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.560630	-0.310152	-4.870782	36360.510990
HLA A*2603	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.610629	-0.260368	-4.870998	40797.107067

HLA A*3002	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.608315	-0.263155	-4.871470	40580.288057
HLA A*3301	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.611130	-0.260368	-4.871498	40844.144930
HLA B*1503	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.507553	-0.364035	-4.871588	32177.534324
HLA A*0202	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.563294	-0.308836	-4.872130	36584.261605
HLA A*3301	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.629397	-0.242879	-4.872276	42598.769511
HLA B*4403	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.612065	-0.260368	-4.872433	40932.182669
HLA B*7301	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.610232	-0.263155	-4.873387	40759.824490
HLA A*3301	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.640585	-0.233064	-4.873649	43710.452461
HLA B*4002	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.641022	-0.233064	-4.874086	43754.457776
HLA A*0301	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.368322	-0.508110	-4.876433	23351.903162
HLA A*6901	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.369565	-0.508110	-4.877675	23418.828089
HLA B*5101	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.516333	-0.364035	-4.880368	32834.679969
HLA B*5401	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.537079	-0.343296	-4.880375	34441.236918
HLA B*1502	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.617351	-0.263155	-4.880506	41433.464125
HLA A*6801	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.640592	-0.242879	-4.883471	43711.161873
HLA A*0101	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.377018	-0.508110	-4.885128	23824.167017
HLA B*4002	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.642589	-0.242879	-4.885468	43912.626384
HLA B*1503	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.543824	-0.343296	-4.887120	34980.346871
HLA A*2301	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.544809	-0.343296	-4.888105	35059.728281
HLA B*0803	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.524709	-0.364035	-4.888744	33474.084008
HLA B*4002	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.628784	-0.260368	-4.889152	42538.663300
HLA A*2602	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.626251	-0.263155	-4.889406	42291.305728
HLA A*3201	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.580819	-0.308836	-4.889655	38090.713042
HLA A*3201	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.627362	-0.263155	-4.890517	42399.662579
HLA A*2602	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.582833	-0.307784	-4.890616	38267.722077
HLA A*0250	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.580993	-0.310152	-4.891145	38105.965018
HLA B*1801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.527166	-0.364035	-4.891202	33664.042238
HLA B*4403	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.658143	-0.233064	-4.891207	45513.790220
HLA B*1502	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.528303	-0.364035	-4.892339	33752.303206
HLA B*3801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.585229	-0.307784	-4.893013	38479.470379
HLA B*1502	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.583171	-0.310152	-4.893323	38297.545167
HLA A*0211	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.550722	-0.343296	-4.894018	35540.390857
HLA A*2603	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.651221	-0.242879	-4.894100	44794.162446
HLA A*6801	1:3-11	9	APNEPGALS	0.822079	-1.082447	-4.634580	-0.260368	-4.894948	43110.198084
HLA A*0250	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.586357	-0.308836	-4.895193	38579.521668
HLA A*3002	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.587783	-0.307784	-4.895567	38706.417442
HLA B*7301	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.587167	-0.308836	-4.896003	38651.594178
HLA A*0211	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.532554	-0.364035	-4.896589	34084.241371
HLA B*1502	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.590844	-0.307784	-4.898628	38980.226207
HLA A*2603	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.665948	-0.233064	-4.899012	46339.142464
HLA A*2602	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.592139	-0.308836	-4.900975	39096.593723
HLA B*1501	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.393779	-0.508110	-4.901889	24761.614100
HLA A*0202	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.594343	-0.307784	-4.902126	39295.492677
HLA A*2301	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.538467	-0.364035	-4.902503	34551.530197
HLA A*2402	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.592797	-0.310152	-4.902949	39155.860906
HLA A*0201	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.395083	-0.508110	-4.903193	24836.072285
HLA B*1509	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.561762	-0.343296	-4.905058	36455.447165
HLA B*5301	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.595508	-0.310152	-4.905660	39401.076063
HLA A*0206	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.562961	-0.343296	-4.906257	36556.168212
HLA A*3301	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.643541	-0.263155	-4.906696	44008.944651

HLA A*3301	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.597888	-0.308836	-4.906724	39617.595281
HLA A*0250	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.600162	-0.307784	-4.907946	39825.607804
HLA B*4501	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.645566	-0.263155	-4.908721	44214.651905
HLA A*2402	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.601032	-0.307784	-4.908815	39905.404926
HLA A*2601	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.400722	-0.508110	-4.908832	25160.639729
HLA B*1509	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.545335	-0.364035	-4.909370	35102.239945
HLA B*4403	1:102-110	9	TPQPDPDAS	0.831657	-1.074536	-4.667466	-0.242879	-4.910344	46501.371274
HLA B*0801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.402472	-0.508110	-4.910582	25262.250979
HLA A*0202	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.546911	-0.364035	-4.910947	35229.893880
HLA A*6801	1:33-41	9	GPGRIPDAG	0.649005	-0.882069	-4.678551	-0.233064	-4.911615	47703.542381
HLA B*5401	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.550431	-0.364035	-4.914466	35516.557425
HLA B*7301	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.571360	-0.343296	-4.914656	37270.058628
HLA B*7301	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.605524	-0.310152	-4.915676	40320.316949
HLA A*2603	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.654656	-0.263155	-4.917811	45149.855812
HLA B*7301	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.610047	-0.307784	-4.917830	40742.408228
HLA B*3801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.576750	-0.343296	-4.920046	37735.472691
HLA B*4601	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.413846	-0.508110	-4.921956	25932.590514
HLA A*3301	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.616038	-0.307784	-4.923822	41308.353296
HLA B*1502	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.582471	-0.343296	-4.925767	38235.853637
HLA A*3002	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.583775	-0.343296	-4.927071	38350.828866
HLA A*2603	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.619078	-0.310152	-4.929230	41598.542685
HLA B*3801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.566299	-0.364035	-4.930335	36838.274969
HLA A*2603	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.621749	-0.308836	-4.930585	41855.205713
HLA B*5701	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.423227	-0.508110	-4.931338	26498.872530
HLA A*3101	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.424322	-0.508110	-4.932432	26565.760686
HLA B*4001	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.425417	-0.508110	-4.933527	26632.817680
HLA A*3201	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.626697	-0.307784	-4.934481	42334.798419
HLA A*6801	1:107-115	9	PDASLGCGD	0.920809	-1.183964	-4.672296	-0.263155	-4.935451	47021.480725
HLA A*6802	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.430060	-0.508110	-4.938170	26919.048095
HLA A*0203	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.431852	-0.508110	-4.939963	27030.392716
HLA A*0250	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.598786	-0.343296	-4.942082	39699.552775
HLA A*2602	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.632005	-0.310152	-4.942157	42855.343730
HLA B*0702	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.434460	-0.508110	-4.942571	27193.197933
HLA A*0250	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.580309	-0.364035	-4.944345	38046.022841
HLA A*2402	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.602552	-0.343296	-4.945848	40045.326490
HLA A*0202	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.603943	-0.343296	-4.947239	40173.783421
HLA B*4402	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.439498	-0.508110	-4.947608	27510.442733
HLA A*2603	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.641358	-0.307784	-4.949142	43788.319939
HLA B*4801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.441459	-0.508110	-4.949570	27634.995592
HLA B*7301	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.587680	-0.364035	-4.951715	38697.205052
HLA B*4002	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.643983	-0.308836	-4.952818	44053.727121
HLA B*5301	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.609678	-0.343296	-4.952974	40707.818249
HLA B*4002	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.647157	-0.307784	-4.954940	44376.884752
HLA B*4002	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.645226	-0.310152	-4.955377	44179.982032
HLA A*2403	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.447392	-0.508110	-4.955502	28015.078858
HLA A*8001	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.447653	-0.508110	-4.955763	28031.906900
HLA A*3301	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.646454	-0.310152	-4.956606	44305.160642
HLA B*4501	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.648219	-0.308836	-4.957055	44485.530993
HLA B*4501	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.647751	-0.310152	-4.957903	44437.665066
HLA A*0212	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.450345	-0.508110	-4.958455	28206.237079
HLA A*2402	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.595513	-0.364035	-4.959548	

									39401.502376
HLA B*4501	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.655143	-0.307784	-4.962926	45200.445065
HLA A*6801	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.658796	-0.307784	-4.966580	45582.292147
HLA B*5301	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.602902	-0.364035	-4.966937	40077.618979
HLA B*3501	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.461193	-0.508110	-4.969303	28919.629462
HLA A*2902	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.462175	-0.508110	-4.970285	28985.100391
HLA A*2603	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.629618	-0.343296	-4.972914	42620.437755
HLA B*4403	1:60-68	9	QPPPVSHPE	0.444789	-0.753625	-4.666223	-0.308836	-4.975059	46368.482435
HLA A*2602	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.632296	-0.343296	-4.975592	42884.101865
HLA B*4403	1:106-114	9	DPDASLGCG	0.706392	-1.014176	-4.668107	-0.307784	-4.975891	46570.099877
HLA A*3201	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.633450	-0.343296	-4.976746	42998.164422
HLA B*4403	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.670358	-0.310152	-4.980510	46812.084034
HLA A*3301	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.637688	-0.343296	-4.980984	43419.856822
HLA A*0219	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.477256	-0.508110	-4.985366	30009.319900
HLA B*4501	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.623930	-0.364035	-4.987965	42065.862977
HLA A*3201	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.624477	-0.364035	-4.988513	42118.920605
HLA A*1101	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.480830	-0.508110	-4.988940	30257.268546
HLA A*6801	1:12-20	9	KGDGPNADG	0.417775	-0.727927	-4.679932	-0.310152	-4.990084	47855.529665
HLA A*6801	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.626171	-0.364035	-4.990207	42283.527540
HLA A*2602	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.626947	-0.364035	-4.990982	42359.082198
HLA A*0216	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.483193	-0.508110	-4.991304	30422.388057
HLA B*4002	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.651475	-0.343296	-4.994771	44820.341890
HLA B*4501	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.658498	-0.343296	-5.001794	45550.985319
HLA B*4002	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.638910	-0.364035	-5.002945	43542.175029
HLA A*3301	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.640360	-0.364035	-5.004395	43687.757359
HLA B*0802	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.497405	-0.508110	-5.005516	31434.411674
HLA A*2603	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.641772	-0.364035	-5.005807	43830.032427
HLA B*2705	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.498989	-0.508110	-5.007099	31549.239096
HLA B*1517	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.502755	-0.508110	-5.010865	31824.025507
HLA B*4403	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.674369	-0.343296	-5.017665	47246.380896
HLA B*5101	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.512111	-0.508110	-5.020221	32517.021873
HLA B*4403	1:149-157	9	GGAGSRGDS	0.871672	-1.235707	-4.657459	-0.364035	-5.021495	45442.195244
HLA A*2501	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.514110	-0.508110	-5.022220	32667.069378
HLA B*3901	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.514850	-0.508110	-5.022960	32722.785283
HLA B*0803	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.516923	-0.508110	-5.025033	32879.295881
HLA A*6801	1:34-42	9	PGRIPDAGD	0.761962	-1.105258	-4.683564	-0.343296	-5.026860	48257.456868
HLA A*0206	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.523184	-0.508110	-5.031294	33356.761976
HLA B*1509	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.528552	-0.508110	-5.036663	33771.663956
HLA B*1801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.533712	-0.508110	-5.041822	34175.267944
HLA B*5401	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.539238	-0.508110	-5.047348	34612.894367
HLA A*2301	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.543730	-0.508110	-5.051840	34972.778098
HLA B*1503	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.546620	-0.508110	-5.054730	35206.268667
HLA A*0211	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.555661	-0.508110	-5.063771	35946.848155
HLA B*7301	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.587536	-0.508110	-5.095647	38684.436956
HLA A*3002	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.587642	-0.508110	-5.095752	38693.855635
HLA B*3801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.589101	-0.508110	-5.097211	38824.067840
HLA A*0202	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.589479	-0.508110	-5.097590	38857.898029
HLA A*2402	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.591385	-0.508110	-5.099495	39028.758496

HLA A*0250	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.600891	-0.508110	-5.109001	39892.453999
HLA B*5301	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.605712	-0.508110	-5.113822	40337.771001
HLA B*1502	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.610143	-0.508110	-5.118253	40751.446119
HLA A*3201	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.633563	-0.508110	-5.141673	43009.331406
HLA A*2602	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.635365	-0.508110	-5.143475	43188.164447
HLA A*3301	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.645815	-0.508110	-5.153925	44240.013991
HLA B*4002	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.652004	-0.508110	-5.160114	44874.931551
HLA B*4501	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.658458	-0.508110	-5.166568	45546.796273
HLA A*2603	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.662687	-0.508110	-5.170797	45992.488396
HLA B*4403	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.673990	-0.508110	-5.182101	47205.247585
HLA A*6801	1:7-15	9	PGALSKGDG	0.487080	-0.995190	-4.679535	-0.508110	-5.187645	47811.796724